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FILE COVERS 1907 - 19 Jun 2002 VOL 136 ISS 25
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=> d his

(FILE 'HOME' ENTERED AT 11:33:14 ON 19 JUN 2002)
SET COST OFF

FILE 'REGISTRY' ENTERED AT 11:33:30 ON 19 JUN 2002

E CHOLESTERYL ESTER TRANSFER PROTEIN/CN
L1 1 S E4
E CETP/CN
E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L2 13 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L3 13 S CETP
L4 13 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
L5 1 S L1 AND L2-L4
L6 24 S L2-L4 NOT L5

FILE 'HCAPLUS' ENTERED AT 11:37:36 ON 19 JUN 2002

L7 876 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L8 883 S CETP
L9 1325 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L10 16 S L5 OR L6
L11 16 S L7-L9 AND L10
L12 57 S ?ARTHEROSCLERO?
L13 34932 S ?ATHEROSCLERO?
L14 19 S ?ARTHERIOSCLERO?
L15 13496 S ?ARTERIOSCLERO?
L16 9 S L11 AND L12-L15
L17 4 S L11 AND VACCIN?
L18 4 S L17 AND L16
E ATHEROSCLEROSIS/CT
E E3+ALL
L19 20165 S E7-E9,E6
L20 32452 S E6,E8,E9/BI
E E5+ALL

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Reference Librarian
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L21 22555 S E5+NT
 L22 8925 S E5/BI
 L23 9 S L11 AND L19-L22
 L24 4 S L16,L23 AND VACCIN?
 L25 5 S L16,L23 NOT L24
 L26 9 S L23-L25
 L27 331 S L7-L9 AND L12-L15,L19-L22
 L28 9 S L27 AND VACCIN?
 L29 24 S L7-L9,L10 AND EPITOP?
 L30 5 S L29 AND (TETANUS OR DIPHTHER? OR TOXOID OR TOXIN OR BCG OR BA
 L31 15 S L26,L28,L30
 L32 19 S L29 NOT L31
 E RITTERSHAUS C/AU
 L33 20 S E3-E6
 E THOMAS L/AU
 L34 219 S E3,E14,E15
 E THOMAS LARRY/AU
 L35 4 S E3
 L36 23 S E26,E29
 L37 6 S L33-L36 AND L7-L10
 L38 6 S L31 AND L37
 L39 9 S L31 NOT L38
 L40 15 S L38,L39
 L41 5 S L40 AND (PY<=1995 OR PRY<=1995 OR AY<=1995)
 L42 15 S L40,L41

FILE 'HCAPLUS' ENTERED AT 11:52:33 ON 19 JUN 2002

=> d all tot 142

L42 ANSWER 1 OF 15 HCAPLUS COPYRIGHT 2002 ACS
 AN 2002:4125 HCAPLUS
 TI An immunotherapeutic approach for the treatment of low plasma
 HDL-Cholesterol
 AU Ryan, Una S.; Rittershaus, Charles W.
 CS AVANT Immunotherapeutics, Inc., Needham, MA, 02494-2725, USA
 SO NATO Science Series, Series I: Life and Behavioural Sciences (2001),
 330(Vascular Endothelium), 26-33
 CODEN: NSSSC9; ISSN: 1566-7693
 PB IOS Press
 DT Journal
 LA English
 CC 15-2 (Immunochemistry)
 Section cross-reference(s): 14
 AB One determinant of plasma HDL-Cholesterol concn. is
cholesteryl ester transfer protein (CETP) activity. Inhibition of **CETP** activity increases
 plasma HDL-C, thus providing a potential therapeutic target for the
 treatment of **atherosclerosis**. Using a **vaccine**
 approach, we immunized New Zealand White rabbits with a peptide contg. a
 region of **CETP** known to be required for neutral lipid
transfer function. **CETP-vaccinated** rabbits
 had significantly reduced plasma **CETP** activity and an altered
 lipoprotein profile compared with control rabbits. In a
cholesterol-fed rabbit model of **atherosclerosis**, the
 fraction of plasma **cholesterol** in HDL was 42% higher, and the
 fraction of plasma **cholesterol** in LDL was 24% lower in the
CETP-vaccinated group compared with the control-
vaccinated group. Moreover, the percentage of the aorta surface
 exhibiting **atherosclerotic** lesion was 39.6% smaller in the
CETP-vaccinated rabbits compared with controls. The
 data reported here demonstrate that **CETP** activity can be reduced
 in vivo by **vaccination** with a peptide derived from **CETP**



GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 ; Search time 26.94 Seconds
(without alignments)
92.737 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDGFLLQMDGFPEHLVDFLQSL S 26

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR-71:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	493	2 A53176	cholesteryl ester
2	134	100.0	493	2 A26941	cholesteryl ester
3	131	97.8	289	2 A38700	cholesteryl ester
4	117	87.3	497	2 I46692	cholesteryl ester
5	56	41.8	587	2 D95247	aspartyl-TRNA synth
6	56	41.8	587	2 A98112	aspartate--TRNA 11
7	54	40.3	310	2 D82199	conserved hypotet
8	53	39.6	426	2 A81904	hypothetical prote
9	53	39.6	590	2 E86870	aspartate--TRNA 11
10	51	38.1	274	2 C83497	conserved hypotet
11	50	37.3	311	1 C64884	gamma protein - Esc
12	50	37.3	311	2 A85749	hypothetical prote
13	50	37.3	311	2 H90869	hypothetical prote
14	49.5	36.9	559	2 D90291	permease, multidru
15	48	35.8	348	1 ADECH	2-dehydro-3-deoxy
16	48	35.8	348	2 C90930	hypothetical prote
17	48	35.8	348	2 G85778	hypothetical prote
18	48	35.8	348	2 AD0704	2-deoxy-D-arabinoh
19	48	35.8	348	2 AD0294	hypothetical prote
20	48	35.8	390	2 D83853	2-dehydro-3-deoxy
21	48	35.8	428	2 C96633	gamma protein - Esc
22	48	35.8	682	1 G71299	probable Serine/Th
23	47	35.1	311	2 AC0663	conserved hypotet
24	46.5	34.7	110	2 A11860	hypothetical prote
25	46.5	34.7	1952	2 T48814	hypothetical prote
26	46	34.3	104	2 A96002	hypothetical prote
27	46	34.3	312	2 G82791	conserved hypotet
28	46	34.3	356	2 H90168	37P-binding protei
29	46	34.3	374	2 G97057	coproporphyrinogen

30	46	34.3	422	2 A49837	clathrin-associate
31	46	34.3	425	2 T23603	hypothetical prote
32	46	34.3	428	2 G86240	hypothetical prote
33	46	34.3	567	2 S60985	probable membrane
34	46	34.3	849	1 T05181	5-receptor kinase
35	46	34.3	886	2 T10890	cysteine proteinase
36	46	34.3	1071	2 T51224	related to small s
37	45.5	34.0	293	2 AF3393	Atases of the p
38	45.5	34.0	738	2 S40992	hypothetical prote
39	45	33.6	177	2 T04228	ribosomal protein
40	45	33.6	265	2 F71119	probable diaphne
41	45	33.6	496	2 B96674	hypothetical prote
42	45	33.6	531	2 B83422	probable serine/th
43	45	33.6	700	2 E69146	sensory transducti
44	45	33.6	779	1 MNVZAL	ribonucleoside-dip
45	45	33.6	900	2 A95340	cation transport p

ALIGNMENTS

RESULT 1
A53176
cholesteryl ester transfer protein - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A53176
C:Paper, M.E.; Renberg, E.F.; Marotti, K.R.; Melchior, G.W.
Arterioscler. Thromb. 11, 1759-1771, 1991
A:Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl
asma high density lipoprotein levels.
A:Reference number: A53176; MUID:92031355
A:Accession: A53176
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <EAP>
A:Cross-references: GB:M86343

Query Match 100.0%; Score 134; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPEHLVDFLQSL S 26
DB 468 RDGFLLQMDGFPEHLVDFLQSL S 493

RESULT 2
A26941
cholesteryl ester transfer protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jul-2000
C:Accession: A26941
C:Drayna, D.; Jarnagin, A.S.; McLean, J.; Henzel, W.; Kohr, W.; Fielding, C.; Lawn, R.
Nature 327, 632-634, 1987
A:Title: Cloning and sequencing of human cholesteryl ester transfer protein cDNA.
A:Reference number: A26941; MUID:87258172
A:Accession: A26941
A:Molecule type: mRNA
A:Residues: 1-493 <DRA>
A:Cross-references: EMBL:M30185; NID:g180259; PIDD:AAA51977.1; PID:g180260
C:Genetics:
A:Gene: GDB:CETP
A:Cross-references: GDB:119773; OMIM:118470
A:Map position: 16q13-16q13
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-493/Product: cholesteryl ester transfer protein #status predicted <MAT>

Query Match 100.0%; Score 134; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
|||||
Db 468 RDGFLLLQMDGFPPEHLVDFLOSL 493

RESULT 3
A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <NR>
A:Cross-references: GB:AE005672; PIDN:AAK76173.1; PID:q14973626; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2114
C:Superfamily: lysine--tRNA ligase

Query Match 97.8%; Score 131; DB 2; Length 289;
Best Local Similarity 96.2%; Pred. No. 8.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
|||||
Db 264 RDGFLLLQMDGFPPEHLVDFLOSL 289

RESULT 4
A:Title: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer prote
A:Reference number: 146692; MUID:89215620
A:Accession: 146692
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-497 <MAG>
A:Cross-references: GB:M27486; NID:q530906; PIDN:AAA31199.1; PID:q530907
C:Genetics:
A:Gene: CETP

Query Match 87.3%; Score 117; DB 2; Length 497;
Best Local Similarity 92.0%; Pred. No. 2.5e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGFLLLQMDGFPPEHLVDFLOSL 26
|||||
Db 473 DGFLLLQMDGFPPEHLVDFLOSL 497

RESULT 5
A:Title: aspartyl-tRNA synthetase [imported] - *Streptococcus pneumoniae* (strain TIGR4)
C:Species: *Streptococcus pneumoniae*
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: D95247
R:Telletlin, H.; Nelson, K.E.; Paulsen, I.T.; Eissen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfe,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

Query Match 97.8%; Score 131; DB 2; Length 289;
Best Local Similarity 96.2%; Pred. No. 8.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
|||||
Db 264 RDGFLLLQMDGFPPEHLVDFLOSL 289

RESULT 4
A:Title: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer prote
A:Reference number: 146692; MUID:89215620
A:Accession: 146692
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-497 <MAG>
A:Cross-references: GB:M27486; NID:q530906; PIDN:AAA31199.1; PID:q530907
C:Genetics:
A:Gene: CETP

Query Match 87.3%; Score 117; DB 2; Length 497;
Best Local Similarity 92.0%; Pred. No. 2.5e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGFLLLQMDGFPPEHLVDFLOSL 26
|||||
Db 473 DGFLLLQMDGFPPEHLVDFLOSL 497

RESULT 5
A:Title: aspartyl-tRNA synthetase [imported] - *Streptococcus pneumoniae* (strain TIGR4)
C:Species: *Streptococcus pneumoniae*
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: D95247
R:Telletlin, H.; Nelson, K.E.; Paulsen, I.T.; Eissen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfe,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <NR>
A:Cross-references: GB:AE005672; PIDN:AAK76173.1; PID:q14973626; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2114
C:Superfamily: lysine--tRNA ligase

Query Match 41.8%; Score 56; DB 2; Length 587;
Best Local Similarity 71.4%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 GFLLLQMDGFPPEH 16
|||||
Db 510 GFLLEAMDYGFPPH 523

RESULT 6
A:Title: aspartate--tRNA ligase (EC 6.1.1.12) [imported] - *Streptococcus pneumoniae* (strain R6
A:Accession: A98112
C:Species: *Streptococcus pneumoniae*
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: A98112
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
A:Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A98112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <NR>
A:Cross-references: GB:AE007317; PIDN:AL00726.1; PID:q15459621; GSPDB:GN00174
C:Genetics:
A:Gene: asps
C:Superfamily: lysine--tRNA ligase
C:Keywords: ligase

Query Match 41.8%; Score 56; DB 2; Length 587;
Best Local Similarity 71.4%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 GFLLLQMDGFPPEH 16
|||||
Db 510 GFLLEAMDYGFPPH 523

RESULT 7
A:Title: conserved hypothetical protein VC1432 [imported] - *Vibrio cholerae* (strain N16961 ser
C:Species: *Vibrio cholerae*
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82199
R:Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
Charadon, D.; Ermolaeva, M.D.; Yamatevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833
A:Accession: D82199
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <NR>
A:Cross-references: GB:AE004222; GB:AE003852; NID:q9655930; PIDN:AAF94589.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:
A:Gene: VC1432
A:Map position: 1
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 40.3%; Score 54; DB 2; Length 310;
Best Local Similarity 64.3%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 12 GPEHLVDFLOSL 25
|||||:|:|:|:|
DB 84 GPEHVLPEYLESL 97

RESULT 8
A:Accession: A81904
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84597.1; PID:9738001
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1350
C:Superfamily: hypothetical protein H10404

Query Match 39.6%; Score 53; DB 2; Length 426;
Best Local Similarity 62.5%; Pred. No. 2.2;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GFLLOMDFGPEHL 18
|||||:|:|:|:|
DB 331 GFVLKHPGPEHL 346

RESULT 9
E86870
A:Alternate names: aspartyl-tRNA synthetase
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: E86870
R:Biological: A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:1137471
A:Accession: E86870
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <STO>
A:Cross-references: GB:AE005176; PID:912725007; PIDN:AAK0663.1; GSPDB:GN00146
A:Experimental source: strain I11403
C:Genetics:
A:Gene: aspS
C:Superfamily: lysine--tRNA ligase
C:Keywords: ligase

Query Match 39.6%; Score 53; DB 2; Length 590;
Best Local Similarity 64.3%; Pred. No. 3.2;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GFLLOMDFGPEHL 16
|||||:|:|:|:|
DB 517 GFLEALDYGPPEH 530

RESULT 10
C83497
A:Accession: C83497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <STO>
A:Cross-references: GB:AE004549; GB:AE004091; NID:99947110; PIDN:AA604581.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1192
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 38.1%; Score 51; DB 2; Length 274;
Best Local Similarity 57.1%; Pred. No. 2.7;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 12 GPEHLVDFLOSL 25
|||||:|:|:|:|
DB 76 GPEHVLPEYLEKSI 89

RESULT 11
C64884
A:Alternate names: conserved hypothetical protein b1344
C:Species: Escherichia coli
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: C64884
R:Biological: F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Zhao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: C64884
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-311 <BIAT>
A:Cross-references: GB:AE000232; GB:U00096; NID:91787600; PIDN:AACT4426.1; PID:917876
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ydaO
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 37.3%; Score 50; DB 1; Length 311;
Best Local Similarity 57.1%; Pred. No. 4.5;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 12 GPEHLVDFLOSL 25
|||||:|:|:|:|
DB 83 GPEHVLPEYLEKL 96

RESULT 12
A85749
A:Accession: A85749
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <STO>
A:Cross-references: GB:AE004549; GB:AE004091; NID:99947110; PIDN:AA604581.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1192
C:Superfamily: conserved hypothetical protein MJ1157

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
 C:Accession: A85749
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 11ter, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoustis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85749
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-311 <STO>
 A:Cross-references: GB:AE005174; NID:g12515408; PIDN:AAG56453.1; GSPDB:GN00145; UWCP:224
 C:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ydaC
 C:Superfamily: conserved hypothetical protein MJ1157

Query Match 37.3%; Score 50; DB 2; Length 311;
 Best Local Similarity 57.1%; Pred. No. 4.5;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 12 GFEHLVDFLOSL 25
 |||||:|:|:|
 DB 83 GFEHLVDFLEKL 96

RESULT 13
 H90869
 hypothetical protein ECs1928 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
 C:Species: *Escherichia coli*
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
 C:Accession: H90869
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: H90869
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-311 <NAV>
 A:Cross-references: GB:BA000007; PIDN:BA835351.1; PID:g13361393; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: ECs1928
 C:Superfamily: conserved hypothetical protein MJ1157

Query Match 37.3%; Score 50; DB 2; Length 311;
 Best Local Similarity 57.1%; Pred. No. 4.5;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 12 GFEHLVDFLOSL 25
 |||||:|:|:|
 DB 83 GFEHLVDFLEKL 96

RESULT 14
 D90291
 permease, multidrug efflux [imported] - *Sulfolobus solfataricus*
 C:Species: *Sulfolobus solfataricus*
 C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C:Accession: D90291
 R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayer, M.J.; Chan-
 arett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
 submitted to Genbank, April 2001
 A:Description: *Sulfolobus solfataricus* complete genome.
 A:Reference number: A99139
 A:Accession: D90291
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-559 <KUR>
 A:Cross-references: GB:AE006641; NID:g13814561; PIDN:AAK41587.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: SS01351

Query Match 35.9%; Score 49.5; DB 2; Length 559;
 Best Local Similarity 42.3%; Pred. No. 11;
 Matches 11; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

QY 3 GFTLLQW---DFGFEHLVDFLOSL 25
 |||||:|:|:|
 DB 360 GFTLLVLPYFNVFPEALITFMGL 385

RESULT 15
 ADECH
 2-dehydro-3-deoxyphosphohexonate aldolase (EC 4.1.2.15) (Trp-sensitive) - *Escherichia*
 N:Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; phospho-2-de
 C:Species: *Escherichia coli*
 C>Date: 22-May-1981 #sequence_revision 31-Oct-1997 #text_change 18-Jun-1999
 C:Accession: H64928; J01131; A31384; A01107
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A:Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of *Escherichia coli* K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: H64928
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-348 <BIAT>
 A:Cross-references: GB:AE000265; GB:U00096; NID:g2367122; PIDN:AAC74774.1; PID:g178679
 A:Experimental source: strain K-12, substrain MG1655
 R:Hudson, G.S.; Rellos, P.; Davidson, B.E.
 Gene 102, 87-91, 1991
 A:Title: Two promoters control the *aroH* gene of *Escherichia coli*.
 A:Reference number: J01131; MUID:91323737
 A:Accession: J01131
 A:Molecule type: DNA
 A:Residues: 1-332, 'S', 334-348 <HUD>
 A:Cross-references: GB:M8266; NID:g145376; PIDN:AAA23497.1; PID:g145378
 R:Ray, J.M.; Yanofsky, C.; Baerle, R.
 J. Bacteriol. 170, 5500-5506, 1988
 A:Title: Mutational analysis of the catalytic and feedback sites of the tryptophan-se
 A:Reference number: A31384; MUID:89035867
 A:Accession: A31384
 A:Molecule type: DNA
 A:Residues: 1-122, 'A', 124-202; 204, 'Q', 206-332, 'RQ', 335-348 <RAY>
 A:Cross-references: GB:J04221
 R:Zurawski, G.; Gunsalus, R.P.; Brown, K.D.; Yanofsky, C.
 J. Mol. Biol. 145, 47-73, 1981
 A:Title: Structure and regulation of *aroH*, the structural gene for the tryptophan-rep
 A:Reference number: A01107; MUID:81263314
 A:Accession: A01107
 A:Molecule type: DNA
 A:Residues: 1-36; 231-332, 'RQ', 335-348 <ZUR>
 A:Cross-references: GB:J01592; GB:J01593
 C:Genetics:
 A:Gene: *aroH*
 A:Map position: 37 min
 C:Function:
 A:Description: aldehyde-lyase; carbon-carbon lyase; this is one of the DAP synthases
 ic acid-7-phosphate
 A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
 A:Note: The first reaction in aromatic amino acid biosynthesis
 A:Key words: feedback-inhibited by tryptophan; the other two DAP synthases are tyrosine-
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
 C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; sh

Query Match 35.8%; Score 48; DB 1; Length 348;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 DEGEPEHLVDF 21
: | | | : | | |
DB 254 EFDLPEHLVDF 265

Search completed: June 18, 2002, 08:06:29
Job time: 38 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:07:01 ; Search time 13.5 Seconds
(without alignments)
74.571 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134
Sequence: 1 RCGFLLQMDRGFPENHLYDFLOSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	134	100.0	493 1	CETP_HUMAN P11597 homo sapien
2	134	100.0	493 1	CETP_MACFA P47896 macaca fasc
3	131	97.8	289 1	CETP_MESAU P25914 mesocricetu
4	117	87.3	497 1	CETP_RABIT P22687 oryctolagus
5	52	38.8	313 1	YDAO_HAETH Q57184 haemophilus
6	50	37.3	311 1	YDAO_ARATH P76055 escherichia
7	50	37.3	311 1	YDAO_ECOLI P76055 escherichia
8	50	37.3	311 1	YDAO_ECOLI P76055 escherichia
9	48	35.8	348 1	AROH_ECOLI P00887 escherichia
10	46.5	34.7	377 1	OPSE_HEKSA Q25158 hemigrasus
11	46	34.3	422 1	AP47_CAEEL P35602 caenorhabdi
12	46	34.3	422 1	AP47_CAEEL P35602 caenorhabdi
13	46	34.3	422 1	AP47_CAEEL P35602 caenorhabdi
14	45.5	34.0	1246 1	YAV2_CAEEL P43504 caenorhabdi
15	45	33.6	177 1	YAV2_CAEEL P43504 caenorhabdi
16	45	33.6	423 1	AIM2_HUMAN Q95409 arabidopsis
17	45	33.6	423 1	AIM2_HUMAN Q95409 arabidopsis
18	45	33.6	423 1	AIM2_HUMAN Q95409 arabidopsis
19	44.5	33.2	782 1	GDFF_MOUSE P26885 african swi
20	44.5	33.2	901 1	POIG_ENMG3 Q35218 mus musculu
21	44.5	33.2	901 1	POIG_ENMG3 Q35218 mus musculu
22	44.5	33.2	901 1	POIG_ENMG3 Q35218 mus musculu
23	44.5	33.2	901 1	POIG_ENMG3 Q35218 mus musculu
24	44	32.8	439 1	AP50_DICDI P17594 encephalomy
25	44	32.8	439 1	AP50_DICDI P17594 encephalomy
26	44	32.8	439 1	AP50_DICDI P17594 encephalomy
27	43.5	32.5	337 1	LEF9_NPVAC Q42669 arabidopsis
28	43.5	32.5	337 1	LEF9_NPVAC Q42669 arabidopsis
29	43.5	32.5	337 1	LEF9_NPVAC Q42669 arabidopsis
30	43.5	32.5	337 1	LEF9_NPVAC Q42669 arabidopsis
31	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
32	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
33	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
34	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
35	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
36	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
37	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
38	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
39	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
40	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
41	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
42	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
43	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
44	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha
45	43	32.1	210 1	PLS3_BACHD Q9K401 bacillus ha

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	493 AA.
CETP_HUMAN				
AC	P11597: Q13987; Q13988;			
DR	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Cholesteryl ester transfer protein precursor (lipid transfer protein 1)			
GN	CETP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=87258172; PubMed=3600759;			
RA	Drayna D., Jarnagin A.S., McLean J., Henzel W., Kohr W., Fielding C., Lavan R.,			
RT	"Cloning and sequencing of human cholesteryl ester transfer protein cDNA."			
RT	Nature 327:632-634(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90241928; PubMed=2334701;			
RA	Agellon L.B., Quinet E.M., Gillette T.G., Drayna D.T., Brown M.L., Tall A.R.;			
RT	"Organization of the human cholesteryl ester transfer protein gene."			
RT	Biochemistry 29:1372-1376(1990).			
RN	[3]			
RP	SEQUENCE OF 1-15 FROM N.A.			
RX	MEDLINE=97112972; PubMed=8943225;			
RA	Oliveria C.F.O., Chouinard R.A., Agellon L.B., Bruce C., Ma L., Walsh A., Breslow J.L., Tall A.R.;			
RT	"Human cholesteryl ester transfer protein gene proximal promoter contains dietary cholesterol positive responsive elements and mediates expression in small intestine and periphery while predominant liver and spleen expression is controlled by 5'-distal sequences. Cis-acting sequences mapped in transgenic mice."			
RT	J. Biol. Chem. 271:31851-31858(1996).			
RN	[4]			
RP	SEQUENCE OF 1-27 FROM N.A.			
RX	MEDLINE=9473500; PubMed=933354;			
RA	Williams S., Hayes L., Eisenboss L., Williams A., Andre C., Abramson R., Thompson J.F., Milos P.M.;			
RT	"Sequencing of the cholesteryl ester transfer protein 5' regulatory region using artificial transposons."			
RT	Gene 197:101-107(1997).			
RL	[5]			
RN	SEQUENCE OF 9-493 FROM N.A.			
RP	TISSUE=Liver;			
RC	Dinucuk J.E., Hart J.T., Wink D.O.;			
RA	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RL	[6]			
RN	VARIANT GIV-459.			
RP	MEDLINE=94013514; PubMed=8408659;			
RX				

34	43	32.1	423 1	AIM1_MOUSE	O9bxs5 h adaptor-t
35	43	32.1	423 1	AIM1_MOUSE	P35585 m adaptor-t
36	43	32.1	702 1	ST1_MYCE	O07151 mycobacteri
37	43	32.1	778 1	RPL1_ASFB7	P42491 african swi
38	42.5	31.7	190 1	VPAA_BACSV	P50726 bacillus su
39	42.5	31.7	358 1	PKX1_HUMAN	P51817 mus sapien
40	42.5	31.7	1816 1	LM44_MOUSE	P97927 mus musculu
41	42.5	31.7	3097 1	CADN_DROME	O15943 drosophila
42	42	31.3	383 1	Y628_MYCNU	P96918 mycobacteri
43	42	31.3	387 1	DHAT_KLEPN	O59477 klebsiella
44	42	31.3	437 1	EP1G_HUMAN	P26541 homo sapien
45	42	31.3	437 1	EP1G_MOUSE	O9d8n0 mus musculu

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RA Takahashi K., Jiang X.-C., Sakai N., Yamashita S., Hirano K., Bujo H.,
RA Yamazaki H., Kusunoki J., Mura T., Kussie P., Matsuzawa Y., Saito Y.,
RA Tall A.;
RT "A missense mutation in the cholesterol ester transfer protein gene
RT with possible dominant effects on plasma high density lipoproteins."
RL J. Clin. Invest. 92:2060-2064(1993).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- DISEASE: PROBABLY INVOLVED IN THE DEVELOPMENT OF ATHEROSCLEROSIS.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
DR EMBL: M30185; AAA51977.1; -
DR EMBL: M32898; AAA51978.1; -
DR EMBL: M32892; AAA51978.1; JOINED.
DR EMBL: M32893; AAA51978.1; JOINED.
DR EMBL: M32894; AAA51978.1; JOINED.
DR EMBL: M32895; AAA51978.1; JOINED.
DR EMBL: M32996; AAA51978.1; JOINED.
DR EMBL: M32997; AAA51978.1; JOINED.
DR EMBL: U71187; AAD14876.1; -
DR EMBL: AF027656; AAB86604.1; -
DR EMBL: M83573; AAB59388.1; -
DR PIR: A26941; A26941.
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP_1.
DR SMART: PF02886; LBP_BPI_CETP_C; 1.
DR SMART: SM00328; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; 1.
KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal;
KW Atherosclerosis; Disease mutation.
FT SIGNAL 1 17
FT CHAIN 18 493 CHOLESTERYL ESTER TRANSFER PROTEIN.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 459 459 D -> G (IN CETP DEFICIENCY).
FT CONFLICT 251 310 /FTID=VAR_004172.
FT CONFLICT 422 422 MISSING (IN REF. 2).
SQ SEQUENCE 493 AA; 54770 MW; 16d47ACDC9B063C CRC64;

Query Match 100.0%; Score 134; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 2,7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

DE 1).
DE CETP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=95411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9203355; PubMed=1931878;
RA Page M.E., Rehberg E.F., Marotti K.R., Melchior G.W.;
RT "Molecular cloning, sequence, and expression of cynomolgus monkey
RT cholesterol ester transfer protein. Inverse correlation between
RT hepatic cholesterol ester transfer protein mRNA levels and plasma
RT high density lipoprotein levels."
RL Arterioscler. Thromb. 11:1759-1771(1991).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
DR EMBL: M86343; AAA36840.1; -
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP_1.
DR SMART: PF02886; LBP_BPI_CETP_C; 1.
DR SMART: SM00328; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; 1.
KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 493
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 493 AA; 54743 MW; 7E82BE3C2A8FAEDD CRC64;

Query Match 100.0%; Score 134; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 2,7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RM [1]
CC SEQUENCE FROM N.A.
RX MEDLINE=91154277; PubMed=1999438;
RA Jiang X.C., Moulin P., Quinet E., Goldberg I.J., Yacoub L.K.,
RA Agellon L.B., Compton D., Schnitzer-Polokoff R., Tall B.R.;
RT "Mammalian adipose tissue and muscle are major sources of lipid
transfer protein mRNA."
RL J. Biol. Chem. 266:4631-4639(1991).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
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CC -----
DR EMBL: M63992; AAA37066.1; -
DR PIR: A38700; A38700.
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP.1.
DR Pfam: PF02886; LBP_BPI_CETP.C; 1.
DR SMART: SM00329; BP12; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; PARTIAL.
KW Lipid transport; Cholesterol metabolism; Glycoprotein.
FT NON_TER 1
FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 289 AA; 32330 MW; CA91A06D83927747 CRC64;

Query Match 97.88; Score 131; DB 1; Length 289;
Best Local Similarity 96.28; Pred. No. 4.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILQMDGFPFPHLLVDFLOSL 26
DB 264 RDGFLILQMDGFPFPHLLVDFLOSLN 289

RESULT 4
CETP_RABIT STANDARD; PRT; 497 AA.
AC P22687;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cholesteryl ester transfer protein precursor (lipid transfer protein
DE 1) (Fragment).
GN CETP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89215620; PubMed=3244015;
RA Nagashima M., McLean J.W., Lawn R.M.;
RT "Cloning and mRNA tissue distribution of rabbit cholesteryl ester
RT transfer protein."
RL J. Lipid Res. 29:1643-1649(1988).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----

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CC -----
DR EMBL: M27486; AAA31199.1; -
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP.1.
DR Pfam: PF02886; LBP_BPI_CETP.C; 2.
DR SMART: SM00328; BP11; 1.
DR SMART: SM00329; BP12; 1.
DR PROSITE: PS00400; LBP_BPI_CETP.1.
KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
FT NON_TER 1
FT SIGNAL <1 1
FT CARIN 2 487
FT CARBOHYD 89 89 CHOLESTERYL ESTER TRANSFER PROTEIN.
FT CARBOHYD 99 99 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 497 AA; 54513 MW; EB2944E1821D0332 CRC64;

Query Match 87.38; Score 117; DB 1; Length 497;
Best Local Similarity 92.08; Pred. No. 1.2e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGFLILQMDGFPFPHLLVDFLOSL 26
DB 473 DGFLILQMDGFPFPHLLVDFLOSL 497

RESULT 5
YDAA_HAEIN STANDARD; PRT; 313 AA.
ID YDAA_HAEIN
AC Q57184; O05059;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein H11371.1.
GN H11371.1.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_Taxid=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542890;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geophagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Yenter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Science 269:496-512(1995).
RN [2]
RP REVISIONS.
RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
RA Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO E.COLI YDAA.
CC -----
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CC -----
DR EMBL: U32817; AAC23019.1; -
DR TIGR: H11371.1; -
DR InterPro: IPR000541; UPF0021.
DR Pfam: PF01171; UPF0021; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 313 AA; 35703 MW; 646711CB802F7252 CRC64;

Query Match 38.8%; Score 52; DB 1; Length 313;
Best Local Similarity 57.1%; Pred. No. 0.93;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Y 12 GPEHVLVDFTQSL 25
| | | | | : : : : |
Db 86 GPEHVLPEYLESL 99

RESULT 6
R102_ARATH STANDARD; PRT; 180 AA.
AC Q9FES8;
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S10-2.
GN RPS10B OR AT5G641520 OR MBK23.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT P1 clones."
RL DNA Res. 4:215-230(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
RA Tracy S.E., Baugh J., Bowser L., Carninci P., Chung M.K.,
RA Goodsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Kallin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shimozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE S10E FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: AB005233; BAB11458.1; -
DR EMBL: AY037240; AAK59840.1; -

DR EMBL: AF375440; AAK53024.1; -
KW Ribosomal protein; Multigene family.
SQ SEQUENCE 180 AA; 19733 MW; 9D8C1E2FED5CA28E CRC64;

Query Match 37.3%; Score 50; DB 1; Length 180;
Best Local Similarity 32.0%; Pred. No. 1.1;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Y 17 KEGVLFKKDFNLPQHLIESVPL 41
: : : : : | : : : : |
Db 17 KEGVLFKKDFNLPQHLIESVPL 41

RESULT 7
YDAO_ECOLI STANDARD; PRT; 311 AA.
ID YDAO_ECOLI
AC P76055; Q47558; -
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydao.
GN YDAO OR B1344.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregory J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 1-40 FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94162733; PubMed=7764507;
RA Yamada M., Yanai S., Takeda A.;
RT "Analysis of products of the Escherichia coli genomic genes and
RT regulation of their expressions: an applicable procedure for genomic
RT analysis of other microorganisms."
RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
CC -1- SIMILARITY: STRONG, TO H. INFLUENZA B H11371.1.
CC -----
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CC -----
DR EMBL: AE000232; AAC74426.1; -
DR EMBL: D21139; BAA04675.1; -
DR EcoGene: EG13357; ydao.
DR InterPro: IPR000541; UPF0021.
DR Pfam: PF01171; UPF0021; 1.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 11 E > A (IN REF. 2).
SQ SEQUENCE 311 AA; 35561 MW; D696057B7C092D79 CRC64;

Query Match 37.3%; Score 50; DB 1; Length 311;
Best Local Similarity 57.1%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Y 12 GPEHVLVDFTQSL 25
| | | | | : : : : |
Db 83 GPEHVLPEYLESL 96

```
RESULT 8
TSD1_ABIGR STANDARD: PRT: 628 AA.
ID TSD1_ABIGR
AC 024475;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Pinene synthase, chloroplast precursor (EC 4.2.3.14) (Beta-geranienolene
DE synthase) ((-)-(1S,5S)-pinene synthase).
GN AG3.18.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxId=46611;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=97413772; PubMed=9268308;
RA Bohmann J., Steele C.L., Croteau R.;
RT Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
RT characterization, and functional expression of myrcene synthase, (-)-
RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.*;
RL J. Biol. Chem. 272:21784-21792(1997).
CC -1- FUNCTION: Involved in defensive oleoresin formation in conifers in
CC response to insect attack or other injury. Involved in monoterpene
CC (C10) olefin biosynthesis. A mixture of alpha- and beta-pinene is
CC produced by this enzyme.
CC -1- CATALYTIC ACTIVITY: Geranyl diphosphate = pinene + diphosphate.
CC -1- COFACTOR: Manganese and potassium.
CC -1- PATHWAY: Oleosinosis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: BY wounding.
CC -1- SIMILARITY: BELONGS TO THE TERPENE SYNTHASE FAMILY.
-----
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-----
DR EMBL: U87909; AAB71085.1; -.
DR HSSP: 040577; 5EAT.
DR Mendel; 27004; Abigr.2508;27004.
DR InterPro: IPR001906; Terp_synth_fam.
DR Pfam; PF01397; Terpene_synth_1.
KW Lyase; Manganese; Trans peptid; Chloroplast.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN 628 ? PINENE SYNTHASE.
FT ACT_SITE 524 524 BY SIMILARITY.
FT ACT_SITE 601 601 BY SIMILARITY.
FT ACT_SITE 605 605 BY SIMILARITY.
SQ SEQUENCE 628 AA; 71505 MW; 230BB8B6F3C8072C CRC64;
-----
Query Match 37.3%; Score 50; DB 1; Length 628;
Best Local Similarity 47.8%; Pred. No. 3.9;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;
-----
QY 6 LLOWDRGPPHLL--VDFLOQSS 26
DB 490 ILTMDIPPHILKEVDFPSKLN 512
-----
RESULT 9
AROH_ECOLI STANDARD: PRT: 348 AA.
ID AROH_ECOLI
AC P00887; P78301;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

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DE Phospho-2-dehydro-3-deoxyheptonate aldolase, trp-sensitive
DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DHP
DE synthase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN AROH OR B1704.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91323737; PubMed=1677907;
RA Hudson G.S., Rellos P., Davidson B.E.;
RT "Two promoters control the aroH gene of Escherichia coli.*";
RL Gene 102:87-91(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89053867; PubMed=2903857;
RA Ray J.M., Yanofsky C., Baerle R.;
RT "Mutational analysis of the catalytic and feedback sites of the
RT tryptophan-sensitive 3-deoxy-D-arabino-heptulosonate-7-phosphate
RT synthase of Escherichia coli.*";
RL J. Bacteriol. 170:5500-5506(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna M.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.*";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Bada T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kashi H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa K.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubraman S., Tegan J., Takeda J.,
RA Takeuchi K., Takeuchi Y., Wada C., Yamamoto Y., Horikuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.*";
RL DNA Res. 3:363-377(1996).
RN [5]
RP SEQUENCE OF 1-36 AND 232-348 FROM N.A.
RX MEDLINE=81267314; PubMed=6167722;
RA Zurawski G., Gunsalus R.P., Brown K.D., Yanofsky C.;
RT "Structure and regulation of aroH, the structural gene for the
RT tryptophan-repressible 3-deoxy-D-arabino-heptulosonic
RT acid-7-phosphate synthase of Escherichia coli.*";
RL J. Mol. Biol. 145:47-73(1981).
RN [6]
RP -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
RN AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
RN ARABINO-HEPTULOSONATE-7-PHOSPHATE (DHP).
RN [7]
RP -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
RN phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
RN phosphate + H(2)O.
RN [8]
RP -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
RN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
RN [9]
RP -1- MISCELLANEOUS: THERE ARE 3 DHP SYNTHASES, AROH IS
RN FEEDBACK-INHIBITED BY TRP. THE OTHER 2 DHP SYNTHASES ARE TYR- AND
RN PHE-SENSITIVE, RESPECTIVELY.
RN [10]
RP -1- SIMILARITY: BELONGS TO CLASS-1 DHP SYNTHETASE FAMILY.
RN [11]
RP -----
RN [12]
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CC -----
CC EMBL: M38266; AAA23497.1; -.
CC DR EMBL: J04221; AAA23493.1; -.
CC DR EMBL: AF000265; AAC74774.1; -.
CC DR EMBL: D90813; BAI5473.1; -.
CC DR EMBL: V00261; CAA23510.1; -.
CC DR EMBL: X04373; CAA27956.1; -.
CC DR PIR: J01131; ADECH.
CC DR HSSP: P00886; 10R7.
CC DR Ecogene: EG10080; aroh.
CC DR Interpro: IPR001785; DAH_synth_1.
CC DR Pfam: PF00793; DAH_synth_1; 1.
CC DR Pfam: PF005060; DAH_synth_1; 1.
CC KM Aromatic amino acid biosynthesis; Lyase; Complete proteome.
CC FT CONFLICT 123 123 E -> G (IN REF. 2).
CC FT CONFLICT 203 205 RAS -> AQ (IN REF. 2).
CC FT CONFLICT 333 333 S -> T (IN REF. 3 AND 4).
CC FT CONFLICT 333 334 SE -> RQ (IN REF. 2 AND 5).
CC SQ SEQUENCE 348 AA; 38721 MW; F293C482447226E6 CRC64;

Query Match 35.8%; Score 48; DB 1; Length 348;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 DECFPEHLVDF 21
Db 254 EFDLPEHLVDF 265

RESULT 10
OPS2_HEMSA STANDARD; PRT; 377 AA.
AC Q25158;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Compound eye opsin BCRH2.
OS Hemigrapsus sanguineus (Crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Grapsoidae; Varunidae; Hemigrapsus.
OX NCBI_TaxID=40176;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Eye.
RA Sakamoto K., Hisatomi O., Tokunaga F., Eguchi E.:
RT "Two opsins from the compound eye of the crab Hemigrapsus
RT sanguineus."
RL J. Exp. Biol. 199;441-450(1996).
CC -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL. THIS OPSIN PRODUCES VISUAL PIGMENTS WITH
CC MAXIMAL ABSORPTION IN THE BLUE-GREEN REGION OF THE SPECTRUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL OF THE SEVEN RETINULAR CELLS
CC (R1-R7) FORMING THE MAIN RHABDOM IN EACH OMATIDIUUM.
CC -1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
CC EMBL: D50584; BAA09133.1; -.
CC DR GCRD: GCR_10677; -.
CC DR Interpro: IPR000276; GPCR_Rhodpsn.

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DR Interpro: IPR001760; Opsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS00238; OPSIN; 1.
DR K1 Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; G-protein coupled receptor.
FT DOMAIN 1 53
FT TRANSMEM 54 78
FT DOMAIN 79 90
FT TRANSMEM 91 115
FT TRANSMEM 116 131
FT TRANSMEM 132 151
FT TRANSMEM 152 170
FT TRANSMEM 171 194
FT TRANSMEM 195 218
FT TRANSMEM 219 246
FT TRANSMEM 247 281
FT TRANSMEM 282 305
FT TRANSMEM 306 313
FT TRANSMEM 314 338
FT TRANSMEM 339 377
FT DOMAIN 382 405
FT BINDING 128 205
FT BINDING 325 325
FT CARBOHYD 3 3
FT SEQUENCE 377 AA; 42114 MW; FD6CC2E0E199A256 CRC64;

Query Match 34.7%; Score 46.5; DB 1; Length 377;
Best Local Similarity 56.2%; Pred. No. 8.1;
Matches 9; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

OY 9 MDECFPEHL-LVDFLQ 23
Db 17 MDECFPEGSIVDFVR 32

RESULT 11
AP47_CAEEL STANDARD; PRT; 422 AA.
ID AP47_CAEEL
AC P35602;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Clathrin coat assembly protein AP47 (Clathrin coat associated protein
DE AP47) (Golgi adaptor Ap-1 47 kDa protein) (HAI 47 kDa subunit)
DE (Clathrin assembly protein assembly protein complex I medium chain).
GN UNC-101.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peldoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC MEDLINE=94116859; PubMed=8288128;
RA Lee J., Jongeward G.D., Sternberg P.W.;
RT "unc-101, a gene required for many aspects of Caenorhabditis elegans
RT development and behavior, encodes a clathrin-associated protein.";
RL Genes Dev. 8:60-73(1994).
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- FUNCTION: REQUIRED FOR MANY ASPECTS OF DEVELOPMENT AND BEHAVIOR,
CC INCLUDING NEGATIVE REGULATION OF OVULAL DIFFERENTIATION.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROHEPramer
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19).
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CC CYTOPLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.

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CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
 CC FAMILY.
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 CC -----
 CC EMBL: L26291; AAA72418.1; -
 CC InterPro: IPR001392; Adap_comp_sub.
 CC Pfam: PF00928; Adap_comp_sub; 1.
 CC PRINTS: PR00314; CLATHRINADPT.
 CC PROSITE: PS00990; CLAT_ADAPTOR_M.1; 1.
 CC PROSITE: PS00991; CLAT_ADAPTOR_M.2; 1.
 CC Coated pits.
 CC SEQUENCE 422 AA; 48297 MW; D57BF5D1EF496D50 CRC64;

Query Match 34.3%; Score 46; DB 1; Length 422;
 Best Local Similarity 42.9%; Pred. No. 11;
 Matches 9; Conservative 4; Mismatches 2; Indels 6; Gaps 1;

OY 1 RDGFLL-----QNDGFPE 15
 DB 104 RDNFVITELDENMDFGFRQ 124

RESULT 12
 PRTT_PORCI STANDARD; PRT: 868 AA.
 AC P4158;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Thiol protease/hemagglutinin prt precursor (EC 3.4.22.-).
 GN PRTT.
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; CF8 group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
 OC Porphyromonas.
 NCBI_TaxID=837;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN-ATCC 53977;
 RA MEDLINE-93114862; PubMed-8093357;
 RA Otogoto J.-I., Kuramitsu H.K.;
 RT "Isolation and characterization of the Porphyromonas gingivalis prt
 RT gene, coding for protease activity.";
 RL Infect. Immun. 61:117-123(1993).
 [2]
 RP REVISIONS. SEQUENCE FROM N.A.
 RC STRAIN-ATCC 53977;
 RA MEDLINE-95105001; PubMed-7806362;
 RA Madden T.E., Clark V.L., Kuramitsu H.K.;
 RT "Revised sequence of the Porphyromonas gingivalis prt cysteine
 RT protease/hemagglutinin gene: homology with streptococcal pyrogenic
 RT exotoxin B/streptococcal proteinase.";
 RL Infect. Immun. 63:238-247(1995).
 CC -1- FUNCTION: APPEARS TO BE SPECIFIC FOR ARGININE-CONTAINING PEPTIDE
 CC BONDS. POSSESSES HEMAGGLUTININ ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC -----

DR EMBL: M83096; -; NOT_ANNOTATED_CDS.
 DR MEROPS: C10.002; -
 DR InterPro: IPR000200; Peptidase_C10.
 DR Pfam: PF01640; Peptidase_C10; 1.
 DR PRINTS: PR00797; STREPTOPAIN.
 DR HYDROLASE: Thiol protease; Signal; Hemagglutinin.
 FT SIGNAL 1 27
 FT PROPEP 28 7
 FT CHAIN 28 7
 FT ACT_SITE 184 184
 FT ACT_SITE 327 327
 FT SEQUENCE 868 AA; 96444 MW; 45436EF32779323 CRC64;

Query Match 34.3%; Score 46; DB 1; Length 868;
 Best Local Similarity 60.0%; Pred. No. 23;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 RDGFLLQNDGFPE 15
 DB 74 KDGFLLVADDFRPE 88

RESULT 13
 YMV2_CAEEL

ID YMV2_CAEEL STANDARD; PRT: 1246 AA.

AC P34504; P34505; P34506; P90907;

DT 01-FEB-1994 (Rel. 28, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Hypothetical 130.6 kDa protein K04H4.2 in chromosome III.

GN K04H4.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pseudocercariae; Caenorhabditis.

NCBI_TaxID=6239;

[1]

SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA MEDLINE-94150718; PubMed-7906398;

RA Willison R., Almscough R., Anderson K., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copesey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,

RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,

RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,

RA Wohlschlag P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL Mature 368:32-38(1994).

[2]

REVISIONS.

RA Durbin R.;

RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: K04H4.2A (SHOWN HERE) AND

CC K04H4.2B; ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: TO CHITIN-BINDING MOTIFS.

CC -----

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CC -----

CC EMBL: Z27078; CAAB1587.1; -

CC EMBL: Z27078; CAAB1588.1; -

CC PIR: S40992; S40992.

DR


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DR 16-OCT-2001 (Rel. 40, last annotation update)
DE Adaptor-related protein complex 1 mu 2 subunit (Clathrin coat
DE assembly protein AP47 2) (Clathrin coat associated protein AP47 2)
DE (Golgi adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit 2) (Clathrin
DE assembly protein assembly protein complex 1 medium chain 2) (AP-mu
DE chain family member mu1b).
GN APIM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99268457; Pubmed=10338135;
RA Ohno H., Tomemori T., Nakatsu F., Okazaki Y., Aguilar R.C.,
RA Foelsch H., Mellman I., Saito T., Shirasawa T., Bonifacio J.S.;
RT "mu1b, a novel adaptor medium chain expressed in polarized epithelial
RT cells.";
RL FEBS Lett. 449:215-220(1999).
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19').
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CC CYTOPLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.
CC -1- PTM: AUTOPHOSPHORYLATED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
CC -----
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CC -----
DR EMBL: AF020797; AAD25870.2; -.
DR InterPro: IPR001392; Adap_comp_sub.
DR Pfam: PF00928; Adap_comp_sub_1.
DR PRINTS: PR00314; CLATHRINADPT.
DR PROSITE: PS00990; CLAT_ADAPTOR_M_1; 1.
DR PROSITE: PS00991; CLAT_ADAPTOR_M_2; 1.
KW Coated pits; Phosphorylation.
SQ SEQUENCE 423 AA; 48108 MW; A3FEFDF8659DD6F7 CRC64;

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Query Match          33.6%; Score 45; DB 1; Length 123;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 4; Mismatches 2; Indels 6; Gaps 1;

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```

QY 1 RDGFLLQ-----MDFGPE 15
   ||:::|||||:
DB 104 RDNFVIYVELDELMDFGPPQ 124

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Search completed: June 18, 2002, 08:13:08
Job time: 367 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:06:36 ; Search time 41.39 Seconds

(without alignments)
108.670 Million cell updates/sec

Title: US-09-943-334-1

Sequence: 1 RDGFLLLQMDGPFEPHLLVDFLOSL 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL-19
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacterioph:*
17: sp.archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	91.8	485	6	09BGS59
2	56	41.8	314	16	09CN39
3	56	41.8	582	16	099XLO
4	56	41.8	387	16	097ND6
5	54	40.3	310	16	09KS29
6	53	39.6	426	16	09JUE9
7	53	39.6	590	16	09CE80
8	51	38.1	274	16	09I4E6
9	50	37.3	180	10	09PEF58
10	50	37.3	623	10	094FMO
11	49.5	36.9	559	17	097YHO
12	49	36.6	416	2	09F2A1
13	49	36.6	426	3	09HES5
14	48	35.8	390	16	09KCE3
15	48	35.8	428	10	022715
16	48	35.8	429	10	094JG7

17	48	35.8	438	10	023140	023140 arabidopsis
18	48	35.8	442	13	090XC0	090XC0 cassiopsis a
19	48	35.8	682	16	083654	083654 treponema p
20	48	35.8	1173	5	09V7J8	09V7J8 drosophila
21	47.5	35.4	227	16	092KX0	092KX0 rhizobium m
22	47.5	35.4	306	16	0992H1	0992H1 streptococcus
23	47	35.1	165	5	015887	015887 trypanosoma
24	47	35.1	311	2	093E30	093E30 salmonella
25	47	35.1	618	10	0948Z0	0948Z0 abies grand
26	46.5	34.7	1992	3	09P6T1	09P6T1 neurospora
27	46	34.3	104	16	092U58	092U58 rhizobium m
28	46	34.3	312	16	09PFT8	09PFT8 xyella fast
29	46	34.3	356	17	0980M3	0980M3 sulfolobus
30	46	34.3	374	16	097J05	097J05 clostridium
31	46	34.3	422	5	002282	002282 caenorhabditis
32	46	34.3	428	10	09SAC9	09SAC9 arabidopsis
33	46	34.3	567	3	012108	012108 saccharomyces
34	46	34.3	694	10	09SVK2	09SVK2 arabidopsis
35	46	34.3	849	10	081906	081906 arabidopsis
36	46	34.3	886	2	093481	093481 porphyromonas
37	46	34.3	1071	3	09P388	09P388 neurospora
38	46	34.3	1252	5	09VTV9	09VTV9 drosophila
39	45.5	34.0	628	10	09SEF1	09SEF1 arabidopsis
40	45	33.6	78	1	0977T3	0977T3 uncultured
41	45	33.6	177	10	09SM09	09SM09 arabidopsis
42	45	33.6	265	17	058456	058456 pyrococcus
43	45	33.6	313	16	092PR1	092PR1 rhizobium m
44	45	33.6	425	4	09BS18	09BS18 homo sapiens
45	45	33.6	425	11	09CWP7	09CWP7 mus musculus

ALIGNMENTS

RESULT 1
09BGS59 ID 09BGS59 PRELIMINARY: PRT: 485 AA.
AC 09BGS59; 01-JUN-2001 (TREMBLrel. 17, created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CHOLESTERYL ESTER TRANSFER PROTEIN (FRAGMENT).
OS Tupaiia glis (Tree shrew)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=9395;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zeng W.W., Chen B.S., Zhang J.;
RT "Cloning and sequencing of tree shrew cholesterol ester transfer
protein (CEPT) cDNA." to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF344033; AAK08086.1; -
DR InterPro: IPR001124; LBP_BPL_CETP.
DR Pfam: PF01273; LBP_BPL_CETP.1.
DR Pfam: PF02886; LBP_BPL_CETP_C.1.
DR SMART: SM00328; BPL1.1.
DR SMART: SM00329; BPL2.1.
DR PROSITE: PS00400; LBP_BPL_CETP.1.
FT NON-TER 1
SQ SEQUENCE 485 AA: 53993 MW: 2605E76D2635C367 CRC64;

Query Match 91.8%; Score 123; DB 6; Length 485;
Best Local Similarity 92.3%; Pred. No. 8.6e-11;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGPFEPHLLVDFLOSL 26
DB 460 DQGFLLQMDGPFEPHLLVDFLOSL 485

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RESULT 2
ID 09CN39 PRELIMINARY; PRT: 314 AA.
AC 09CN39;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN PM0606.
GN PM0606.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE-21145866; PubMed-11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT *Complete genomic sequence of Pasteurella multocida Pm70.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006096; AAK02690.1;
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 314 AA; 36080 MW; 3CDEA33486CF62ED CRC64;

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Query Match 41.8%; Score 56; DB 16; Length 314;
Best Local Similarity 64.3%; Pred. No. 1.3;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Oy 12 GFFLLQMDVGFPPH 25
Db 85 GFFLLQMDVGFPPH 98

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RESULT 3
ID 099XLO PRELIMINARY; PRT: 582 AA.
AC 099XLO;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12).
GN ASPS OR SPY2156.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SERO TYPE M1;
RX MEDLINE-21192684; PubMed-11296296;
RA Ferrerelli J.D., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Szatate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren O., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT *Complete genome sequence of an M1 strain of Streptococcus pyogenes.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- CATALYTIC ACTIVITY: ATP -> L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC -1- PYROPHOSPHATE + L-AMINO ACID + TRNA(AMINO ACID)
CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
CC -1- TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-
CC -1- ASPARAGINYL-TRNA(ASN)).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR EMBL; AE006633; AAK34793.1; -.
DR HSSP; P36419; IEFW.
DR InterPro; IPR002106; AA_TRNA_Ligase_II.
DR InterPro; IPR004115; GAD.
DR InterPro; IPR004364; trna-synt_2.
DR InterPro; IPR002312; trna-synt_asp.
DR InterPro; IPR002313; trna-synt_lys_2.
SQ SEQUENCE 587 AA; 66297 MW; AECFE6B31C94452A CRC64;

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DR InterPro; IPR004365; trna_anti.
DR Pfam; PF02938; GAD; 1.
DR Pfam; PF00152; trna-synt_2; 2.
DR Pfam; PF01336; trna_anti; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PRINTS; PR00982; TRNASYNTHYS.
DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
KM ATP-binding; Aminoacyl-TRNA synthetase; Complete proteome; Ligase;
KM Protein biosynthesis.
SQ SEQUENCE 582 AA; 66028 MW; DBA8ABFDE49F4FBC CRC64;

```

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Query Match 41.8%; Score 56; DB 16; Length 582;
Best Local Similarity 71.4%; Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Oy 3 GFFLLQMDVGFPPH 16
Db 510 GFFLLQMDVGFPPH 523

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RESULT 4
ID 097ND6 PRELIMINARY; PRT: 587 AA.
AC 097ND6;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ASPARTYL-TRNA SYNTHETASE.
GN SP2114.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11GR4;
RX MEDLINE-21357209; PubMed-11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwin M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouiri H., Wolf A.M., Uffertback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT *Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.*;
RL Science 293:498-506(2001).
DR EMBL; AE007500; AAK76173.1; -.
DR TIGR; SP2114; -.
DR InterPro; IPR002106; AA_TRNA_Ligase_II.
DR InterPro; IPR004115; GAD.
DR InterPro; IPR004364; trna-synt_2.
DR InterPro; IPR002312; trna-synt_asp.
DR InterPro; IPR002313; trna-synt_lys_2.
DR InterPro; IPR004365; trna_anti.
DR Pfam; PF02938; GAD; 1.
DR Pfam; PF00152; trna-synt_2; 2.
DR Pfam; PF01336; trna_anti; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PRINTS; PR00982; TRNASYNTHYS.
DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
KM Aminoacyl-TRNA synthetase; Complete proteome.
SQ SEQUENCE 587 AA; 66297 MW; AECFE6B31C94452A CRC64;

```

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Query Match 41.8%; Score 56; DB 16; Length 587;
Best Local Similarity 71.4%; Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCt-2001 (TREMblrel. 18, Last annotation update)
 DE HYPOtHEtICAL PROTEIN PA1192.
 GN PA1192.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PA01;
 RA MEDLINE=20437337; PubMed=10984043;
 RA Slover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltier L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT *Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.*;
 RU Nature 406:959-964(2000).
 DR EMBL; AE004549; AAC04581.1; -;
 DR InterPro: IPR000541; UPF0021.
 DR Pfam: PF01171; UPF0021; 1.
 KW Hypothetical protein; Complete Proteome.
 SO SEQUENCE 274 AA; 31260 MW; 4C042FA0198FA4F6 CRC64;

Query Match 38.18; Score 51; DB 16; Length 274;
 Best Local Similarity 57.18; Pred. No. 6.5;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Oy 12 GPFHLLVDFLOSL 25
 Db 76 GPFHLLVDFLOSL 89

RESULT 9
 ID 09FFS8 PRELIMINARY; PRT; 180 AA.
 AC 09FFS8;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE SIMILARITY TO 40S RIBOSOMAL PROTEIN S10 (ATG641520/MRK23_4).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA MEDLINE=97471969; PubMed=9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asemizu E., Fukami M.,
 RA Miya Jima N., Tabata S.;
 RT *Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 mb regions covered by twenty physically assigned
 RT pl clones.*;
 RL DNA Res. 4:215-230(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shin P.,
 RA Treacy S.E., Bann J., Bowser L., Carninci P., Chung M.K.,
 RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
 RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
 RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT *Arabidopsis cDNA clones.*;
 RT Submitted (May-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB005233; BAB11458.1; -;
 DR EMBL; AT037240; AAK5840.1; -;
 DR EMBL; AF375440; AAK53024.1; -;
 KW Ribosomal protein.
 SO SEQUENCE 180 AA; 19733 MW; 908C1E2FED5CA28E CRC64;

Query Match 37.3%; Score 50; DB 10; Length 180;
 Best Local Similarity 32.0%; Pred. No. 5.8;
 Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDPFGFPHLLVDFLOSL 25
 Db 17 KEGVLFARKDFNLPDPLEISVPL 41

RESULT 10
 ID 094FW0 PRELIMINARY; PRT; 623 AA.
 AC 094FW0;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE PINE NE SYNTHASE (FRAGMENT).
 OS Abies grandis (Grand fir).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
 NCBI_TaxID=46611;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21297238; PubMed=11404343;
 RA Trapp S.C., Croteau R.B.;
 RT *Genomic organization of plant terpene synthases and molecular
 RT evolutionary implications.*;
 RL Genetics 158:811-832(2001).
 DR EMBL; AF326517; AAK83564.1; -;
 PT NON_TER
 SO SEQUENCE 623 AA; 70948 MW; 823B82B8113467B CRC64;

Query Match 37.3%; Score 50; DB 10; Length 623;
 Best Local Similarity 47.8%; Pred. No. 23;
 Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

Oy 6 LLQMDPFGFPHLL--VDFLOSL 26
 Db 485 LLQMDPFGFPHLLKEVDFPSKLN 507

RESULT 11
 ID 097YH0 PRELIMINARY; PRT; 559 AA.
 AC 097YH0;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PERMEASE, MULTIDRUG EFFLUX.
 GN SSO1351.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35092 / DSM 1617 / P2;
 RA MEDLINE=21332296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Anavez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moers A., Etrauso G., Fletcher C., Gordon P.M.K.,
 RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Folstropp N.,
 RA Garret R.A., Ragan M.A., Senses C.W., Van der Oost J.;
 RT *The complete genome of the crenarchaeon Sulfolobus solfataricus P2.*;

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL: AE006749; AAK41587.1; -
 KW Complete proteome.
 SQ SEQUENCE 559 AA; 60490 MW; ADOC0C903F6DB157F CRC64;

Query Match 36.9%; Score 49.5; DB 17; Length 559;
 Best Local Similarity 42.3%; Pred. No. 24;
 Matches 11; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

OY 3 GFLLLQ---DFGPEHLVDFLOSL 25
 DB 360 GFLLLPLPVNPNYPERALITIFMGL 385

RESULT 12
 ID 09F2A1 PRELIMINARY; PRT: 416 AA.
 AC 09F2A1:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE DSRP.
 GN DSRP.
 OS Chromatium vinosum.
 OC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
 OC Allochromatium.
 OX NCBI_TaxID=1049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D DSM 180;
 RA Polt-Sperling A.S., Dahl C.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U84760; AAG1085.1; -
 SQ SEQUENCE 416 AA; 45664 MW; B0B554FEBC71DC21 CRC64;

Query Match 36.6%; Score 49; DB 2; Length 416;
 Best Local Similarity 58.8%; Pred. No. 21;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 3 GFLLLQMDGFEHLV 19
 DB 103 GLVLMVDIGRPERLIV 119

RESULT 13
 ID 09HE5 PRELIMINARY; PRT: 426 AA.
 AC 09HE5:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CLATHRIN-ASSOCIATED ADAPTOR MEDIUM CHAIN.
 GN SPBP16F9.07.
 OS Schizosaccharomyces pombe (Pislon yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA Aert R., Robben J., Volckaert G., Wood V., Rajandream M.A.,
 BA Bartel B.G.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AKA41603; CAC08546.1; -
 DR InterPro: IPR001392; Adap_comp_sub.
 DR Pfam: PF00328; Adap_comp_sub.1.
 DR PRINTS: PR00314; CLATHRINADPT.
 DR PROSITE: PS00890; CLATHRINADPT_M.1; 1.
 SQ SEQUENCE 426 AA; 48955 MW; 91FEB137C63AED3 CRC64;

Query Match 36.6%; Score 49; DB 3; Length 426;
 Best Local Similarity 41.4%; Pred. No. 22;
 Matches 12; Conservative 3; Mismatches 8; Indels 6; Gaps 1;

OY 1 RDGFLLDQ-----MDGFEHLVDFLO 23
 DB 104 RDNFVLYELDELMDGFEPTETKILQ 132

RESULT 14
 ID 09KCE3 PRELIMINARY; PRT: 390 AA.
 AC 09KCE3:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CYSTATINONE BETA-LYASE.
 GN MPTC OR BH1628.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=8665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
 halodurans and genomic sequence comparison with Bacillus subtilis.*;
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AP001512; BAB05347.1; -
 DR HSP: P00935; ICS1.
 DR InterPro: IPR000277; Cys_Met_Meta_PP.
 DR InterPro: IPR002026; Urease_gamma.
 DR Pfam: PF01053; Cys_Met_Meta_PP.1.
 DR PROSITE: PS00866; Cys_Met_Meta_PP.1.
 KW Lyase; Complete proteome.
 SQ SEQUENCE 390 AA; 42918 MW; 73BACD4C9533425 CRC64;

Query Match 35.8%; Score 48; DB 16; Length 390;
 Best Local Similarity 47.6%; Pred. No. 28;
 Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

OY 1 RDGFLLDQMDGFEHLVDF 21
 DB 356 RDCLRLRSLVGLKPEBLMADF 376

RESULT 15
 ID 022715 PRELIMINARY; PRT: 428 AA.
 AC 022715:
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE CLATHRIN COAT ASSEMBLY PROTEIN.
 GN F8A5.29.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
 RA A. N., Arango R., Brendel V., Buehler E., Dewar K., Feng J., Kim C.,
 RA Li Y., Oji O., Osborne B.I., Shih P., Sun H., Toriumi M.,
 RA Vysotskaya V.S., Yu G., Ecker J., Theologis A., Davis R.W.;
 RT *Genomic sequence of Arabidopsis.*;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 : Search time 51.68 Seconds
(without alignments)
35.881 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134

Sequence: 1 RDGFLLOMDGPEHLLVDLQSLIS 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
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22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	26	17	AAW06128
2	134	100.0	26	17	AAV13801
3	134	100.0	26	21	AAV91228
4	134	100.0	46	21	AAV91232
5	134	100.0	46	21	AAV91233
6	134	100.0	476	17	AAW06127
7	134	100.0	476	18	AAW46446
8	134	100.0	476	20	AAW02466
9	134	100.0	493	15	AAW03032
10	134	100.0	493	20	AAV49556
11	134	100.0	493	20	AAV49568

12	134	100.0	493	22	AAW5636
13	121	90.3	496	20	AAV02469
14	117	87.3	26	20	AAV13802
15	117	87.3	26	21	AAV91231
16	117	87.3	46	21	AAV91240
17	117	87.3	46	21	AAV91241
18	117	87.3	477	20	AAV02468
19	117	87.3	496	17	AAW06133
20	117	87.3	496	18	AAW46445
21	117	87.3	496	20	AAV02467
22	111	82.8	22	20	AAV13815
23	111	82.8	22	20	AAV13821
24	107	79.9	22	20	AAV13809
25	85	63.4	31	17	AAW06129
26	85	63.4	31	20	AAV02470
27	83	61.9	16	21	AAV91229
28	83	61.9	35	21	AAV91236
29	83	61.9	36	21	AAV91235
30	83	61.9	36	21	AAV91234
31	83	61.9	36	21	AAV91237
32	83	61.9	50	17	AAW06131
33	79	59.0	16	21	AAV91230
34	79	59.0	36	21	AAV91238
35	79	59.0	36	21	AAV91239
36	79	59.0	50	17	AAW06132
37	79	59.0	50	18	AAW46447
38	56	41.8	97	18	AAW44126
39	56	41.8	587	18	AAW31916
40	56	41.8	587	22	AAU37899
41	53	39.6	11	18	AAW24294
42	52	38.8	584	22	AAU35117
43	52	38.8	589	22	AAU35285
44	51.5	38.4	353	20	AAW97881
45	50.5	37.7	67	21	AAV59432

ALIGNMENTS

RESULT	1
AAW06128	standard: Peptide: 26 AA.
AAW06128	
XX	
AC	AAW06128:
XX	
DT	07-FEB-1997 (first entry)
XX	
DE	Human cholesteryl ester transfer protein C-terminal B-cell epitope.
XX	
KW	Cholesteryl ester transfer protein: CETP; antigen: vaccine;
KW	cardiovascular disease; atherosclerosis; B-cell epitope.
OS	Homo sapiens.
XX	
PN	W09634888-A1
XX	
PD	07-NOV-1996.
XX	
PF	01-MAY-1996; 96MO-US06147.
XX	
PR	01-MAY-1995; 95US-0432483.
XX	
XX	(TCELL-) T CELL SCI INC.
PA	
XX	Rittershaus CW, Thomas J.L.
PI	
XX	
XX	WPI, 1996-506103/50.
DR	
XX	
PT	Cholesteryl ester transfer protein B cell epitope linked to T cell
PT	epitope used to generate vaccine to regulate CETP activity for
PT	decreasing the risk of developing a cardiovascular disease e.g.
PT	atherosclerosis
XX	

PS Claim 5; Page 41; 72pp; English.

XX
XX A B-cell epitope (AAW06128) comprising the C-terminal 26 amino acids
CC of human liver mature cholesteryl ester transfer protein (CETP)
CC (see also AAW06127) is involved in a neutral lipid binding or a
CC transfer activity of CETP. It can be linked to a universal or
CC broad range immunogenic T-cell epitope, such as that found at amino
CC acids 830-843 of tetanus toxoid protein, to produce a synthetic
CC vaccine (see also AAW06129) that elicits an immune response against
CC endogenous CETP activity, thereby treating or preventing
CC cardiovascular disease, such as atherosclerosis. It may also be
CC incorporated into a multivalent vaccine (see also AAW06131)
CC including another CETP B-cell epitope.

XX
XX Sequence 26 AA:

SQ

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFRPEHLIVDFLOSLS 26
DB 1 rdgfilllqmdifgpehlivdfllgs1s 26
|||||

RESULT 2
AAV13801
ID AAV13801 standard; peptide; 26 AA.
XX
XX AAV13801;
XX
XX 08-JUL-1999 (first entry)
XX
XX Rabbit CETP immunogenic fragment.

DE
XX
XX CETP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW antibody production; cholesteryl ester transfer; therapy;
KW high density lipoprotein; HDL cholesterol concentration;
KW pro-atherogenic dyslipoproteinaemia.
XX
XX Oryctolagus sp.
XX
XX WO9915655-A1.
XX
XX 01-APR-1999.
XX
XX 17-SEP-1998; 98WO-US19366.
XX
XX 19-SEP-1997; 97US-0934367.
XX
XX (MONS) MONSANTO CO.
XX
XX Glenn K, Needleman P;
XX
XX WPI; 1999-276984/23.
XX
XX New recombinant DNA vaccines
XX
XX Claim 15; Page 85; 99pp; English.

XX
XX This sequence represents an immunogenic fragment of the rabbit
CC cholesteryl ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenous immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.

XX
XX Sequence 26 AA:

SQ

Query Match 100.0%; Score 134; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFRPEHLIVDFLOSLS 26
DB 1 rdgfilllqmdifgpehlivdfllgs1s 26
|||||

RESULT 3
AAV91228
ID AAV91228 standard; peptide; 26 AA.
XX
XX AAV91228;
XX
XX 22-MAY-2000 (first entry)
XX
XX Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:106.
XX
XX DE
XX Promiscuous T-cell epitope; measles virus F protein; WVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW interleukin-6; interleukin-6 releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW plasmidium falciparum; circumsporozoite; anti-malarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
XX Homo sapiens.
XX
XX WO9966957-A2.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-US19975.
XX
XX 20-JUN-1998; 98US-0100412.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY;
XX
XX WPI; 2000-160564/14.
XX
XX New artificial T helper cell epitope and derived immunogens with target
XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX or human immune deficiency virus -
XX
XX Claim 10; Page 49; 129pp; English.

XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin-6
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAV91121 represents a promiscuous T helper epitope
CC from the measles virus F (WVF) protein and sequences AAV91122-Y91142,

CC AA91220 and AA91245-Y91246 represent synthetic Th epitopes based on the
CC MYF Th epitope. Sequence AA91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AA91208 is a
CC human CD4 CD82-like domain antigenic site, and AA91209-Y90211 are the MYH Th
CC infection of T cells. AA90212 is a modified version of a human HIV
CC (immunoglobulin E) CH3 domain, and AA90213-Y90219 are Th epitope/ID5E CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AA91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AA91221-Y91222 comprise this porozoite and a Th
CC epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AA91224-Y91225 comprise the CS antigen and an MYF Th
CC epitope, and may be used in a malaria vaccine. AA91228-Y91231 represent
CC CEMP-derived peptides and AA91232-Y91241 are immunogens comprising a
CC CEMP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AA91248-Y91251 and
CC AA91258-Y91273 are antigenic peptides comprising MYH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AA91198 and AA91199 are respectively an immunostimulatory invasion
CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the invention.
CC Note: Sequence AA91227 is also designated SEQ ID NO:106 in the
CC specification.

Sequence 26 AA;

Query Match	100.0%;	Score 134;	DB 21;	Length 26;
Best Local Similarity	100.0%;	Pred. No. 1,2e-13;		
Matches 26; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```

OY 1 RDGELLQWDEGFPENHLVDFLOSL 26
    |||||
Db 1 rdgelllqmdfgfpehlldvdfiqsls 26

```

RESULT	4
AA91232	
ID	AA91232 standard; peptide; 46 AA.

AC	AA91232;
XX	
DT	22-MAY-2000 (first entry)

Modified MVT Th epitope/CTP peptide, SEQ ID NO:110

KM Promiscuous T-cell epitope: measles virus F protein; WVF.
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin-6; IL-6; proinflammatory cytokine; IL-6; IL-6; IL-6;
KM interleukin-6; IL-6; proinflammatory cytokine; IL-6; IL-6; IL-6;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesterol ester transport protein; anti-arteriosclerotic.

OS Chimeric - Measles virus.
OS Chimeric - Homo sapiens.

PN W09966957-A2.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus -
XX
XX
XX Claim 11: Page 104; 129pp; English.

PS Claim 11; Page 104; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CEMP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of uterineising hormone releasing hormone (LHRH) for contraception; treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AA91121 represents a promiscuous T helper epitope from the measles virus P (MVP) protein and sequences AA91122-991144, AA91226 and AA91245-991246 represent synthetic Th epitopes based on the MVP Th epitope. Sequence AA91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AA91144-991155 are synthetic epitopes derived from this HBV epitope. AA91156-991196, AA91227 and AA91242-991244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AA91200 is somatostatin, and AA91201-991207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AA91208 is a human CD4 CD82-like domain antigenic site, and AA91209-990211 are MVA Th epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV infection of T cells. AA990212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AA990213-990219 are Th epitope/19E CH3 antigenic peptides which may be used in the treatment of allergies. AA91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AA91221-991222 comprise this peptide and a Th epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AA91224-991225 comprise the CS antigen and an MVA Th epitope, and AA91224-991225 comprise the CS antigen and an MVA Th epitope and may be used in a malaria vaccine. AA91228-991231 represent CEMP-derived peptides and AA91232-991241 are immunogens comprising a CEMP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AA91247 and AA91252-991257 are HIV-1 neutralising B-cell epitopes, and AA91248-991251 and AA91258-991273 are antigenic peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AA91198 and AA91199 are respectively an immunostimulatory invasive protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

SQ Sequence 46 AA;

Query Match	100.08;	Score 134;	DB 21;	Length 46;
Best Local Similarity	100.08;	Pred. No. 2,3e-13;		
Matches 26; conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```
OY      1 RDGFLLLQMDGFPFHHLLVDFLOSLS 26
          |||||
Db       21 rdfglllqmdfgfpehlldvdlqlsls 46
```

RESULT 5
 ID AAY91233 standard; peptide; 46 AA.
 AC AAY91233;
 XX AAY91233;
 DE 22-MAY-2000 (first entry)
 XX Modified MWV Th epitope/CETP peptide, SEQ ID NO:111.
 XX
 XX Promiscuous T-cell epitope; measles virus F protein; MWV;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin hormone releasing hormone; LHRH; contraceptive; antitumor;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalaria; CETP;
 XX cholesterol ester transport protein, anti-arteriosclerotic.
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 PN MO9966957-A2.
 PD 29-DEC-1999.
 PF 21-JUN-1999; 99WO-US13975.
 PR 20-JUN-1998; 98US-0100412.
 PA (UNBEL-) UNITED BIOMEDICAL INC.
 PI Wang CY;
 PI WPI; 2000-160564/14.
 DR
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 PS
 PS Claim 11; Page 104-105; 129pp; English.
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MWV) protein and sequences AAY91122-Y91142,
 CC AAY911226 and AAY91143-Y91246 represent synthetic Th epitopes based on
 CC MWV Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91127 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a

PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX
 PS Claim 2: Page 44-47; 72pp: English.
 XX
 CC Human liver mature cholesteryl ester transfer protein (CETP) (AAM06127)
 CC plays a role in altering the relative profile of circulating
 CC lipoproteins to one associated with an increased risk of
 CC cardiovascular disease. B-cell epitopes (see also AAM06128) of CETP
 CC can be used in novel peptide vaccines (see also AAM06129, AAM06131)
 CC that elicit an immune response against endogenous CETP activity,
 CC thereby treating or preventing cardiovascular disease, such as
 CC atherosclerosis.
 XX
 SQ Sequence 476 AA:
 XX
 Query Match 100.0%; Score 134; DB 17; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLOMDRGPEPHLLVDFLOSL 26
 Db 451 rdgflilqmdrgfpehllvdflosls 476
 RESULT 7
 AAM46446
 ID AAM46446 standard; Peptide: 476 AA.
 AC AAM46446;
 DT 18-MAY-1998 (first entry)
 XX
 DE Human mature cholesteryl ester transfer protein (CETP).
 XX
 KW Cholesteryl ester transfer protein; CETP; cholesteryl ester;
 KW high density lipoprotein; HDL; very low density lipoprotein; VLDL;
 KW low density lipoprotein; LDL; atherosclerosis; neutral lipid blinding;
 KW transfer activity; immunogenic; B cell epitope; antibody; T2;
 KW DNA plasmid-based vaccine; broad range helper T cell epitope;
 KW treatment; cardiovascular disease.
 KM
 XX
 OS Homo sapiens.
 XX
 PN WO9741227-A1.
 XX
 PD 06-NOV-1997.
 XX
 PF 01-MAY-1997; 97WO-US07294.
 XX
 PR 21-FEB-1997; 97US-0802967.
 XX
 PR 01-MAY-1996; 96US-0640713.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Thomas LJ;
 XX
 DR WPI: 1997-549731/50.
 DR N-PSDB: AAV05127.
 XX
 PT DNA plasmid-based vaccine encodes CETP B cell and helper T cell
 PT epitope(s) - used for elevating high density lipoprotein levels, and
 PT for treating cardiovascular disease
 XX
 PS Claim 6: Pages 36-38; 67pp: English.
 XX
 CC The present sequence represents a human mature cholesteryl ester transfer
 CC protein (CETP). CETPs mediate the transfer of cholesteryl esters from
 CC high density lipoprotein (HDL) to very low density lipoprotein (VLDL) and
 CC low density lipoprotein (LDL). An increased CETP activity
 CC produces an atherogenic lipoprotein profile and induces atherosclerosis.
 CC A 13 amino acid stretch in the human CETP (Phe463 to Leu475), and also

CC possibly Asp460, are particularly important for neutral lipid binding and
 CC transfer activity. This region has been shown to be immunogenic as a B
 CC cell epitope of CETP, and a monoclonal antibody (TP2) directed at this
 CC region has been shown to inhibit neutral lipid transfer. A second B cell
 CC epitope is defined by Arg349 to Ile367. Antibodies to this second epitope
 CC would allow the formation of immune complexes involving CETP, and promote
 CC the removal of the complexed CETP. This peptide region was selected for
 CC its potential antigenicity and high possibility for surface expression
 CC on native CETP. Sequences encoding these 2 epitopes can be used in a DNA
 CC plasmid-based vaccine which comprises sequences encoding at least 1 B
 CC cell epitope of CETP linked in frame with at least one segment encoding
 CC a broad range helper T cell epitope. The vaccines can be used to elevate
 CC the ratio of circulating HDL to circulating LDL, VLDL or total
 CC cholesterol in a human. It can also be used for decreasing the level of
 CC endogenous CETP activity in a human. The vaccine can be used to produce
 CC anti-CETP antibodies in vivo and for treating cardiovascular disease.
 XX
 SQ Sequence 476 AA:
 XX
 Query Match 100.0%; Score 134; DB 18; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLOMDRGPEPHLLVDFLOSL 26
 Db 451 rdgflilqmdrgfpehllvdflosls 476
 RESULT 8
 AAY02466
 ID AAY02466 standard; protein: 476 AA.
 AC AAY02466;
 DT 14-JUL-1999 (first entry)
 XX
 DE Human cholesteryl ester transfer protein (CETP).
 XX
 KW Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CETP;
 KW high-density lipoprotein-associated cholesterol; metabolism;
 KW low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
 KW cholesterol; atherosclerosis; heart disease.
 KM
 XX
 OS Homo sapiens.
 XX
 PN WO9920302-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22145.
 XX
 PR 20-OCT-1997; 97US-0954643.
 XX
 PA (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI: 1999-302645/25.
 DR N-PSDB: AAX35807.
 XX
 PT Vaccine against cholesteryl ester transfer protein
 XX
 PS Disclosure: Page 44-46; 61pp: English.
 XX
 CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein
 CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol; for
 CC inhibiting development of atherosclerotic lesions; to lower circulating

CC Levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents human CERP.
 CC

SO Sequence 476 AA:

Query Match 100.0%; Score 134; DB 20; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFTLLQMDGFPPEHLIVDFLOSLG 26
 DB 451 rdgftllqmdgfppehlivdfllqsls 476

RESULT 9

AA60342
 ID AAR60342 standard; protein; 491 AA.

AC AAR60342;

DI 01-MAR-1995 (first entry)

DE Partial human lipid transfer protein.

KW lipid transfer protein; LTP; monoclonal antibody; immunoassay;
 KW antigen determining group.

OS Homo sapiens.

PH Key Location/Qualifiers
 FT Peptide 16..43

FT Peptide /label= peptide 1
 FT /note= "claim 1; antigen determining group"

FT Peptide 209..221
 FT /label= peptide 2

FT Peptide /note= "claim 1; antigen determining group"

FT Peptide 275..288
 FT /label= peptide 3

FT Peptide /note= "claim 1; antigen determining group"

FT Peptide 303..322
 FT /label= peptide 4

FT Peptide /note= "claim 1; antigen determining group"

FT Peptide 360..370
 FT /label= peptide 5

FT Peptide /note= "claim 1; antigen determining group"

PN JP06169793-A.

XX 21-JUN-1994.

XX 02-DEC-1992; 92JP-0349842.

XX 02-DEC-1992; 92JP-0349842.

XX (EIKE) EIKEN KAGAKU KK.

XX WPI: 1994-237601/29.

XX A monoclonal antibody recognising human lipid transfer protein -
 FT useful for immunoassay

XX Disclosure: Fig 1; 14pp; Japanese.

XX This sequence shows a partial human lipid transfer protein,
 CC containing specific peptide groups that are antigen determining. The
 CC monoclonal antibody of the invention recognises any of these
 CC peptides. The Mab can be used in an immunoassay for LTP.

SO Sequence 491 AA:

Query Match 100.0%; Score 134; DB 15; Length 491;
 Best Local Similarity 100.0%; Pred. No. 3.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFTLLQMDGFPPEHLIVDFLOSLG 26
 DB 466 rdgftllqmdgfppehlivdfllqsls 491

RESULT 10

AA49556
 ID AAY49556 standard; protein; 493 AA.

AC AAY49556;

DI 13-JAN-2000 (first entry)

DE Human cholesterol ester transfer protein sequence.

KW Human; coding sequence polymorphism; vascular pathology gene;
 KW polymorphic site; phenotype correlation; forensic; paternity testing;
 KW medicine; genetic analysis; vascular disease.

OS Homo sapiens.

PN M09950454-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06473.

XX 01-APR-1998; 98US-0054272.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Lander ES, Daley GO, Cargill M, Ireland JS, Rozen SG;

XX WPI: 1999-620066/53.

XX N-PSDB; AA232165.

XX Determination of polymorphisms in genes, especially those identifying
 FT predisposition to vascular disease

XX Disclosure: Fig 9; 134pp; English.

XX AA232159 to AA232194 represent reference alleles for specifically
 CC claimed nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected
 CC from 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic
 CC analysis. AAY49550 to AAY49573 represent the proteins which correspond
 CC to some of the reference alleles.

SO Sequence 493 AA:

Query Match 100.0%; Score 134; DB 20; Length 493;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFTLLQMDGFPPEHLIVDFLOSLG 26
 DB 468 rdgftllqmdgfppehlivdfllqsls 493

RESULT 11

AA49568
 ID AAY49568 standard; protein; 493 AA.

XX

AC	AAV49568;
XX	
DT	13-JAN-2000 (first entry)
DE	Human cholesterol[ester transfer protein sequence.
KM	Human; coding sequence polymorphism; vascular pathology gene;
KW	polymorphic site; phenotype correlation; forensics; paternity testing;
XX	medicine; genetic analysis; vascular disease.
OS	Homo sapiens.
PN	W09950454.v2.
PD	07-OCT-1999.
PF	26-MAR-1999; 99WO-US06473.
PR	01-APR-1998; 98US-0054272.
XX	
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.
PI	Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
XX	WPI; 1999-620065/53.
DR	N-PDB; AA32188.
PT	Determination of polymorphisms in genes, especially those identifying
PT	predisposition to vascular disease .
PS	Disclosure: Fig 32; 134pp; English.
CC	AA32159 to AA32194 represent reference alleles for specifically
CC	claimed nucleic acid sequences from the present invention which comprise
CC	polymorphic sites as given in a table in the specification, selected
CC	from 92 single nucleotide polymorphisms in which the nucleotide at the
CC	polymorphic site is different from a nucleotide at the same site in a
CC	reference allele. The nucleic acids, and primers and probes, are used to
CC	identify polymorphisms, which may predispose an individual to disease,
CC	especially a vascular disease. They can also be used in phenotype
CC	correlations, forensicis, paternity testing, medicine or genetic
CC	analysis. AAV49550 to AAV49573 represent the proteins which correspond
CC	to some of the reference alleles.
XX	
SO	Sequence 493 AA:
OY	Query Match 100.0%; Score 134; DB 20; Length 493; Best Local Similarity 100.0%; Pred. No. 3.2e-12; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 RDGFLIOMDFGPPEHLVDPLQSLS 26 468 rdgflilqmdfgfpehlvdfiqsls 493
RESULT 12	
ID	AAAG5636 standard; Protein; 493 AA.
XX	
AC	AAG5636;
XX	
DT	07-JAN-2002 (first entry)
DE	Human cholesterol ester transfer protein (CETP).
XX	
XX	CETP; arteriosclerosis; cholesterol ester transfer protein; HDL;
KW	high density lipoprotein; human.
XX	
OS	Homo sapiens.
XX	
TH	Key
FT	Peptide Location/Qualifiers 1..17

Query	Subject	Score	DB	Length	Ident	Gaps
QY 1 RDGFLQLQMDFGFPEHLVDFLQSL 26	Humanised rabbit cholesteryl ester transfer protein (CETP).	100.0%	DR 22	493	0	0
DB 468 rdgflqlqmdfgfpehlvdfllqsls 493						
Result 13						
AAV02469						
ID AAV02469	standard; protein; 496 AA.					
AC AAV02469;						
DE 14-JUL-1999	(first entry)					
FM Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CETP; high-density lipoprotein-associated cholesteryl metabolism;						
KW low-density lipoprotein-associated cholesteryl; atherosclerotic lesion; cholesterol; atherosclerosis; heart disease.						
XX Synthetic.						
OS Oryctolagus sp.						
PN W09920302-A1.						
PD 29-APR-1999.						
PF 20-OCT-1998;	98MO-US22145.					
PR 20-OCT-1997;	97US-0954643.					
PA (AVAN-) AVANT	IMMUNOTHERAPEUTICS INC.					

PI Rittershaus CW, Thomas LD;
 XX WPI: 1999-302645/25.
 DR Vaccine against cholesteryl ester transfer protein
 XX
 XX Disclosure; Page 53-54; 61pp; English.
 PS
 CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein
 CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents a humanised rabbit CETP.
 XX
 SQ Sequence 496 AA;
 XX
 Query Match 90.3%; Score 121; DB 20; Length 496;
 Best Local Similarity 96.0%; Pred. No. 3.1e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 DGFLLQMDGFPEHLVDFLOSL 26
 DB 472 dgclllqmdfgfpehlldvflqsls 496
 |||||||||||||||||||||
 RESULT 14
 AAY13802
 ID AAY13802 standard; peptide: 26 AA.
 XX
 XX AAY13802;
 AC
 XX 08-JUL-1999 (first entry)
 DT
 XX Rabbit CETP immunogenic fragment.
 DE
 XX CETP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Oryctolagus sp.
 XX
 PN WO9915655-A1.
 PD 01-APR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 XX (MONS) MONSANTO CO.
 PA
 XX Glenn K, Needleman P;
 PI WPI: 1999-276984/23.
 DR
 XX
 PT New recombinant DNA vaccines
 XX
 PS Claim 15; Page 94; 9pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transfer protein (CETP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CETP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the

CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CETP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 SQ Sequence 26 AA;
 XX
 Query Match 87.3%; Score 117; DB 20; Length 26;
 Best Local Similarity 92.0%; Pred. No. 4.8e-11;
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 2 DGFLLQMDGFPEHLVDFLOSL 26
 DB 2 dgclllqmdfgfpehlldvflqsls 26
 |||||||||||||||||||||
 RESULT 15
 AAY91231
 ID AAY91231 standard; peptide: 26 AA.
 XX
 XX AAY91231;
 AC
 XX 22-MAY-2000 (first entry)
 DT
 XX Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:109.
 DE
 XX Promiscuous T-cell epitope; measles virus F protein; MYF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin-6 hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antitrial; PMOY;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmidium falciparum; circumsporozoite; anti-malarial; CETP;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO9966957-A2.
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 XX (UNBI-) UNITED BIOMEDICAL, INC.
 PA
 XX Wang CY;
 PI WPI: 2000-160564/14.
 DR
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Claim 10; Page 62; 12pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes and the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmidium falciparum, cholesteryl ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous

Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAY91208 is a human CD4/CD82-like domain antigenic site, and AAY91209-Y90211 are MVA Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90218 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent CEMP-derived peptides and AAY91232-Y91241 are immunogens comprising a CEMP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasion protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

Sequence 26 AA:

Query Match 87.3%; Score 117; DB 21; Length 26;

Best Local Similarity 92.0%; Pred. No. 4,8e-11;

Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGFLLQWDFGPEHLVDFLOSL 26

DB 2 dgcillqmdfgfphkhlvdltqsls 26

Search completed: June 18, 2002, 08:08:27
Job time: 156 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 ; Search time 205.61 Seconds
(without alignments)
44.509 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134
Sequence: 1 RDGFLQLQMDGFPENHLVDFLQSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/paa/US07.COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08.COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081.COMB.pep.*
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25: /cgn2_6/ptodata/2/paa/US101.COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US60.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134	100.0	26	1 PCT-US99-13975B-106	Sequence 106, App
2	134	100.0	26	8 US-08-432-483-1	Sequence 1, Appl
3	134	100.0	26	8 US-08-432-483A-1	Sequence 1, Appl
4	134	100.0	26	11 US-08-785-997-29	Sequence 29, Appl
5	134	100.0	26	11 US-08-788-882-29	Sequence 29, Appl
6	134	100.0	26	13 US-08-934-367-29	Sequence 29, Appl
7	134	100.0	26	13 US-08-945-289-1	Sequence 1, Appl

8	134	100.0	26	17 US-09-386-591-29	Sequence 29, Appl
9	134	100.0	26	17 US-09-387-340-29	Sequence 29, Appl
10	134	100.0	26	21 US-09-701-588-106	Sequence 106, App
11	134	100.0	26	23 US-09-943-334-1	Sequence 1, Appl
12	134	100.0	26	23 US-09-943-548-1	Sequence 1, Appl
13	134	100.0	46	1 PCT-US99-13975B-110	Sequence 110, App
14	134	100.0	46	1 PCT-US99-13975B-111	Sequence 111, App
15	134	100.0	46	21 US-09-701-588-110	Sequence 110, App
16	134	100.0	46	21 US-09-701-588-111	Sequence 111, App
17	134	100.0	470	19 US-09-518-598-14	Sequence 14, Appl
18	134	100.0	470	22 US-09-872-128-14	Sequence 14, Appl
19	134	100.0	476	11 US-08-640-713-4	Sequence 4, Appl
20	134	100.0	476	11 US-08-785-997-28	Sequence 28, Appl
21	134	100.0	476	11 US-08-788-882-28	Sequence 28, Appl
22	134	100.0	476	12 US-08-802-967A-4	Sequence 4, Appl
23	134	100.0	476	13 US-08-934-367-28	Sequence 28, Appl
24	134	100.0	476	13 US-08-945-289-4	Sequence 4, Appl
25	134	100.0	476	13 US-08-854-643-1	Sequence 1, Appl
26	134	100.0	476	17 US-09-386-591-28	Sequence 1, Appl
27	134	100.0	476	17 US-09-387-340-28	Sequence 28, Appl
28	134	100.0	476	19 US-09-529-762-1	Sequence 1, Appl
29	134	100.0	476	23 US-09-943-334-4	Sequence 4, Appl
30	134	100.0	476	23 US-09-943-548-4	Sequence 4, Appl
31	134	100.0	493	11 US-08-785-997-30	Sequence 30, Appl
32	134	100.0	493	11 US-08-788-882-30	Sequence 30, Appl
33	134	100.0	493	13 US-08-934-367-30	Sequence 30, Appl
34	134	100.0	493	14 US-09-054-272-14	Sequence 14, Appl
35	134	100.0	493	14 US-09-054-272-14	Sequence 14, Appl
36	134	100.0	493	17 US-09-386-591-30	Sequence 30, Appl
37	134	100.0	493	17 US-09-387-340-30	Sequence 30, Appl
38	134	100.0	493	22 US-09-802-643-12	Sequence 12, Appl
39	134	100.0	496	13 US-08-954-643-6	Sequence 6, Appl
40	121	90.3	496	19 US-09-529-762-6	Sequence 6, Appl
41	117	87.3	26	1 PCT-US99-13975B-109	Sequence 109, Appl
42	117	87.3	26	11 US-08-785-997-50	Sequence 50, Appl
43	117	87.3	26	11 US-08-788-882-50	Sequence 50, Appl
44	117	87.3	26	13 US-08-934-367-50	Sequence 50, Appl
45	117	87.3	26	17 US-09-386-591-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
Sequence 106, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL, INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL,
TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158PC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-106

Query Match 100.0%; Score 134; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

RESULT 2
US-08-432-483-1
Sequence 1, Application US/08432483
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179 (TCS-95179)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino acids of
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
JOURNAL: cholesterol ester transfer CDNA
VOLUME: 327
ISSUE:
PAGES: 632-634

DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-432-483-1

Query Match 100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

RESULT 3
US-08-432-483A-1
Sequence 1, Application US/08432483A
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,483A
FILING DATE: 1-May-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179 (TCS-95179)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino acids of
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
JOURNAL: cholesterol ester transfer CDNA
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-432-483A-1

Query Match 100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGFPEHLLVDFLQSL 26
1 RDGFLLLQMDFGFPEHLLVDFLQSL 26

RESULT 4
US-08-785-997-29

Sequence 29, Application US/08785997

GENERAL INFORMATION:

APPLICANT: Needleman, Philip

APPLICANT: Glenn, Kevin

TITLE OF INVENTION: An Immunological Process for Increasing

TITLE OF INVENTION: the HDL Cholesterol Concentration

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Welsh & Katz, Ltd

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/785,997

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Gansson Ph.D., Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)655-1500

TELEFAX: (312)655-1501

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PUBLICATION INFORMATION:

AUTHORS: Swenson, T. L.

AUTHORS: et al.,

JOURNAL: J. Biol. Chem.

VOLUME: 264

PAGES: 14318-14326

DATE: 1989

US-08-785-997-29

Query Match 100.0%; Score 134; DB 11; Length 26;

Best Local Similarity 100.0%; Pred. No. 1,5e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGFPEHLLVDFLQSL 26
1 RDGFLLLQMDFGFPEHLLVDFLQSL 26

RESULT 5
US-08-788-882-29

Sequence 29, Application US/08788882

GENERAL INFORMATION:

APPLICANT: Needleman, Philip

APPLICANT: Glenn, Kevin

APPLICANT: Krul, Elaine

APPLICANT: Gansson, Edward P.

TITLE OF INVENTION: An Immunological Process and Constructs

TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/788,882

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gansson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)655-1500

TELEFAX: (312)655-1501

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PUBLICATION INFORMATION:

AUTHORS: Swenson, T. L.

AUTHORS: et al.,

JOURNAL: J. Biol. Chem.

VOLUME: 264

PAGES: 14318-14326

DATE: 1989

US-08-788-882-29.

Query Match 100.0%; Score 134; DB 11; Length 26;

Best Local Similarity 100.0%; Pred. No. 1,5e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGFPEHLLVDFLQSL 26
1 RDGFLLLQMDFGFPEHLLVDFLQSL 26

RESULT 6
US-08-934-367-29

Sequence 29, Application US/08934367

GENERAL INFORMATION:

APPLICANT: Needleman, Philip

APPLICANT: Glenn, Kevin

TITLE OF INVENTION: An Immunological Process and Constructs

TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/934,367
3 FILING DATE:
4 CLASSIFICATION: 514
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Gamson Ph.D., Edward P.
7 REGISTRATION NUMBER: 29,381
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (312)655-1501
10 TELEFAX: (312)655-1501
11 INFORMATION FOR SEQ ID NO: 29:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 26 amino acids
14 TYPE: amino acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: peptide
18 PUBLICATION INFORMATION:
19 AUTHORS: Swenson, T. L.
20 JOURNAL: J. Biol. Chem.
21 VOLUME: 264
22 PAGES: 14318-14326
23 DATE: 1989
24 US-08-934-367-29

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 RDGFLLLQMDGFPPEHLVDFLQSL 26
DB 1 RDGFLLLQMDGFPPEHLVDFLQSL 26

1 RESULT 7
2 US-08-945-289-1
3 Sequence 1, Application US/08945289
4 GENERAL INFORMATION:
5 APPLICANT: Rittershaus, Charles, W.
6 APPLICANT: Thomas, Lawrence J.
7 TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
8 TITLE OF INVENTION: TRANSFER PROTEIN (CTEP) ACTIVITY
9 NUMBER OF SEQUENCES: 9
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Yankwich & Associates
12 STREET: 130 Bishop Allen Drive
13 CITY: Cambridge
14 STATE: Massachusetts
15 COUNTRY: USA
16 ZIP: 02139
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: Windows 95
21 SOFTWARE: Word 97
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/945,289
24 FILING DATE: October 17, 1997
25 CLASSIFICATION: 514
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/432,483
28 FILING DATE: May 1, 1995
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Leon R. Yankwich
31 REGISTRATION NUMBER: 30,237
32 REFERENCE/DOCKET NUMBER: TCS-411.1P US
33 INFORMATION FOR SEQ ID NO: 1:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 26 amino acids
36 TYPE: amino acid

1 TOPOLOGY: linear
2 MOLECULE TYPE: peptide
3 HYPOTHETICAL:
4 ANTI-SENSE:
5 FEATURE:
6 NAME/KEY: Carboxyl terminal 26 amino
7 NAME/KEY: acids of human CTEP
8 LOCATION:
9 PUBLICATION INFORMATION:
10 AUTHORS: Drayna, Dennis, et al.
11 TITLE: Cloning and sequencing of human cholesterol ester transfer cDNA
12 JOURNAL: Nature
13 VOLUME: 327
14 ISSUE:
15 PAGES: 632-634
16 DATE: 18-JUN-1987
17 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
18 US-08-945-289-1

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 RDGFLLLQMDGFPPEHLVDFLQSL 26
DB 1 RDGFLLLQMDGFPPEHLVDFLQSL 26

1 RESULT 8
2 US-09-386-591-29
3 Sequence 29, Application US/09386591
4 GENERAL INFORMATION:
5 APPLICANT: Needleman, Philip
6 APPLICANT: Glenn, Kevin
7 TITLE OF INVENTION: An Immunological Process and Constructs
8 TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
9 TITLE OF INVENTION: Vaccination
10 NUMBER OF SEQUENCES: 52
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Welsh & Katz, Ltd.
13 STREET: 120 South Riverside Plaza, 22nd Floor
14 CITY: Chicago
15 STATE: IL
16 COUNTRY: USA
17 ZIP: 60606
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: Patent Release #1.0, Version #1.30
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/09/386,591
25 FILING DATE:
26 CLASSIFICATION:
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Gamson Ph.D., Edward P.
29 REGISTRATION NUMBER: 29,381
30 REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (312)655-1501
33 TELEFAX: (312)655-1501
34 INFORMATION FOR SEQ ID NO: 29:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 26 amino acids
37 TYPE: amino acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: peptide
41 PUBLICATION INFORMATION:
42 AUTHORS: Swenson, T. L.
43 JOURNAL: J. Biol. Chem.

VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-386-591-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPEHLLVDFLOSLS 26
DB 1 RDGFLLQMDGFPEHLLVDFLOSLS 26

RESULT 9
US-09-387-340-29
Sequence 29, Application US/09387340
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamson, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-387-340-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPEHLLVDFLOSLS 26
DB 1 RDGFLLQMDGFPEHLLVDFLOSLS 26

RESULT 10
US-09-701-588-106
Sequence 106, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
IMMUNOGENS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Marla H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-1580S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 106
US-09-701-588-106

Query Match 100.0%; Score 134; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPEHLLVDFLOSLS 26
DB 1 RDGFLLQMDGFPEHLLVDFLOSLS 26

RESULT 11
US-09-943-334-1
Sequence 1, Application US/09943334
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US/09/943,334
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1

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SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CERP
US-09-943-334-1

Query Match          100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
Db 1 RDGFLLLQMDGFPPEHLVDFLOSL 26

RESULT 12
US-09-943-548-1
Sequence 1, Application US/09943548
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Thomas, Lawrence J. OF CHOLESTERYL ESTER TRANSFER PROTEIN (CERP) ACTIVITY
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CERP) ACTIVITY
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,548
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CERP
US-09-943-548-1

Query Match          100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
Db 1 RDGFLLLQMDGFPPEHLVDFLOSL 26

RESULT 13
PCT-US99-13975B-110
Sequence 110, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL.
TITLE OF INVENTION: EPITOPE AS IMMUNE STIMULATORS FOR SYNTHETIC
TITLE OF INVENTION: PEPTIDE IMMUNOGENS
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Liu
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158P01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
PCT-US99-13975B-110

Query Match          100.0%; Score 134; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
Db 21 RDGFLLLQMDGFPPEHLVDFLOSL 46

RESULT 14
PCT-US99-13975B-111
Sequence 111, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL.
TITLE OF INVENTION: EPITOPE AS IMMUNE STIMULATORS FOR SYNTHETIC
TITLE OF INVENTION: PEPTIDE IMMUNOGENS
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Liu
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158P01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
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; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 PCT-US99-139758-111

Query Match 100.0%; Score 134; DB 1; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.8e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPPEHLVDFLQSLS 26
 |||
 DB 21 RDGFLLQMDGFPPEHLVDFLQSLS 46

RESULT 15
 US-09-701-588-110
 ; Sequence 110, Application US/09701588
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Chang Yi
 ; TITLE OF INVENTION: NOVEL IHRH PEPTIDE
 ; NUMBER OF SEQUENCES: 122
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morgan & Finnegan, L.L.P.
 ; STREET: 345 Park Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10154-0054
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC Windows
 ; SOFTWARE: Word 97
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/701,588
 ; FILING DATE: 29-NOV-2000
 ; CLASSIFICATION: <unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/100,414
 ; FILING DATE: 20-JUNE-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Matla H. Llin
 ; REGISTRATION NUMBER: 29,323
 ; REFERENCE/DOCKET NUMBER: 1151-158US1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-758-4800
 ; TELEFAX: 212-751-6849
 ; INFORMATION FOR SEQ ID NO: 110
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 46 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 110
 US-09-701-588-110

Query Match 100.0%; Score 134; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.8e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPPEHLVDFLQSLS 26
 |||
 DB 21 RDGFLLQMDGFPPEHLVDFLQSLS 46

Search completed: June 18, 2002, 08:11:59
 Job time: 368 sec

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 ; Search time 26.26 Seconds
(without alignments)
83.832 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134
1 RDGFLLQMDGFPPEHLVDFLQSLT 26

Sequence: BLOSUM62

Scoring table: GAPOP 10.0 , Gapext 0.5

Searched: 257105 seqs, 84670655 residues

Total number of hits satisfying chosen parameters: 257.05

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep:*
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7: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	470	5	US-09-446-415B-6
2	53	39.6	11	5	US-09-523-033A-3
3	50	37.3	80	5	US-09-935-625-631
4	50	37.3	80	5	US-09-935-625-19787
5	50	37.3	180	5	US-09-935-625-1494
6	50	37.3	180	5	US-09-935-625-21627
7	50	37.3	183	5	US-09-935-625-592
8	50	37.3	183	5	US-09-935-625-19733
9	50	37.3	628	6	US-10-041-007-22
10	48	35.8	348	7	US-60-360-039-850
11	48	35.8	390	7	US-60-360-039-17233
12	47.5	35.4	434	7	US-60-360-039-13240
13	46	34.3	428	5	US-09-573-655B-740
14	46	34.3	428	5	US-09-573-655B-787
15	46	34.3	754	5	US-09-935-625-557
16	46	34.3	826	5	US-09-935-625-556
17	46	34.3	849	5	US-09-935-625-555
18	45	33.6	442	6	US-10-106-698-6383
19	44	32.8	324	5	US-09-935-625-5733
20	44	32.8	324	5	US-09-935-625-9347
21	44	32.8	352	5	US-09-935-625-5732
22	44	32.8	352	5	US-09-935-625-9346
23	44	32.8	371	5	US-09-935-625-5731
24	44	32.8	371	5	US-09-935-625-9345
25	44	32.8	401	5	US-09-935-625-5737
26	44	32.8	401	5	US-09-935-625-9351

27	44	32.8	435	7	US-60-360-039-17062	Sequence 17062, A
28	44	32.8	444	5	US-09-935-625-5228	Sequence 5228, Ap
29	44	32.8	444	5	US-09-935-625-5736	Sequence 5736, Ap
30	44	32.8	444	5	US-09-935-625-7740	Sequence 7740, Ap
31	44	32.8	444	5	US-09-935-625-9350	Sequence 9350, Ap
32	44	32.8	472	5	US-09-935-625-5227	Sequence 5227, Ap
33	44	32.8	472	5	US-09-935-625-5735	Sequence 5735, Ap
34	44	32.8	472	5	US-09-935-625-7739	Sequence 7739, Ap
35	44	32.8	472	5	US-09-935-625-9349	Sequence 9349, Ap
36	44	32.8	492	5	US-09-935-625-5226	Sequence 5226, Ap
37	44	32.8	492	5	US-09-935-625-7738	Sequence 7738, Ap
38	43.5	32.5	216	7	US-60-360-039-9644	Sequence 9644, Ap
39	43.5	32.5	430	6	US-10-145-415-8	Sequence 8, Appl1
40	43.5	32.5	430	6	US-10-145-415-12	Sequence 12, Appl1
41	43.5	32.5	430	6	US-10-145-415-20	Sequence 20, Appl1
42	43.5	32.5	430	6	US-10-145-415-30	Sequence 30, Appl1
43	43	32.1	80	5	US-09-620-393B-4183	Sequence 4183, Ap
44	43	32.1	90	5	US-09-620-393B-8965	Sequence 8965, Ap
45	43	32.1	99	5	US-09-620-393B-4182	Sequence 4182, Ap

ALIGNMENTS

RESULT 1
US-09-446-415B-6
Sequence 6, Application US/09446415B
GENERAL INFORMATION:
APPLICANT: Beamter, Lesa J.
APPLICANT: Eisenberg, David F.
TITLE OF INVENTION: BACTERIAL/PERMEABILITY-INCREASING PROTEIN:
TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
TITLE OF INVENTION: MOLECULAR MODELING OF RELATED PROTEINS
FILE REFERENCE: 110034US02
CURRENT APPLICATION NUMBER: US/09/446,415B
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 08/879,565
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: 5)
US-09-446-415B-6
Query Match 100.0%, Score 134, DB 5, Length 470;
Best Local Similarity 100.0%, Pred. No. 4.3e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 445 RDGFLLQMDGFPPEHLVDFLQSLT 470
OY 1 RDGFLLQMDGFPPEHLVDFLQSLT 26
DB 445 RDGFLLQMDGFPPEHLVDFLQSLT 470
RESULT 2
US-09-523-033A-3
Sequence 3, Application US/09523033A
GENERAL INFORMATION:
APPLICANT: Kwok, Deborah Y.
APPLICANT: Brostoff, Steven W.
TITLE OF INVENTION: METHOD FOR INCREASING HDL CHOLESTEROL LEVEL
FILE REFERENCE: TCS-428.0 US-1
CURRENT APPLICATION NUMBER: US/09/523,033A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 08/482,454

PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-523-033A-3

Query Match 39.6%; Score 53; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSLS 26
Db 1 HLLVDFLOSLS 11

RESULT 3
US-09-935-625-631
Sequence 631, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 631
LENGTH: 80
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..80
OTHER INFORMATION: Ceres Seq. ID no. 1977520
US-09-935-625-631

Query Match 37.3%; Score 50; DB 5; Length 80;
Best Local Similarity 32.0%; Pred. No. 1.7;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RDGFLIQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFARKDFNLPQHPLESV PNL 41

RESULT 4
US-09-935-625-19787
Sequence 19787, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 19787
LENGTH: 80
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..80
OTHER INFORMATION: Ceres Seq. ID no. 1977520
US-09-935-625-19787

Query Match 37.3%; Score 50; DB 5; Length 80;

Best Local Similarity 32.0%; Pred. No. 1.7;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RDGFLIQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFARKDFNLPQHPLESV PNL 41

RESULT 5
US-09-935-625-1494
Sequence 1494, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 1494
LENGTH: 180
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..180
OTHER INFORMATION: Ceres Seq. ID no. 3058194
US-09-935-625-1494

Query Match 37.3%; Score 50; DB 5; Length 180;
Best Local Similarity 32.0%; Pred. No. 4.1;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RDGFLIQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFARKDFNLPQHPLESV PNL 41

RESULT 6
US-09-935-625-21627
Sequence 21627, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 21627
LENGTH: 180
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..180
OTHER INFORMATION: Ceres Seq. ID no. 3058194
US-09-935-625-21627

Query Match 37.3%; Score 50; DB 5; Length 180;
Best Local Similarity 32.0%; Pred. No. 4.1;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RDGFLIQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFARKDFNLPQHPLESV PNL 41

RESULT 7
US-09-935-625-592
Sequence 592, Application US/09935625

OY 1 RDGFLLOMDFGPEHLLVDF 21
 ||| | : ||| :
 Db 356 RDGLRLSVGLEKPEELMADF 376

RESULT 12

US-60-039-13240
 ; Sequence 13240, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Tongwei
 ; APPLICANT: Chen, Xiandeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 13240
 ; LENGTH: 434
 ; TYPE: PRT
 ; ORGANISM: Aspergillus nidulans
 US-60-039-13240

Query Match

35.4%; Score 47.5; DB 7; Length 434;
 Best Local Similarity 52.4%; Pred. No. 24;
 Matches 11; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

OY 7 LQMDFGPE-HLLVDFLOSLS 26
 ||:| ||| : ||| : |

Db 272 LQLDIGAPEINHVDALKGLT 292

RESULT 13

US-09-573-655B-240
 ; Sequence 240, Application US/09573655B
 ; GENERAL INFORMATION:
 ; APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-0876P
 ; CURRENT APPLICATION NUMBER: US/09/573,655B
 ; CURRENT FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 3281
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 240
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-09-573-655B-240

Query Match

34.3%; Score 46; DB 5; Length 428;
 Best Local Similarity 29.4%; Pred. No. 40;
 Matches 10; Conservative 10; Mismatches 4; Indels 10; Gaps 2;

OY 1 RDGFLLOMDFGPEHLLVDFLOS 24
 ||| : ||| : | : | : |

Db 107 RDNFVVVVELDMDMDFGYQFTFARILSEFIKT 140

RESULT 14

US-09-573-655B-787
 ; Sequence 787, Application US/09573655B
 ; GENERAL INFORMATION:
 ; APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-0876P
 ; CURRENT APPLICATION NUMBER: US/09/573,655B

; CURRENT FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 3281
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 787
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-09-573-655B-787

Query Match

34.3%; Score 46; DB 5; Length 428;
 Best Local Similarity 29.4%; Pred. No. 40;
 Matches 10; Conservative 10; Mismatches 4; Indels 10; Gaps 2;

OY 1 RDGFLLOMDFGPEHLLVDFLOS 24
 ||| : ||| : | : | : |

Db 107 RDNFVVVVELDMDMDFGYQFTFARILSEFIKT 140

RESULT 15

US-09-935-625-557
 ; Sequence 557, Application US/09935625
 ; GENERAL INFORMATION:
 ; APPLICANT: N. ALEXANDROV et al
 ; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
 ; FILE REFERENCE: 2750-1481P
 ; CURRENT APPLICATION NUMBER: US/09/935,625
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 3336
 ; SEQ ID NO 557
 ; LENGTH: 754
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: 1..754
 ; OTHER INFORMATION: Ceres Seq. ID no. 1825655
 US-09-935-625-557

Query Match

34.3%; Score 46; DB 5; Length 754;
 Best Local Similarity 52.2%; Pred. No. 72;
 Matches 12; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

OY 2 DGFLLQMDFGPEHLLVDFLOS 20
 ||| : ||| : | : | : |

Db 260 DDFLLKSVKLPDFEIPENHLYD 282

Search completed: June 18, 2002, 08:07:29
 Job time: 98 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 : Search time 21.83 Seconds
(without alignments)
29,091 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134

Sequence: 1 RDGFLLMDFGPFPHLLVDFLOSL 26

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTRUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	134	100.0	470 3 US-08-879-565-14	Sequence 14, Appl
2	134	100.0	476 4 US-09-171-969-4	Sequence 4, Appl
3	117	87.3	495 4 US-09-171-969-2	Sequence 2, Appl
4	79	59.0	50 4 US-09-171-969-7	Sequence 7, Appl
5	56	41.8	97 1 US-08-844-280-4	Sequence 4, Appl
6	56	41.8	97 4 US-09-006-726-4	Sequence 4, Appl
7	56	41.8	587 1 US-08-844-280-2	Sequence 2, Appl
8	56	41.8	587 4 US-09-006-726-2	Sequence 2, Appl
9	51.5	38.4	353 4 US-09-118-442-6	Sequence 2, Appl
10	51.5	38.4	353 4 US-09-118-442-6	Sequence 2, Appl
11	44.5	33.2	428 1 US-08-050-132A-2	Sequence 6, Appl
12	44.5	33.2	428 3 US-08-750-222A-2	Sequence 2, Appl
13	44.5	33.2	428 3 US-08-815-652B-2	Sequence 2, Appl
14	44.5	33.2	428 3 US-08-254-353A-2	Sequence 2, Appl
15	44.5	33.2	428 5 PCT-US97-0537A-2	Sequence 2, Appl
16	44.5	33.2	428 5 PCT-US95-07084-2	Sequence 2, Appl
17	44	32.8	472 2 US-08-622-168A-2	Sequence 2, Appl
18	44	32.8	472 2 US-08-622-168A-4	Sequence 4, Appl
19	43	32.1	422 2 US-08-403-852D-17	Sequence 17, Appl
20	43	32.1	422 3 US-08-510-646B-18	Sequence 18, Appl
21	43	32.1	422 4 US-09-231-818-17	Sequence 17, Appl
22	42	31.3	387 3 US-08-968-563-37	Sequence 37, Appl
23	42	31.3	387 4 US-08-969-683A-37	Sequence 37, Appl
24	41	30.6	418 4 US-08-795-430-13	Sequence 13, Appl
25	41	30.6	564 4 US-09-211-704A-8	Sequence 8, Appl
26	41	30.6	669 4 US-08-704-711A-3	Sequence 3, Appl
27	40.5	30.2	462 4 US-09-036-987A-18	Sequence 18, Appl

28	40.5	30.2	462 4	US-09-370-700-18	Sequence 18, Appl
29	40	29.9	433 2	US-08-919-624-1	Sequence 1, Appl
30	40	29.9	578 1	US-08-766-014-4	Sequence 4, Appl
31	40	29.9	808 1	US-08-766-014-3	Sequence 3, Appl
32	40	29.9	872 1	US-08-766-014-2	Sequence 2, Appl
33	40	29.9	906 2	US-08-609-230A-9	Sequence 9, Appl
34	40	29.9	907 3	US-08-990-140-4	Sequence 4, Appl
35	40	29.9	907 4	US-09-546-238-4	Sequence 4, Appl
36	40	29.9	940 4	US-08-810-712-7	Sequence 7, Appl
37	39.5	29.5	1174 2	US-08-446-345-36	Sequence 36, Appl
38	39	29.1	268 4	US-08-652-877-4	Sequence 4, Appl
39	39	29.1	268 4	US-08-476-515A-4	Sequence 4, Appl
40	39	29.1	363 1	US-08-484-105-20	Sequence 20, Appl
41	39	29.1	363 1	US-08-484-105-20	Sequence 20, Appl
42	39	29.1	582 2	US-08-899-244-2	Sequence 2, Appl
43	39	29.1	582 4	US-09-224-772-2	Sequence 2, Appl
44	39	29.1	582 4	US-09-227-804-2	Sequence 2, Appl
45	39	29.1	607 4	US-09-211-704A-10	Sequence 10, Appl

ALIGNMENTS

```
RESULT 1
US-08-879-565-14
; Sequence 14, Application US/08879565A
; Patent No. 6093573
; GENERAL INFORMATION:
; APPLICANT: Beamet, Lesa J.
; APPLICANT: Carroli, Stephen F.
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF
; TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN
; FILE REFERENCE: 1103/110340US01
; CURRENT APPLICATION NUMBER: US/08/879,565A
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: cholesterol ester transfer protein (CTP) (Figure
; US-08-879-565-14

Query Match          100.0%; Score 134; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 8.7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLMDFGPFPHLLVDFLOSL 26
Db 445 RDGFLLMDFGPFPHLLVDFLOSL 470

RESULT 2
US-09-171-969-4
; Sequence 4, Application US/09171969
; Patent No. 6284533
; GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: PLASMIN-D-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff, Ltd.
; STREET: 75 State Street, Suite 2300
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1807
; COMPUTER READABLE FORM:
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1  MEDIUM TYPE: Floppy disk
2  COMPUTER: IBM PC compatible
3  OPERATING SYSTEM: PC-DOS/MS-DOS
4  SOFTWARE: Morderefect 6.1
5  CURRENT APPLICATION DATA:
6  APPLICATION NUMBER: US/09/171,969
7  FILING DATE: 01 May 1997 (01.05.97)
8  CLASSIFICATION: 514
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 08/640,713
11 FILING DATE: 01 May 1996 (01.05.96)
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 08/802,967
14 FILING DATE: 21 February 1997 (21.02.97)
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Leon R. Yankwich
17 REGISTRATION NUMBER: 30,237
18 REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
19 INFORMATION FOR SEQ. ID NO. 4:
20 SEQUENCE CHARACTERISTICS:
21     LENGTH: 476 amino acids
22     TYPE: amino acid
23     TOPOLOGY: linear
24 MOLECULE TYPE: peptide
25 HYPOTHEITICAL:
26 ANTI-SENSE:
27 FEATURE:
28 NAME/KEY: amino acid sequence of mature human
29 NAME/KEY: CPTP
30 LOCATION:
31 PUBLICATION INFORMATION:
32 AUTHORS: Dietzma, Dennis, et al.
33 TITLE: Cloning and sequencing of human
34     cholesteryl ester transfer CDNA
35 JOURNAL: Nature
36 VOLUME: 327
37 ISSUE:
38 PAGES: 632 - 634
39 DATE: 18-JUN-1987
40 RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476
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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/640,713
: FILING DATE: 01 May 1996 (01.05.96)
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/802,967
: FILING DATE: 21 February 1997 (21.02.97)
: ATTORNEY/AGENT INFORMATION:
: NAME: Leon R. Yankwich
: REGISTRATION NUMBER: 30,237
: REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 50 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL:
: ANTI-SENSE:
: FEATURE: amino acid sequence of peptide encoded
: FEATURE: by bases 10 to 159 of SEQ ID NO:5
: NAME/KEY:
: LOCATION:
: US-09-171-969-7

Query Match 59.0%; Score 79; DB 4; Length 50;
Best Local Similarity 93.8%; Pred. No. 4.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPPELLVDLFQSL 26
Db 35 GGPPELLVDLFQSL 50

RESULT 5
US-08-844-280-4
: Sequence 4, Application US/08844280
: Patent No. 5747315
: GENERAL INFORMATION:
: APPLICANT: Lawlor, Elizabeth
: TITLE OF INVENTION: No. 5747315el Compounds
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-0939
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/844,280
: FILING DATE: 18-APR-1997
: CLASSIFICATION: ?
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 9607993.4
: FILING DATE: 18-APR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Gilmul, Edward R
: REGISTRATION NUMBER: 38,891
: REFERENCE/DOCKET NUMBER: P31457-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-4478
: TELEFAX: 610-270-5090
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 97 amino acids
: TYPE: amino acid
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: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-844-280-4

Query Match 41.8%; Score 56; DB 1; Length 97;
Best Local Similarity 71.4%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GFLLDMDGFFPH 16
Db 33 GFLLDMDGFFPH 46

RESULT 6
US-09-006-726-4
: Sequence 4, Application US/09006726
: Patent No. 6210940
: GENERAL INFORMATION:
: APPLICANT: Lawlor, Elizabeth J.
: TITLE OF INVENTION: No. 6210940el Compounds
: FILE REFERENCE: P31457-2-D1
: CURRENT APPLICATION NUMBER: US/09/006,726
: EARLIER FILING DATE: 1998-01-14
: EARLIER APPLICATION NUMBER: 08/844,280
: EARLIER FILING DATE: 1997-04-18
: EARLIER APPLICATION NUMBER: US9607993.4
: EARLIER FILING DATE: 1996-04-18
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 97
: TYPE: PPT
: ORGANISM: Streptococcus pneumoniae
: US-09-006-726-4

Query Match 41.8%; Score 56; DB 4; Length 97;
Best Local Similarity 71.4%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GFLLDMDGFFPH 16
Db 33 GFLLDMDGFFPH 46

RESULT 7
US-08-844-280-2
: Sequence 2, Application US/08844280
: Patent No. 5747315
: GENERAL INFORMATION:
: APPLICANT: Lawlor, Elizabeth
: TITLE OF INVENTION: No. 5747315el Compounds
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-0939
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/844,280
: FILING DATE: 18-APR-1997
: CLASSIFICATION: ?
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 9607993.4
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? FILING DATE 18-APR-1996
? ATTORNEY/AGENT INFORMATION:
?
? NAME: Gilmli, Edward R
?
? REGISTRATION NUMBER: 38,891
?
? REFERENCE/DOCKET NUMBER: P31457-2
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: 610-270-4478
?
? TELEFAX: 610-270-5090
?
? TELEX:
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? INFORMATION FOR SEQ ID NO: 2:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 587 amino acids
?
? TYPE: amino acid
?
? STRANDEDNESS: single
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
? OS-08-844-280-2

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Query Match	41.8%;	Score 56;	DB 1;	Length 587;
Best Local Similarity	71.4%;	Pred. No. 0.43;		
Matches	10; conservative	1; Mismatches	3; Indels	0; Gaps 0;

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OY      3  GELLQMDFGPEH 16
          |||  ||: |||  |
Db      510 GELLEAMDYGFPPH 523

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RESULT 8
 US-09-006-726-2
 Sequence 2, Application US/09006726
 Patent No. 6210940
 GENERAL INFORMATION:
 APPLICANT: LAWLOF, Elizabeth J.
 TITLE OF INVENTION: NO. 6210940e1 compounds
 FILE REFERENCE: P31457-2-D1
 CURRENT APPLICATION NUMBER: US/09/006,726
 CURRENT FILING DATE: 1998-01-14
 EARLIER APPLICATION NUMBER: 09/844,280
 EARLIER FILING DATE: 1997-04-18
 EARLIER APPLICATION NUMBER: US9607993.4
 EARLIER FILING DATE: 1996-04-18
 NUMBER OF SEQ. ID NOS: 6
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 2
 LENGTH: 567
 TYPE: PRN
 ORGANISM: *Streptococcus pneumoniae*
 US-09-006-726-2

Query Match	41.8%;	Score 56;	DB 4;	Length 587;
Best Local Similarity	71.4%;	Pred. NO. 0.43;		
Matches 10;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;

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QY      3 GELLQMDFGPPEH 16
          |||  ||: |||  |
Db     510 GELLEAMDYGFPPH 523
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RESULT 9
 US-09-118-442-6
 : Sequence 6, Application US/09118442B
 : Patient No. 6197561
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Martino-Catt, Susan J.
 :
 : APPLICANT: Wang, Hongyu
 :
 : APPLICANT: Beach, Larry R.
 :
 : APPLICANT: Wang, Kun
 :
 : APPLICANT: Bowen, Benjamin A.
 :
 : TITLE OF INVENTION: Genes Controlling Phytate Metabolism In
 :
 : TITLE OF INVENTION: Plants and Uses Thereof
 :
 : FILE REFERENCE: 0706

```

?
? CURRENT APPLICATION NUMBER: 05/09/118,442B
? CURRENT FILING DATE: 1998-07-17
? EARLIER APPLICATION NUMBER: 60/055,446
? EARLIER FILING DATE: 1997-08-11
? EARLIER APPLICATION NUMBER: 60/055,526
? EARLIER FILING DATE: 1997-08-08
? EARLIER APPLICATION NUMBER: 60/053,944
? EARLIER FILING DATE: 1997-07-28
? NUMBER OF SEQ ID NOS: 31
? SOFTWARE: fastSeq for Windows Version 3.0
? SEQ ID NO: 6
? LENGTH: 353
? TYPE: PRT
? ORGANISM: Zea mays
US-09-118-442-6

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Query Match	38.48;	Score 51.5;	DB 4;	length 353;
Best Local Similarity	38.2%;	Pred. No. 1.3;		
Matches 13; Conservative	6;	Mismatches 6;	Indels 9;	Gaps 2.

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QY      1 RDGFLLLQMDGFP-----EHLVLVDLFQSL 26
          |||:::||          ||| ||| |||
Db      303 RDREYVIDMNY-FPGYGMNPGYEHVFTDFLLSLA 335

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RESULT 10
US-09-677-064-6
; Sequence 6, Application US/09677064
; Patent No. 6281224
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; TITLE OF INVENTION: Genes Controlling Phytae Metabolism In
; TITLE OF INVENTION: Plants and Uses Thereof
; FILE REFERENCE: 0706D
; CURRENT APPLICATION NUMBER: US/09/677,064
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/18,442
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays
US-09-677-064-6

```

Query Match	38.48;	Score 51.5;	DB 4;	Length 353;
Best Local Similarity	38.28;	Pred. No. 1.3;		
Matches 13; Conservative	6;	Mismatches 6;	Indels 9;	Gaps 2

QY 1 RDGELLQMDGFP-----EHLVDLFQSL 26
|||::||| |||::|||::|||
Db 303 RDRFYVIDMNY-FPGYGMFGYEHEVFTDFLLSLA 335

```

RESULT 11
US-08-050-132A-2
; Sequence 2, Application US/08050132A
; Patent No. 5661007
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, JOHN M.
; APPLICANT: CELESTE, ANTHONY
; TITLE OF INVENTION: BWP-9 COMPOSITIONS

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:06:29 ; Search time 26.91 Seconds
(without alignments)
110.571 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162

Sequence: 1 COYIKANSKFIGITREFGFPHLLVDFQSLS 31

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	52.5	493	2 A53176	cholesteryl ester
2	85	52.5	493	2 A26941	cholesteryl ester
3	82	50.6	289	2 A38700	cholesteryl ester
4	81	50.0	497	2 I46692	cholesteryl ester
5	70	43.2	1315	1 BTCLTN	tenoxtolysin (EC 3
6	56.5	34.9	458	2 T32634	hypothetical prote
7	54	33.3	310	2 D82199	conserved hypotet
8	52.5	32.4	1071	2 T51224	related to small s
9	52	32.1	348	2 AD0294	2-dehydro-3-deoxy
10	52	32.1	386	2 T28176	hypothetical prote
11	51	31.5	215	2 H97154	sporulation factor
12	51	31.5	274	2 C83497	conserved hypotet
13	51	31.5	289	2 S74959	lipidic acid synthet
14	51	31.5	348	1 ADECH	2-dehydro-3-deoxy
15	51	31.5	348	2 C90930	hypothetical prote
16	51	31.5	348	2 G85778	hypothetical prote
17	51	31.5	348	2 AD0704	3-deoxy-D-arabinoh
18	51	31.5	899	2 T42976	hypothetical prote
19	50	30.9	212	2 B71161	hypothetical prote
20	50	30.9	311	1 C64884	ydo protein - Esc
21	50	30.9	311	2 A85749	hypothetical prote
22	50	30.9	311	2 H90869	hypothetical prote
23	49.5	30.6	406	2 A71109	probable phosphate
24	49	30.2	212	2 C75002	chea histidine kin
25	49	30.2	233	2 T01867	hypothetical prote
26	49	30.2	252	2 T03873	photosystem II oxy
27	49	30.2	254	2 T02873	probable photosyst
28	48.5	29.9	810	2 JC4857	hypoxia-inducible
29	48.5	29.9	813	2 JC5809	hypoxia-inducible

30	48.5	29.9	826	2 138972	hypoxia-inducible
31	48	29.6	213	2 AD2533	hypothetical prote
32	48	29.6	478	2 H90445	hypothetical prote
33	48	29.6	564	2 I64134	D-lactate dehydrog
34	47.5	29.3	252	2 C75007	competence-damage
35	47.5	29.3	395	2 T44512	hypothetical prote
36	47.5	29.3	1298	2 T18360	Os-1p - Neurospora
37	47	29.0	229	1 G64371	conserved hypotet
38	47	29.0	269	2 T15635	hypothetical prote
39	47	29.0	311	2 AC0663	conserved hypotet
40	47	29.0	348	2 I40070	2-dehydro-3-deoxy
41	47	29.0	442	2 A11314	triglycer factor tlg
42	47	29.0	512	2 JC7599	cisplatin(CDP) re
43	47	29.0	611	2 T28171	hypothetical prote
44	47	29.0	758	2 E81140	5-methyltetrahydro
45	47	29.0	1034	2 A95262	probable formate d

ALIGNMENTS

RESULT 1

A53176

cholesteryl ester transfer protein - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C>Date: 12-May-1994 #sequence-revision 12-May-1994 #text-change 07-May-1999

C/Accession: A53176

R:Pepe, W.E.; Renberg, E.F.; Marcotti, K.R.; Melchior, G.W.

A:Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl

asma high density lipoprotein levels.

A:Reference number: A53176; MUID:92031355

A:Accession: A53176

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-493 <FAP>

A:Cross-references: GB:M86343

Query Match

Best Local Similarity 52.5%; Score 85; DB 2; Length 493;

Best Local Similarity 94.1%; Pred. No. 8.7e-05;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 ERGPEHLLVDFQSLS 31

DB 477 DFGPEHLLVDFQSLS 493

cholesteryl ester transfer protein precursor - human

A26941

C:Species: Homo sapiens (man)

C>Date: 19-Nov-1998 #sequence-revision 19-Nov-1998 #text-change 21-Jul-2000

C/Accession: A26941

R:Dreyna, D.; Darnaglin, A.S.; McLean, J.; Henzel, W.; Kohr, W.; Fielding, C.; Lawn, R

Mature 327, 632-634, 1987

A:Title: Cloning and sequencing of human cholesteryl ester transfer protein cDNA.

A:Reference number: A26941; MUID:87258172

A:Accession: A26941

A:Molecule type: mRNA

A:Residues: 1-493 <DRA>

A:Cross-references: EMBL:M30185; NID:g180259; PIDN:AA51977.1; PIR:g180260

C:Genetics:

A:Gene: GDB:CEMP

A:Cross-references: GDB:119773; OMIM:118470

A:Map position: 16q13-16q13

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-493/Product: cholesteryl ester transfer protein #status predicted <MAT>

Query Match

Best Local Similarity 52.5%; Score 85; DB 2; Length 493;

Best Local Similarity 94.1%; Pred. No. 8.7e-05;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSLS 31
:|||||:|||||:|||||
Db 477 DFGPEHLVDFLOSLS 493

RESULT 3
A38700
cholesteryl ester transfer protein - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 05-Nov-1999
C:Accession: A38700
R:Jiang, X.C.; Moulin, P.; Quinet, E.; Goldberg, I.J.; Yacoub, L.K.; Agellon, L.B.; Comp
J. Biol. Chem. 266, 4631-4639, 1991
A:Title: Mammalian adipose tissue and muscle are major sources of lipid transfer protein
A:Reference number: A38700; MUID:91154277
A:Accession: A38700
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-289 <JIA>
A:Cross-references: GB:M63992; NID:q191342; PIDN:AAA37066.1; PID:q191343
A>Note: the authors translated the codon CTG for residue 68 as Gly, GGC for residue 69 as
as Ser, and TTC for residue 267 as Ser

Query Match 50.6%; Score 82; DB 2; Length 289;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSLS 31
:|||||:|||||:|||||
Db 273 DFGPEHLVDFLOSLS 289

RESULT 4
146692
cholesteryl ester transfer protein - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46692
R:Nagashima, M.; McLean, J.W.; Lawm, R.M.
J. Lipid Res. 29, 1643-1649, 1988
A:Title: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer prote
A:Reference number: I46692; MUID:89215620
A:Accession: I46692
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-497 <NMG>
A:Cross-references: GB:M27486; NID:q530906; PIDN:AAA31199.1; PID:q530907
A:Gene: CETP

Query Match 50.0%; Score 81; DB 2; Length 497;
Best Local Similarity 88.2%; Pred. No. 0.00035;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSLS 31
:|||||:|||||:|||||
Db 481 DFGPEHLVDFLOSLS 497

RESULT 5
BTCLTN
tetroxylisin (EC 3.4.24.68) precursor - Clostridium tetani
N:Alternate names: tetanus neurotoxin
C:Species: Clostridium tetani
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
C:Accession: A23689; A25757; A25194; B25194; S69348; S09364
R:Eisell, U.; Jarusch, W.; Goretzki, K.; Henschel, A.; Engels, J.; Weller, U.; Hudel, M.
EMBO J. 5, 2495-2502, 1986
A:Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botu
A:Reference number: A23689; MUID:87053814

A:Accession: A25689
A:Molecule type: DNA
A:Residues: 1-1315 <EIS>
A:Cross-references: GB:X04436; NID:q40769; PIDN:CAA2803.1; PID:q40770
R:Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A:Title: The complete nucleotide sequence of tetanus toxin.
A:Reference number: A25757; MUID:87040747
A:Accession: A25757
A:Molecule type: DNA
A:Residues: 1-1315 <FAI>
A:Cross-references: GB:X06214; NID:q40773; PIDN:CAA29564.1; PID:q40774
R:Experimental source: strain CN3911
R:Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
J. Bacteriol. 165, 21-27, 1986
A:Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C 1
A:Reference number: A25194; MUID:86085672
A:Accession: A25194
A:Molecule type: DNA
A:Residues: 743-1315 <FA2>
A:Cross-references: GB:M12739; NID:q144920; PIDN:AAA23282.1; PID:q144921
A:Accession: B25194
A:Molecule type: protein
A:Residues: 865-894 <FA3>
R:Matluda, M.; Iel, D.L.; Sugimoto, N.; Ozutsu, K.; Okabe, T.
Infect. Immun. 57, 3588-3593, 1989
A:Title: Isolation, purification, and characterization of fragment B, the NH-2-termin
A:Reference number: A60759; MUID:90035436
A:Accession: A60759
A:Molecule type: protein
A:Residues: 461-475 <MAT>
R:Demotz, S.; Lanzavecchia, L.; Eisell, U.; Niemann, H.; Wildmann, C.; Corradin, G.
J. Immunol. 142, 394-402, 1989
A:Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A:Reference number: J50098; MUID:88093918
A:Contents: annotation; epitope region
R:Schiaffo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta,
Nature 359, 832-835, 1992
A:Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteo
A:Reference number: S27125; MUID:93063293
A:Contents: annotation
R:de Filippis, V.; Vangelista, L.; Schiaffo, G.; Tonello, F.; Montecucco, C.
Eur. J. Biochem. 229, 61-69, 1995
A:Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotox
A:Reference number: S69348; MUID:95262688
A:Accession: S69348
A:Molecule type: protein
A:Residues: 2-31 <DEF>
C:Comment: The source of this protein was an extrachromosomal plasmid.
C:Comment: The precursor is cleaved by endogenous proteinase activity to form light (C
dual chains are not toxic when separated). The amino end of the heavy chain (fragment
C:Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to gang
C:Comment: This potent neurotoxin binds to peripheral neuronal synapses, its internal
presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of
C:Function:
A:Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in syn
A:Superfamily: tetanus toxin
C:Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F:2-457/Product: tetroxylisin light chain (fragment A) #status predicted <TTT>
F:461-1315/Product: tetroxylisin heavy chain (fragment B.C) #status experimental <TTT>
F:461-864/Domain: channel forming (fragment B) #status predicted <TTT>
F:865-1315/Domain: ganglioside binding (fragment C) #status predicted <TTT>
F:233-237/Binding site: zinc (His) #status predicted
F:234/Active site: Glu #status predicted

Query Match 43.2%; Score 70; DB 1; Length 1315;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYTKANSKRGITTE 15
:|||||:|||||:|||||
Db 830 QYTKANSKRGITTE 843

RESULT 6
T32634
hypothetical protein F4268.9 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C:Accession: T32634
R:Gatung, S.; Holmes, A.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of *C. elegans* cosmid F4268.
A:Reference number: Z21203
A:Accession: T32634
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-458 <GAT>
A:Cross-references: EMBL:AF038618; PDB:AA692068.1; GSPDB:GN00022; CESP:F4268.9
A:Experimental source: strain Bristol N2; clone F4268
C:Genetics:
A:Gene: CESP:F4268.9
A:Map position: 4
A:Introns: 119/1; 171/3; 227/1; 313/3; 398/1
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F4268.9

Query Match 34.9%; Score 56.5; DB 2; Length 458;
Best Local Similarity 40.0%; Pred. No. 1.6;
Matches 12; Conservative 6; Mismatches 9; Indels 3; Gaps 1;
QY 1 CQYKANSKFGITGFGPEHLVDFL 30
| | | | | : : : : :
Db 232 CNYKNNKYLGRKSSGTHQ---LDFLOKL 258

RESULT 7
D82199
conserved hypothetical protein VC1432 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82199
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chaudson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Olin, H.; Dragol, I.; Sellers, F.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: M01D:20406833
A:Accession: D82199
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <HEI>
A:Cross-references: GB:AE004222; GB:AE003852; NID:99655930; PDB:AAF94589.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1432
A:Map position: 1
C:Superfamily: conserved hypothetical protein M1157

Query Match 33.3%; Score 54; DB 2; Length 310;
Best Local Similarity 64.3%; Pred. No. 2.5;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 17 GPEHLVDFL 30
| | | | | : : : : :
Db 84 GPEHLVDFL 97

RESULT 8
T51224
related to small s protein [imported] - *Neurospora crassa*
N:Alternate names: protein B24M2.200
C:Species: *Neurospora crassa*
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000

C:Accession: T51224
R:Schulze, U.; Align, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: T51224
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1071 <SCH>
A:Cross-references: EMBL:AL390354; GSPDB:GN00116; NCSP:B24M2.200
C:Genetics:
A:Gene: NCSP:B24M2.200
A:Map position: 6
A:Introns: 954/1; 981/2

Query Match 32.4%; Score 52.5; DB 2; Length 1071;
Best Local Similarity 40.0%; Pred. No. 17;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 1;
QY 1 CQYKA---NSKFGITGFGPEHLVDFL 27
| | | | | : : : : :
Db 659 CPWIKQDHNSLTLTKSGFPEHSDIDFI 688

RESULT 9
AD0294
2-dehydro-3-deoxyphosphopentose aldolase (EC 4.1.2.15) [imported] - *Yersinia pestis*
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD0294
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
H.; M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barral
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; M01D:21470413; PMID:11586360
A:Accession: AD0294
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <KUR>
A:Cross-references: GB:AL590842; PDB:CA021216.1; PID:915980406; GSPDB:GN00175
C:Genetics:
A:Gene: arch
A:Superfamily: phospho-2-dehydro-3-deoxyphosphopentose aldolase
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 32.1%; Score 52; DB 2; Length 348;
Best Local Similarity 64.3%; Pred. No. 5.8;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 13 ITGFGPEHLVDF 26
| | | | | : : : : :
Db 253 LRFEDLPEHLVDF 265

RESULT 10
T28176
hypothetical protein ORF15 - *Melanoplus sanguinipes entomopoxvirus* (strain Tuscon)
C:Species: *Melanoplus sanguinipes entomopoxvirus*
A:Variety: isolate Tuscon
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28176
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of *Melanoplus sanguinipes entomopoxvirus*.
A:Reference number: Z20484; M01D:99102612
A:Accession: T28176
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-386 <AF0>
A:Cross-references: EMBL:AF063866; NID:94049647; PDB:AA097854.1; PID:94049694

A: Experimental source: isolate Tuscon
C: Genetics:
A: Note: MSV015

Query Match 32.1%; Score 52; DB 2; Length 386;
Best Local Similarity 55.0%; Pred. No. 6.5;
Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 IKANSKFIGITGEPPEHL 23

DB 232 IKLNCFCCITDFKLELV 251

RESULT 11

H97154
sporulation factor spoIIM, uncharacterized membrane protein [imported] - Clostridium ac
C: Species: Clostridium acetobutylicum
C: Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C: Accession: H97154
R: Mulling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4836, 2001
A: Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A: Reference number: A96900; MUID: 21359325; PMID: 21359325
A: Accession: H97154
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-215 <KAN>
A: Cross-references: GB:AE001437; PIDN:AAK80027.1; PID: g15025055; GSPDB:GN00168
A: Experimental source: Clostridium acetobutylicum ATCC824
C: Genetics:
A: Gene: CAC2068

Query Match 31.5%; Score 51; DB 2; Length 215;
Best Local Similarity 40.9%; Pred. No. 4.8;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 10 FIGITGEPPEHLVDLOSLS 31

DB 87 FLGITMTGIVPILIDLLKGS 108

RESULT 12
C83497
conserved hypothetical protein PA1192 [imported] - Pseudomonas aeruginosa (strain PA01)

C: Species: Pseudomonas aeruginosa
C: Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C: Accession: C83497

R: Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
Edman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A: Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A: Reference number: AB2950; MUID: 2043737
A: Accession: C83497
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-274 <STO>

A: Cross-references: GB:AE004549; GB:AE004091; NID: g9947110; PIDN: AAG04581.1; GSPDB: GN001
A: Experimental source: strain PA01
C: Genetics:
A: Gene: PA1192
C: Superfamily: conserved hypothetical protein MJ1157

Query Match 31.5%; Score 51; DB 2; Length 274;
Best Local Similarity 57.1%; Pred. No. 6.3;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 17 GPEHMLVDLOSLS 30

5

DB 76 GPEHMLPEYLKSI 89

RESULT 13

S74959

lipidic acid synthetase (EC 2.8.1.-) 1 - Synechocystis sp. (strain PCC 6803)

N: Alternate names: protein slr1598

C: Species: Synechocystis sp.

A: Variety: PCC 6803 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C: Date: 25-Apr-1997

C: Accession: S74959

R: Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A: Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

S

A: Reference number: S74322; MUID: 97061201

A: Accession: S74959

A: Status: nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-289 <KAN>

A: Cross-references: EMBL: D90902; GB: AB001339; NID: g1652027; PIDN: BAA1699.1; PID: g165

A: Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C: Genetics:

A: Gene: lrpA-1

A: Start codon: GTG

C: Function:

A: Description: catalyzes sulfur insertion as one step in the biosynthesis of lipote a

A: Pathway: lipote biosynthesis

C: Superfamily: Lipote acid synthase

C: Keywords: Lipote biosynthesis; sulfurtransferase

Query Match 31.5%; Score 51; DB 2; Length 289;
Best Local Similarity 31.6%; Pred. No. 6.7;
Matches 12; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

OY 2 QYIKANSKFIGITGEPPEHL-----LYDFLOSLS 31

DB 230 QYIDPSQKHLGKVEFVPEDPVWRIGESIGFLQVYS 267

RESULT 14

ADECH

2-dehydro-3-deoxyphosphoheptone aldolase (EC 4.1.2.15) (TTP-sensitive) - Escherich

N: Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; phospho-2-de

C: Species: Escherichia coli

C: Date: 22-May-1981 #sequence_revision 31-Oct-1997 #text_change 18-Jun-1999

C: Accession: H64928; J01131; A31384; A01107

R: Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A: Title: The complete genome sequence of Escherichia coli K-12.

A: Reference number: A64720; MUID: 97426617

A: Accession: H64928

A: Status: nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-348 <BIAT>

A: Cross-references: GB:AE000265; GB:U00096; NID: g2367122; PIDN: AAC74774.1; PID: g17879

A: Experimental source: strain K-12, substrain MG1655

R: Hudson, G.S.; Kelios, P.; Davidson, B.E.

Gene 102, 87-91, 1991

A: Title: Two promoters control the *aroH* gene of Escherichia coli.

A: Reference number: J01131; MUID: 91323737

A: Accession: J01131

A: Molecule type: DNA

A: Residues: 1332, 'S', 334-348 <HUD>

A: Cross-references: GB: M38265; NID: g145376; PIDN: AAA23497.1; PID: g145378

R: Ray, J.M.; Yanofsky, C.; Baerle, R.

J. Bacteriol. 170, 5500-5506, 1988

A: Title: Mutational analysis of the catalytic and feedback sites of the tryptophan-se

A: Reference number: A31384; MUID: 89053867

A: Accession: A31384

A:Molecule type: DNA
 A:Residues: 1-122, 'A', 124-202, 204, 'Q', 206-332, 'RQ', 335-348 <RAY>
 A:Cross-references: GB:J04221
 R:Zurawski, G.; Gunsalus, R.P.; Brown, K.D.; Yanofsky, C.
 J. Mol. Biol. 145, 47-73, 1981
 A:Title: Structure and regulation of *aroH*, the structural gene for the tryptophan-repress
 A:Reference number: A01107; MUID:81267314
 A:Accession: A01107
 A:Molecule type: DNA
 A:Residues: 1-36, 231-332, 'RQ', 335-348 <ZUR>
 A:Cross-references: GB:J01592; GB:J01593
 C:Genetics:
 A:Gene: *aroH*
 A:Map position: 37 min
 C:Function:
 A:Description: aldehyde-lyase; carbon-carbon lyase; this is one of the DAHP synthases th
 ic acid-7-phosphate
 A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
 A>Note: the first reaction in aromatic amino acid biosynthesis
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
 C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; shik

Query Match 31.5%; Score 51; DB 1; Length 348;
 Best Local Similarity 75.0%; Pred. No. 8.2;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 EFGFPEHLVDF 26
 11 11111111
 DB 254 EFDLPEHLVDF 265

RESULT 15
 C90930
 Hypothetical protein ECs2411 [Imported] - Escherichia coli (strain O157:H7, substrain R)
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence=revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: C90930
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shida, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: C90930
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <RAY>
 A:Cross-references: GB:BA00007; PIDN:BA035834.1; PID:q13361878; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: ECs2411
 C:Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase

Query Match 31.5%; Score 51; DB 2; Length 348;
 Best Local Similarity 75.0%; Pred. No. 8.2;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 EFGFPEHLVDF 26
 11 11111111
 DB 254 EFDLPEHLVDF 265

Search completed: June 18, 2002, 08:06:30
 Job time: 39 sec

100

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:13:08 ; Search time 13.5 Seconds
(without alignments)
88,912 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYIKANSKFIGITFEFGPEHLVDFLOSLIS 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	52.5	493	1 CERP_HUMAN	P11597 homo sapien
2	85	52.5	493	1 CERP_MACPA	P17896 macaca fasc
3	82	50.6	289	1 CERP_MESAU	P25914 mesocricetu
4	81	50.0	497	1 CERP_RABIT	P22687 coryctolagus
5	70	43.2	1314	1 TERY_CLOTE	P04958 clostridium
6	52	32.1	313	1 YDAO_HAELN	P37184 haemophilus
7	51	31.5	289	1 LIP1_SYNY3	P72980 synechocyst
8	51	31.5	348	1 AROH_ECOLI	P00887 escherichia
9	50	30.6	311	1 YDAO_ECOLI	P76087 escherichia
10	49.5	30.9	406	1 Y640_PYRHO	P58374 pyrococcus
11	49	30.2	935	1 AD22_XENLA	P42596 xenopus lae
12	48.5	29.9	832	1 HIRA_MOUSE	P61221 mus musculu
13	48.5	29.9	826	1 HIRA_MOUSE	P16865 homo sapien
14	48	29.6	204	1 PYRC_SERNA	P39331 serralia ma
15	48	29.6	564	1 LDHD_HAELN	P45295 haemophilus
16	48	29.6	626	1 MP44_FOWPV	P31500 fowipox vir
17	48	29.6	911	1 MAN1_HUMAN	P39248 homo sapien
18	47.5	29.3	252	1 YD05_PYPAB	P39495 pyrococcus
19	47	29.0	229	1 Y575_METJA	P57995 methanococ
20	47	29.0	348	1 AROH_BUCAP	P46245 buchnera ap
21	47	29.0	442	1 TIC_TREPA	P08359 treponema p
22	47	29.0	757	1 METE_PASKO	P37883 streptococ
23	47	29.0	758	1 METE_METMB	P37883 streptococ
24	46.5	28.7	394	1 GATP_MOUSE	P03242 nelssetia m
25	46.5	28.7	591	1 MP44_VACCA	P23336 mus musculu
26	46.5	28.7	591	1 MP44_VACCC	P23336 mus musculu
27	46.5	28.7	591	1 MP44_VACCC	P23336 mus musculu
28	46.5	28.7	591	1 MP44_VACCC	P23336 mus musculu
29	46.5	28.7	591	1 MP44_VACCC	P23336 mus musculu
30	46	28.4	816	1 SUS3_ORYSA	P16713 vaccinia vl
31	46	28.4	314	1 HEM9_CHLTR	P32991 variola vir
32	46	28.4	516	1 LBE9_MPVAC	P04402 chrysa sativ
33	46	28.4	899	1 V120_HSVSA	P1465 autographa t

34	45	27.8	348	1 AROH_BUCAI	P57224 buchnera ap
35	45	27.8	429	1 GDP2_HUMAN	O9AK05 homo sapien
36	45	27.8	590	1 MP44_TYDV	O9AK05 homo sapien
37	45	27.8	648	1 KAPC_DICDI	P34099 dictyostel
38	45	27.8	756	1 METE_HAELN	P45331 haemophilus
39	45	27.8	886	1 LEUR_YEAST	P08638 saccharomyc
40	44.5	27.5	376	1 Y550_BUCAI	P57615 buchnera ap
41	44.5	27.5	640	1 UL35_HCMVA	P16766 human cytom
42	44	27.2	70	1 ESM6_DROME	O97179 drosophila
43	44	27.2	478	1 YARR_RHISN	P55641 rhizobium s
44	44	27.2	870	1 PAS1_HUMAN	O99814 homo sapien
45	44	27.2	874	1 PAS1_MOUSE	P97481 mus musculu

ALIGNMENTS

RESULT 1
ID CERP_HUMAN STANDARD: PRT: 493 AA.
AC P11597; Q13987; Q13988;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
DE 1)
GN CERP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
[1]
RP MEDLINE-67258172; PubMed-3600759.
RX Drayna D., Jarnagin A.S., McLean J., Henzel W., Kohr W., Fielding C.,
Lawn R.;
RT "Cloning and sequencing of human cholesteryl ester transfer protein
RT cDNA.";
RL Nature 327:632-634(1987).
[2]
RP MEDLINE-90241928; PubMed-2334701;
RX Agellon L.B., Quinet E.M., Gillette T.G., Drayna D.T., Brown M.L.,
Tall A.R.;
RL "Organization of the human cholesteryl ester transfer protein gene.";
[3]
RP MEDLINE-97112972; PubMed-8943225;
RX Oliveira C.F.O., Chouinard R.A., Agellon L.B., Bruce C., Ma L.,
Walsh A., Breslow J.L., Tall A.R.;
RL "Human cholesteryl ester transfer protein gene proximal promoter
RL contains dietary cholesterol positive responsive elements and mediates
RL expression in small intestine and periphery while predominant liver
RL and spleen expression is controlled by 5'-distal sequences. Cis-acting
RL sequences mapped in transgenic mice.";
RL J. Biol. Chem. 271:31831-31838(1996).
[4]
RP MEDLINE-97473500; PubMed-9332354;
RX Williams S., Hayes L., Eisenboss U., Williams A., Andre C.,
Abramson R., Thompson J.F., Milos P.M.;
RL "Sequencing of the cholesteryl ester transfer protein 5' regulatory
RL region using artificial transposons.";
RL Gene 197:101-107(1997).
[5]
RP MEDLINE-94013514; PubMed-8408659;
RX MEDLINE-94013514; PubMed-8408659;


```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91154277; PubMed-1999438;
RA Jang X.C., Moulin P., Guinet E., Goldberg I.J., Yacoub I.K.,
RA Agellon L.B., Compton D., Schritzer-Polokoff R., Tall A.R.;
RT "Mammalian adipose tissue and muscle are major sources of lipid
transfer protein mRNA."
RL J. Biol. Chem. 266:4631-4639(1991).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
DR EMBL: M63992; AAA37066.1; -
DR PIR: A38700; A38700
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP; 1.
DR Pfam: PF02886; LBP_BPI_CETP_C; 1.
DR SMART: SM00329; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; PARTIAL.
KW Lipid transport; Cholesterol metabolism; Glycoprotein.
FT NON_TER 1
FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 289 AA; 32330 MW; CA91A06D83927747 CRC64;
SO
Query Match 50.6%; Score 82; DB 1; Length 289;
Best Local Similarity 88.2%; Pred. No. 4,7e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 15 EFGPEHLVDFLOSLS 31
Db 273 DFGPEHLVDFLOSLS 289
RESULT 4
CETP_RABIT STANDARD; PRT; 497 AA.
AC P22687;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
DE 1) (Fragment).
GN CETP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89215620; PubMed-3244015;
RA Nagashima M., McLean J.W., Lawn R.M.;
RT "Cloning and mRNA tissue distribution of rabbit cholesteryl ester
transfer protein."
RL J. Lipid Res. 29:1643-1649(1988).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----

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CC -----
DR EMBL: M27486; AAA31199.1; -
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP; 1.
DR Pfam: PF02886; LBP_BPI_CETP_C; 1.
DR SMART: SM00328; BPI1; 1.
DR SMART: SM00329; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; 1.
KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 2 497
FT CARBOHYD 89 89 CHOLESTERYL ESTER TRANSFER PROTEIN.
FT CARBOHYD 99 99 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 497 AA; 54513 MW; E82944E1821D0332 CRC64;
SO
Query Match 50.0%; Score 81; DB 1; Length 497;
Best Local Similarity 88.2%; Pred. No. 0.00012;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 15 EFGPEHLVDFLOSLS 31
Db 481 DFGPEHLVDFLOSLS 497
RESULT 5
TETX_CLOTE STANDARD; PRT; 1314 AA.
AC P04958;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tetanus toxin precursor (Ec 3.4.24.68) (Tentoxylysin).
DE Tetanus toxin tetanl.
OS Clostridium tetani.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87053614; PubMed-3536478;
RA Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J.,
RA Weller U., Jarausch W., Habermann E., Niemann H.;
RT "Tetanus toxin: Primary structure, expression in E. coli, and
RT homology with botulinum toxins."
RL EMBO J. 5:2495-2502(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-CN3911;
RX MEDLINE-87040747; PubMed-3774547;
RA Fairweather N.F., Lyness V.A.;
RT "The complete nucleotide sequence of tetanus toxin."
RL Nucleic Acids Res. 14:7809-7812(1986).
RN [3]
RP SEQUENCE OF 742-1314 FROM N.A.
RX MEDLINE-86085672; PubMed-3510187;
RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;
RT "Cloning, nucleotide sequencing, and expression of tetanus toxin
RT fragment C in Escherichia coli."
RL J. Bacteriol. 165:21-27(1986).
RN [4]

```

RP PARTIAL SEQUENCE. AND DISULFIDE BONDS.
 RA MEDLINE-90201034; PubMed-2108021;
 RA Krieglstein K., Henschel A., Weller U., Habermann E.;
 RT Arrangement of disulfide bridges and positions of sulfhydryl groups
 in tetanus toxin.";
 RL Eur. J. Biochem. 188:39-45(1990).
 RN [5]
 RP PARTIAL SEQUENCE.
 RX MEDLINE-92037649; PubMed-1935979;
 RA Krieglstein K.G., Henschel A.H., Weller U., Habermann E.;
 RT "Limited proteolysis of tetanus toxin. Relation to activity and
 identification of cleavage sites.";
 RL Eur. J. Biochem. 202:41-51(1991).
 RN [6]
 RP IDENTIFICATION AS ZINC-PROTEASE.
 RX MEDLINE-93010948; PubMed-1396558;
 RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
 RA Montecucco C.;
 RT "Tetanus toxin is a zinc protein and its inhibition of
 neurotransmitter release and protease activity depend on zinc.";
 RL Nature 359:832-835(1992).
 RN [7]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE-93063293; PubMed-1331807;
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RA Dasgupta B.R., Montecucco C.;
 RT "Tetanus and botulinum-B neurotoxins block neurotransmitter release
 by proteolytic cleavage of synaptobrevin.";
 RL Nature 359:832-835(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ÅNGSTRÖMS) OF 874-1314.
 RX MEDLINE-97475217; PubMed-934741;
 RA Umland T.C., Wingerl L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
 RA Sax M.;
 RT "Structure of the receptor binding fragment HC of tetanus
 neurotoxin.";
 RL Nat. Struct. Biol. 4:788-792(1997).
 CC -1- FUNCTION: "TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77
 BOND OF SYNAPTOSOMAL-2."
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-|-PHE-77 BOND IN
 SYNAPTOSOMAL-2.
 CC -1- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
 YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
 AND ARE NON-TOXIC AFTER SEPARATION.
 CC -1- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
 GANGLIOSIDE RECEPTORS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
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 CC -----
 DR EMBL: X04436; CAA28033.1; -
 DR EMBL: M12739; AAA23282.1; -
 DR EMBL: X06214; CAA29564.1; -
 DR PIR: A25689; BRCTNW
 DR PDB: 1AF9; 29-APR-98.
 DR PDB: 1ABD; 14-OCT-98.
 DR MEROPS: M27.001; -
 DR InterPro: IPR000139; Bontoxilysin.
 DR InterPro: IPR000130; Zn_MTPeptide.
 DR Pfam: PF01742; Peptidase_M27; 1.
 DR PRINTS: PR00760; BONTOXILYSIN.
 DR ProDom: PD001963; Bontoxilysin; 1.

DR PROSITE: PS00142; ZINC-PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
 RN 3D-structure.
 FT INT. MET 0
 FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.
 FT CHAIN 1314 TETANUS TOXIN HEAVY CHAIN.
 FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACN SITE 233 233 BY SIMILARITY.
 FT METAL 236 236 ZINC (CATALYTIC) (BY SIMILARITY).
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 669 689 POTENTIAL.
 FT DISULFID 438 466 INTERCHAIN.
 FT DISULFID 1076 1092
 SQ SEQUENCE 1314 AA; 150550 MW; 134C3657133EF81D CRC64;
 Query Match 43.2%; Score 70; DB 1; Length 1314;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYKANSKFIGITE 15
 Db 829 QYKANSKFIGITE 842
 |||||||||||||
 YDAO_HAEIN
 ID YDAO_HAEIN STANDARD; PRT; 313 AA.
 AC Q57184; 005059;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein H11371.1.
 GN H11371.1.
 OS Haemophilus influenzae.
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus.
 CC NCBI_TaxId=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE-95350630; PubMed-7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Lin L.-I., Glodek A., Kelley J.M.,
 RA Wetlihan J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen B.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Ghem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP REVISIONS.
 RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO E.COLI YDAO.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U32817; AAC33019.1; -
 DR TIGR: H11371.1; -
 DR InterPro: IPR000541; UPR0021.
 DR Pfam: PF01171; UPR0021; 1.
 KW Hypothetical protein; Complete proteome.

```

SQ  SEQUENCE      313 AA:      35703 MW:      646717CB802EF7252 CRR64;

Query Match      32.1%, Score 52; DB 1; Length 313;
Best Local Similarity 57.1%; Pred. No. 1.8;
Matches      8; Conservative      5; Mismatches      1; Indels      0; Gaps      0;

OY      17 GPPEHLIVDFQLSL 30
      |||||:|:|:|:|:|:|:
DB      86 GPPEHLVPEYLESI 99

RESULT      7
LIPI_SYNY3
ID LIPI_SYNY3      STANDARD:      PRT;      289 AA.
AC P72980;
DT 15-JUL-1998 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable lipoteic acid synthetase 1 (LIP-SYN 1) (lipoteic synthase 1).
GN LIPI1 OR SLR1598.
OS Synechocystis sp. (Strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_Taxid=1148;
RN      [1]
RP      SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231.
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kikuchi T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naro K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res.3:109-136(1996).
CC -1- FUNCTION: SYNTHESIS OF ALPHA-(+)-LIPOTEIC ACID. IT MAY BE INVOLVED
CC IN THE SULFUR INSERTION CHEMISTRY IN LIPOATE BIOSYNTHESIS (BY
CC SIMILARITY).
CC -1- PATHWAY: LIPOATE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL, D90902; BAA16999.1; -
DR InterPro: IPR003698; Lipoteic_synth.
DR Pfam: PF02546; Lipoteic_synth; 1.
DR Iron_sulfur; Complete proteome.
KW METAL      60
KW METAL      60
FT METAL      64
FT METAL      64
FT METAL      67
FT METAL      67
SQ SEQUENCE      289 AA: 32485 MW: EE57E8482AC3379 CRG64;

Query Match      31.5%; Score 51; DB 1; Length 289;
Best Local Similarity 31.6%; Pred. No. 2.4;
Matches      12; Conservative      7; Mismatches      11; Indels      8; Gaps      1;

OY      2 QYIRANSKFIGITEFGPEHL-----LVDFQLSL 31
      ||::|:|:|:|:|:|:|:
DB      230 QYLPSOKHGLGVEKFTYPRDFQDMRYIGSTIGFLQVYS 267

RESULT      8
AROH_ECOLI

```

AD AROH_ECOLI1 STANDARD; PRT; 348 AA.

OC P00887; P783301.

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Phospho-2-dehydro-3-deoxyheptonate aldolase, Trp-sensitive

DE (EC 4.1.2.13) (Phospho-2-keto-3-deoxyheptonate aldolase) (DAHP

DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).

DE AROH OR B1704.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_taxid:562;

XX [1]

RP SEQUENCE FROM N.A.

RM MEDLINE=9133737; PubMed=1677907;

RX Hudson G.S., Relloso P., Davidson B.E.;

RA "Two promoters control the aroH gene of Escherichia coli.";

RL Gene 102:87-91(1991).

RN [2]

RP SEQUENCE FROM N.A.

RM MEDLINE=89053867; PubMed=2903857;

RX Ray J.M., Yanofsky C., Baerle R.;

RA "Mutational analysis of the catalytic and feedback sites of the

RT tryptophan-sensitive 3-deoxy-D-arabino-heptulosonate-7-phosphate

RT synthase of Escherichia coli.";

RL J. Bacteriol. 170:5500-5506(1988).

RN [3]

RP SEQUENCE FROM N.A.

RM MEDLINE=97251357; PubMed=9097039;

RX Kasai H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,

RA Nakano H., Koshimoto K., Kimura S., Kitakawa M., Kitagawa M.,

RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

RA Nakade S., Nakamura Y., Nishimatsu S., Nishio Y., Oshima T., Saito N.,

RA Stampel G., Seki Y., Sivasubramanian S., Tagami H., Takeda J.,

RA Takeuchi K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;

RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 28.0-40.1 min region on the linkage map.";

RL DNA Res. 3:363-377(1996).

RN [5]

RP SEQUENCE OF 1-36 AND 232-348 FROM N.A.

RX MEDLINE=81267314; PubMed=6167722;

RA Zurawski G., Gunsalus K.P., Brown K.D., Yanofsky C.;

RA "Structure and regulation of aroH, the structural gene for the

RT tryptophan-repressible 3-deoxy-D-arabino-heptulosonate

RT acid-7-phosphate synthetase of Escherichia coli.";

RL J. Mol. Biol. 145:47-73(1981).

CC -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)

CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-

CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).

CC -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-

CC phosphate + phosphate -> phosphoenolpyruvate + D-erythrose 4-

CC phosphate + H(2)O.

CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN

CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).

CC -1- MISCELLANEOUS: THERE ARE 3 DAHP SYNTHASES, AROH IS

CC FEEDBACK-INHIBITED BY TRP. THE OTHER 2 DAHP SYNTHASES ARE TYR- AND

CC PHE-SENSITIVE, RESPECTIVELY.

CC -1- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

RX MEDLINE-98034461; PubMed-9368100;
 RA Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
 RA Bradfield C.A.; Molecular characterization of the murine Hif-1 alpha locus.";
 RL Gene Expr. 6:287-299(1997).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV;
 RX MEDLINE-97354184; PubMed-9210478;
 RA Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
 RA Gassmann M.;
 RT "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
 RT organization, expression and characterization of an alternative first
 RT exon and 5' flanking sequence.";
 RL Eur. J. Biochem. 246:135-165(1997).
 [4]
 RP SEQUENCE OF 13-822 FROM N.A.
 RC TISSUE-Hepatocytes;
 RX MEDLINE-96254028; PubMed-8660378;
 RA Wenger R.H., Rolfs A., Marti H.H., Guenet J.-L., Gassmann M.;
 RT "Nucleotide sequence, chromosomal assignment and mRNA expression of
 RT mouse hypoxia-inducible factor-1 alpha.";
 RL Biochem. Biophys. Res. Commun. 223:54-59(1996).
 [5]
 RP SEQUENCE OF 22-85 FROM N.A.
 RC TISSUE-Hepatocytes;
 RA O'Rourke J.F.;
 RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE INDUCTION OF OXYGEN REGULATED GENES.
 CC SPECIFICALLY RECOGNIZES AN 8 BP HYPOXIA RESPONSE ELEMENT (HRE).
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. HETERODIMER OF AN ALPHA AND A BETA (ARNT) SUBUNITS.
 CC THE ALPHA SUBUNIT IS UNIQUE TO HIF-1 WHEREAS HIF-1 BETA (ARNT) CAN
 CC DIMERIZE WITH OTHER BHLH-PAS PROTEINS. INTERACTS WITH HSP90 (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- DOMAIN: BOTH HYPOXIA RESPONSIVENESS AND TRANSCRIPTION CAPABILITY
 CC RESIDE WITHIN THE C-TERMINAL PART.
 CC -1- PTM: REQUIRES PHOSPHORYLATION FOR DNA-BINDING.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.
 CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

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 DR EMBL; U59496; AAC52730.1; -;
 DR EMBL; AF003695; AAC53455.1; -;
 DR EMBL; Y09085; CAI70306.1; -;
 DR EMBL; Y13656; CAI70306.1; JOINED.
 DR EMBL; Y09085; CAI70305.1; -;
 DR EMBL; AF004155; AAC53461.1; -;
 DR EMBL; AF004141; AAC53461.1; JOINED.
 DR EMBL; AF004142; AAC53461.1; JOINED.
 DR EMBL; AF004143; AAC53461.1; JOINED.
 DR EMBL; AF004144; AAC53461.1; JOINED.
 DR EMBL; AF004145; AAC53461.1; JOINED.
 DR EMBL; AF004146; AAC53461.1; JOINED.
 DR EMBL; AF004147; AAC53461.1; JOINED.
 DR EMBL; AF004148; AAC53461.1; JOINED.
 DR EMBL; AF004149; AAC53461.1; JOINED.
 DR EMBL; AF004150; AAC53461.1; JOINED.
 DR EMBL; AF004151; AAC53461.1; JOINED.
 DR EMBL; AF004152; AAC53461.1; JOINED.
 DR EMBL; AF004153; AAC53461.1; JOINED.
 DR EMBL; AF004154; AAC53461.1; JOINED.

DR EMBL; X95580; CAA64833.1; -;
 DR EMBL; X95002; CAA64458.1; -;
 DR MGI; MGI:106918; HLF1.
 DR InterPro: IPR003015; HLH_Myc.
 DR InterPro: IPR001092; HLH_dlm.
 DR InterPro: IPR001321; Hypoxindf1A.
 DR InterPro: IPR001610; PAC.
 DR InterPro: IPR000014; PAS.
 DR Pfam: PF00785; PAC; 1.
 DR Pfam: PF00989; PAS; 2.
 DR PRINTS; PRO1080; HYPOXIA1FLA.
 DR SMART; SM00353; HLH; 1.
 DR SMART; SM00086; PAC; 1.
 DR SMART; SM00091; PAS; 2.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
 DR PROSITE; PS0112; PAS; 2.
 DR Repeat: DNA-binding: Nuclear protein; Transcription regulation;
 KW Activator; Phosphorylation.
 KM DNA_BIND 17 30 BASIC DOMAIN
 FT 1 17 30
 FT DOMAIN 31 71
 FT 1 31 71
 FT DOMAIN 80 155
 FT 1 80 155
 FT DOMAIN 228 298 PAS 1.
 FT 1 228 298
 FT DOMAIN 302 345 PAC.
 FT 1 302 345
 FT CONFLICT 31 31 S -> T (IN REF. 1).
 FT CONFLICT 128 128 A -> T (IN REF. 2 AND 3).
 FT CONFLICT 351 351 I -> L (IN REF. 1).
 FT CONFLICT 511 511 E -> L (IN REF. 1).
 FT CONFLICT 511 511 E -> L (IN REF. 1).
 FT CONFLICT 686 686 K -> N (IN REF. 3 AND 4).
 FT CONFLICT 785 785 E -> V (IN REF. 4)
 FT CONFLICT 785 785
 FT SEQUENCE 822 AA; 91858 MW; E717ADCE4CA9D/95 CRC64;

 QY 3 YIKAN-SKEITGERPEHLVDF 26
 DB 111 YISDNVNMKTGLOFELAGHSYDF 135

 RESULT 13
 ID HIFA_HUMAN STANDARD; PRT; 826 AA.
 AC 016665;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (ARNT interacting
 DE protein) (Member of PAS protein 1) (MOP1) (HIF1 alpha).
 GN HIF1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID-9606;
 RN 1;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
 RA MEDLINE-95296340; PubMed-7539918.
 RA Wang G.L., Jiang B.H., Rue F.A., Semenza G.L.;
 RT "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
 RT heterodimer regulated by cellular O₂ tension.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Hepatoma;
 RX MEDLINE-97236817; PubMed-9079689;
 RA Hogenesch J.B., Verdew G.H., Bradfield C.A., Jackiv V.H., Brown R.C., Gu Y.-Z.,
 RA Pray-Grant M., Verdew G.H., Bradfield C.A.;
 RT "Characterization of a subset of the basic-helix-loop-helix-PAS
 RT superfamily that interacts with components of the dioxin signaling
 RT pathway.";
 RL J. Biol. Chem. 272:8581-8593(1997).
 [3]

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:12:49 : Search time 41.35 Seconds

(without alignments)
129,569 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYKANSKFGITGEFGPEHLVDFIQSLIS 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_podic:*
13: sp_virus:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioid:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	78	48.1	485	6	Q9BG59	G9bg59 tupaia glis
2	70	43.2	1310	2	O93N27	Q93n27 clostridium
3	56.5	34.9	458	5	O44506	O44506 caenorhabditis
4	56.5	34.9	609	3	O12601	O12601 candida albicans
5	56	34.6	314	16	Q9CN39	Q9cn39 pasteurella
6	54	33.3	310	16	Q9KS29	Q9ks29 vibrio cholerae
7	54	33.3	469	12	Q910P5	Q910p5 melon yellow
8	52.5	32.4	108	11	Q9Q294	Q9q294 cavia porcella
9	52.5	32.4	1071	3	Q9P388	Q9p388 neospora
10	52	32.1	386	12	Q9YH77	Q9yh77 melon yellow
11	51	31.5	215	16	Q91AF6	Q91af6 pseudomonas
12	51	31.5	274	16	Q91AF6	Q91af6 pseudomonas
13	51	31.5	469	12	Q9MB52	Q9mb52 physalis
14	51	31.5	899	12	Q91TK4	Q91tk4 atelinae
15	50.5	31.2	771	2	Q9S309	Q9s309 porphyromon
16	50	30.9	212	17	O58223	O58223 pyrococcus

17	50	30.9	493	4 Q9NX26	Q9nx26 homo sapien
18	50	30.9	493	4 Q9NX26	Q9nx26 homo sapien
19	49	30.2	165	5 O15887	O15887 trypanosoma
20	49	30.2	198	10 Q940L5	Q940l5 arabidopsis
21	49	30.2	212	17 Q9UYF5	Q9uyf5 pyrococcus
22	49	30.2	233	10 O81513	O81513 arabidopsis
23	49	30.2	252	10 O40701	O40701 oryza sativa
24	49	30.2	254	10 O65103	O65103 oryza sativa
25	49	30.2	513	3 Q9C1X4	Q9c1x4 schizosaccharomyces
26	48.5	29.9	103	6 Q9N110	Q9n110 ovine
27	48.5	29.9	106	11 Q9DA88	Q9da88 mus musculus
28	48.5	29.9	258	11 Q9CYA8	Q9cy88 mus musculus
29	48.5	29.9	735	4 Q96PY9	Q96py9 homo sapien
30	48.5	29.9	823	6 Q9XTA5	Q9xta5 bos taurus
31	48.5	29.9	823	11 Q9MTU9	Q9mtu9 rattus norvegicus
32	48.5	29.9	825	11 Q35800	Q35800 rattus norvegicus
33	48.5	29.9	826	4 Q9UPH1	Q9uph1 homo sapien
34	48	29.6	440	16 Q9CMT1	Q9cm11 pasteurella
35	48	29.6	478	17 Q97WC2	Q97wc2 sulfolobus
36	48	29.6	832	16 Q9BG05	Q9bg05 rhizobium
37	48	29.6	1173	5 Q9V7J8	Q9v7j8 dirosophila
38	47.5	29.3	374	16 Q9CKE4	Q9cke4 pasteurella
39	47.5	29.3	390	2 Q9F739	Q9f739 shigella sonnei
40	47.5	29.3	395	2 Q9S0R2	Q9s0r2 pleistomonas
41	47.5	29.3	403	2 O55045	O55045 shigella sonnei
42	47.5	29.3	1079	5 Q9VN30	Q9vn30 dirosophila
43	47.5	29.3	1298	3 Q91318	Q91318 neospora
44	47.5	29.3	1307	3 Q9C101	Q9c101 magnaporthe
45	47	29.0	189	5 Q95R25	Q95r25 babesia rossi

ALIGNMENTS

RESULT 1
Q9BG59 PRELIMINARY: PRT: 485 AA.
ID Q9BG59
AC Q9BG59
DT 01-JUN-2001 (Tremblrel, 17, Created)
DT 01-JUN-2001 (Tremblrel, 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE CHOLESTERYL ESTER TRANSFER PROTEIN (FRAGMENT).
OS Tupaia glis (Tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=9395;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zeng W.W., Chen B.S., Zhang J.;
RT *Cloning and sequencing of tree shrew cholesteryl ester transfer protein (CETP) cDNA.
RU Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334033; AAK08086.1; .
DR InterPro; IPR001124; LBP_BPL_CETP.
DR Pfam; PF02886; LBP_BPL_CETP_1.
DR SMART; SM00328; BP11; 1.
DR SMART; SM00329; BP12; 1.
DR PROSITE; PS00400; LBP_BPL_CETP; 1.
DR NON_TER
FT SEQUENCE 485 AA; 53993 MW; 2605E76D2635C367 CRC64;

Query Match 48.1%; Score 78; DB 6; Length 485;
Best Local Similarity 88.2%; Pred. No. 0.0026;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFIQSLIS 31
DB 469 DFGPEHLVDFIQSLIS 485

RESULT 2
 ID 093N27 PRELIMINARY; PRT; 1310 AA.
 AC 093N27;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE TETANUS TOXIN (FRAGMENT).
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shumlin Z., Dianliang L.;
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF389424; AAK72964.2; -.
 FT NON_TER 1 1
 FT SEQUENCE 1310 AA; 150316 MW; 9EADDC914418E450 CRC64;
 SQ

Query Match 43.2%; Score 70; DB 2; Length 1310;
 Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
 DB 831 OYKANSKFIGITE 844

RESULT 3
 ID 044506 PRELIMINARY; PRT; 458 AA.
 AC 044506;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 51.1 KDA PROTEIN.
 F42G8.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peltoderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Gattung S., Holmes A.;
 RT "The sequence of C. elegans cosmid F42G8.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submision.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF038618; AAB92068.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 458 AA; 51070 MW; 9F4DF23D8CDABBD5 CRC64;
 SO

Query Match 34.9%; Score 56.5; DB 5; Length 458;
 Best Local Similarity 40.0%; Pred. No. 4;
 Matches 12; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

OY 1 CQYTKANSKFIGITFEFGPEHLVDFLOSL 30
 DB 232 CNYIKNNKYLGRKSSGFHQ---LDFIQRL 258

RESULT 4
 ID 012601 PRELIMINARY; PRT; 609 AA.
 AC 012601;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE BETA-D-GLUCOSIDASE PRECURSOR (EC 3.2.1.21).
 GN BGLB.
 OS Candida wickerhamii.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Microsporici Saccharomycetales; Candida.
 OX NCBI_TaxID=35521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CAPRIOTTI;
 RX MEDLINE=96031564; PubMed=7574590;
 RA Skory C.D., Freer S.N.;
 RT "Cloning and characterization of a gene encoding a cell-bound,
 RT extracellular beta-glucosidase in the yeast Candida wickerhamii.";
 DL Appl. Environ. Microbiol. 61:518-525(1995).
 DR EMBL; U13672; AAC49036.1; -.
 DR HSSP; P26205; ICBG.
 DR InterPro; IPR001360; Glyco_hydro_1.
 DR Pfam; PF00232; Glyco_hydro_1; 3.
 KW Signal; Hydrolase; Glycosidase.
 FT SIGNAL 1 21
 FT CHAIN 22 609
 FT SEQUENCE 609 AA; 68034 MW; 9C5624E3B3F1734E CRC64;
 SO

Query Match 34.9%; Score 56.5; DB 3; Length 609;
 Best Local Similarity 60.0%; Pred. No. 5.5;
 Matches 15; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY 11 IGITFEGFP-----EHLVDFLOSL 30
 DB 510 IFTTFEGFPWRGKLVDFQYDDL 534

RESULT 5
 ID 09CN39 PRELIMINARY; PRT; 314 AA.
 AC 09CN39;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN PM0606.
 GN PM0606.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL; AE006096; AAK02690.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 314 AA; 36080 MW; 3C0EA33486CP62BD CRC64;
 SO

Query Match 34.6%; Score 56; DB 16; Length 314;
 Best Local Similarity 64.3%; Pred. No. 3.1;

Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 17 GPEHVLVDLQSL 30
 |||||:||||:
 DB 85 GPEHVLPEYLQSL 98

RESULT 6
 ID 09KS29 PRELIMINARY; PRT; 310 AA.
 AC 09KS29;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN VC1432.
 GN VC1432.
 OS Vibrio cholerae
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Urquhart L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae";
 RL Nature 406:477-483(2000).
 DR EMBL: AE004222; AAF94589.1; -.
 DR TIGR: VC1432; -.
 KW Complete proteome.
 SQ SEQUENCE 310 AA; 35120 MW; 13FE328403241448 CRC64;

Query Match 33.3%; Score 54; DB 16; Length 310;
 Best Local Similarity 64.3%; Pred. No. 6.1;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 17 GPEHVLVDLQSL 30
 |||||:||||:
 DB 84 GPEHVLPEYLQSL 97

RESULT 7
 ID 0910P5 PRELIMINARY; PRT; 469 AA.
 AC 0910P5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NONSTRUCTURAL PROTEIN.
 GN NSS.
 OS melon yellow spot virus.
 OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
 OX NCBI_TaxID=89471;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TOSPO-MELO;
 RA Kato K., Hanada K.;
 RT "Characterization of the S RNA segment of melon yellow spot virus";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB038343; BAB18310.1; -.
 SQ SEQUENCE 469 AA; 53117 MW; 1B0BA052FC0D769B CRC64;

Query Match 33.3%; Score 54; DB 12; Length 469;
 Best Local Similarity 35.3%; Pred. No. 9.6;
 Matches 12; Conservative 8; Mismatches 6; Indels 8; Gaps 1;

OY 5 KANSKPGIT-----EKGPEHVLVDLQSL 30
 |||||:||||:
 DB 413 KNSSEFVYLSRTMSPFWKEPPEOHLVDYNEFL 446

RESULT 8
 ID 09Q294 PRELIMINARY; PRT; 108 AA.
 AC 09Q294;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HIF1-ALPHA PROTEIN (FRAGMENT).
 GN HIF1-ALPHA.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriicongnathii; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HARTLEY; TISSUE=HEART;
 RA Aguan K., Thompson L., Weiner C.P.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF193574; AAF04124.1; -.
 DR InterPro: IPR003015; HLH_dlm.
 DR InterPro: IPR000014; PAS.
 DR SMART: SM00353; HLH; 1.
 DR PROSITE: PS00036; HELIX_LOOP_HELIX; UNKNOWN_1.
 FT NON_TER 1 108
 FT NON_TER 1 108
 SQ SEQUENCE 108 AA; 12409 MW; B010BF6258DAACE3 CRC64;

Query Match 32.4%; Score 52.5; DB 11; Length 108;
 Best Local Similarity 40.7%; Pred. No. 3.1;
 Matches 11; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

OY 3 YIKAN-SKFIGITGEGPEHVLVDLQSL 28
 |||||:||||:
 DB 82 YISDNVKNKMGITQFELTGHVDFDTQ 108

RESULT 9
 ID 09P388 PRELIMINARY; PRT; 1071 AA.
 AC 09P388;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE RELATED TO SMALL S PROTEIN.
 GN B24W22.200.
 GN Neurospora crassa.
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohnsels J., Brandt P., Partmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390354; CAB93388.1; -.
 SQ SEQUENCE 1071 AA; 120743 MW; EF954CFB6CE58BD2 CRC64;

Query Match 33.4%; Score 52.5; DB 3; Length 1071;
 Best Local Similarity 40.0%; Pred. No. 41;
 Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 1;

SO SEQUENCE 469 AA; 53204 MW; 732435E83C3FC27D CRC64;

Query Match 31.5%; Score 51; DB 12; Length 469;

Best Local Similarity 36.7%; Pred. No. 27;
Matches 11; Conservative 7; Mismatches 4; Indels 8; Gaps 1;

OY 5 KANSKFIGIT-----ERGFPEHLVDF 26

DB 413 KNSSEFWLSTKMTSPWKEPPEQHLVDY 442

RESULT 14

ID O9YTK4 PRELIMINARY; PRT; 899 AA.

AC O9YTK4;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE ORF 63.

OS Ateline herpesvirus 3.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae; Rhadinovirus.

OY NCBI_TaxID=85618;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-73;

RX MEDLINE-20091363; PubMed-10623770;

RA Albrecht J.C.;

RT "Primary structure of the Herpesvirus Ateles genome.";

RL J. Virol. 74:1033-1037 (2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-73;

RA Albrecht J.C., Fleckenstein B.;

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF083424; AAC95587.1; "

SO SEQUENCE 899 AA; 103389 MW; 19440A7944DE2531 CRC64;

Query Match 31.5%; Score 51; DB 12; Length 899;

Best Local Similarity 44.0%; Pred. No. 56;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITERGFPEHLVDF 26

DB 124 OYTSNSTFTGTETPIVNNVILTF 148

RESULT 15

ID O9S309 PRELIMINARY; PRT; 771 AA.

AC O9S309;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE IMMUNOREACTIVE 87KD ANTIGEN PG92.

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; CFM group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;

OC Porphyromonas.

OX NCBI_TaxID=837;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-W50;

RA Ross B.C., Barr I., Patterson M., Agius C., Rothel L., Margetts M.,

RT "Porphyromonas gingivalis polypeptides and nucleic acids.";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF175724; AAD51077.1; "

SO SEQUENCE 771 AA; 86667 MW; 75016BF66848C9B9 CRC64;

Best Local Similarity 50.0%; Pred. No. 56;
Matches 11; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

OY 13 IYERGFPE--HLVDFIQSLIS 31

DB 162 LTERAFPEEGEGHILLNLGOALS 183

Search completed: June 18, 2002, 08:12:52
Job time: 376 sec

Query Match 31.2%; Score 50.5; DB 2; Length 771;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 08:08:27 : Search time 51.68 Seconds
(without alignments)
66.627 Million cell updates/sec

Title: US-09-943-334-2
Perfect score: 162
Sequence: 1 CQYKANSKRIGTERGPEHLLVDFLOSLSL 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.032802:*

1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
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11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
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15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
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18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	31	17	AAW06129
2	162	100.0	31	20	AAW02470
3	142.5	88.0	50	17	AAW06131
4	129.5	79.9	50	17	AAW06132
5	129.5	79.9	50	18	AAW46447
6	87	53.7	35	21	AAV91236
7	85	52.5	22	20	AAV13815
8	85	52.5	22	20	AAV13821
9	85	52.5	26	17	AAW06128
10	85	52.5	26	20	AAV13801
11	85	52.5	26	21	AAV91228

12	85	52.5	46	21	AAV91232	Modified MYF Th ep
13	85	52.5	46	21	AAV91233	Modified MYF Th ep
14	85	52.5	476	17	AAW06127	Human cholesteryl
15	85	52.5	476	18	AAW46446	Human mature chole
16	85	52.5	476	20	AAW02466	Human cholesteryl
17	85	52.5	491	15	AAW60342	Partial human lipid
18	85	52.5	493	20	AAV49556	Human cholesteryl
19	85	52.5	493	20	AAV49568	Human cholesteryl
20	85	52.5	493	22	AAW65636	Humanised rabbit c
21	85	52.5	496	20	AAV02469	Modified MYF Th ep
22	84.5	52.2	36	21	AAV91234	Modified MYF Th ep
23	84.5	52.2	124	21	AAW45501	Modified MYF Th ep
24	84	51.9	36	21	AAV91235	Modified MYF Th ep
25	84	51.9	36	21	AAV91237	Modified MYF Th ep
26	83.5	51.5	126	21	AAW45490	Modified human int
27	83	51.2	16	21	AAV91229	Human cholesteryl
28	81.5	50.3	750	21	AAV92631	Mutant human prost
29	81.5	50.3	750	21	AAV92632	Mutant human prost
30	81.5	50.3	750	21	AAV92633	Mutant human prost
31	81.5	50.3	750	21	AAV92634	Mutant human prost
32	81.5	50.3	750	21	AAV92635	Mutant human prost
33	81.5	50.3	750	21	AAV92636	Mutant human prost
34	81.5	50.3	750	21	AAV92643	Mutant human prost
35	81	50.0	22	20	AAV13802	Rabbit CERP immuno
36	81	50.0	26	20	AAV13809	Rabbit CERP immuno
37	81	50.0	26	21	AAV91231	Modified MYF Th ep
38	81	50.0	46	21	AAV91240	Modified MYF Th ep
39	81	50.0	46	21	AAV91241	Modified rabbit ch
40	81	50.0	477	20	AAW02468	Modified cholesteryl
41	81	50.0	496	17	AAW06133	Mature rabbit chol
42	81	50.0	496	18	AAW46445	Rabbit cholesteryl
43	81	49.7	36	21	AAV91238	Modified MYF Th ep
44	80.5	49.7	36	21	AAV91239	Modified MYF Th ep
45	80	49.4	36	21	AAV91239	Modified MYF Th ep

ALIGNMENTS

RESULT 1	AAW06129	standard; Peptide; 31 AA.
ID	AAW06129	
XX	AAW06129:	
AC		
XX		
DT	07-FEB-1997 (first entry)	
XX		
DE	Anti-cholesteryl ester transfer peptide vaccine.	
XX		
KW	Cholesteryl ester transfer protein; CERP; antigen; vaccine;	
KW	cardiovascular disease; atherosclerosis.	
XX		
OS	Synthetic.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 1	/note= "C-terminal Cys residue is present for use in linking the peptide to itself or other molecules"
FT		
FT	Region	2..15
FT		/label= T-cell epitope comprises amino acids
FT		/note= T-cell epitope comprises amino acids
FT	Region	16..31
FT		/label= B-cell epitope
FT		/note= B-cell epitope comprises the C-terminal 16 amino acids of human CERP (claim 5)."
PM	W09634888-A1.	
XX		
XX		
PD	07-NOV-1996.	
XX		
PF	01-MAY-1996:	96WO-US06147.

XX 01-MAY-1995; 95US-0432483.
 XX (TCCL-) T CELL SCI INC.
 PA Rittershaus CW, Thomas LJ;
 PI WPI; 1996-506103/50.
 DR
 XX Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CETP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 PS
 XX Claim 8; Page 41-42; 72pp; English.
 CC A synthetic peptide vaccine comprises an immunogenic helper T-cell
 CC epitope of tetanus toxoid protein covalently linked to the
 CC C-terminal B-cell epitope of human cholesteryl ester transfer
 CC protein (CETP) (see also AAM06127) that is involved in a neutral
 CC lipid binding or a transfer activity of CETP. The vaccine elicits
 CC an immune response against endogenous CETP activity, and is used to
 CC treat or prevent a cardiovascular disease, such as atherosclerosis.
 CC
 SQ Sequence 31 AA;

Query Match 100.0%; Score 162; DB 17; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CQYKANSKFIQTGEPPEHLVDFLOSLS 31
 |||||
 DB 1 cgyikanskfigitelfephlvdfiqsls 31

RESULT 2

AA02470
 ID AAY02470 standard; protein; 31 AA.

AC AAY02470;

DT 14-JUL-1999 (first entry)

DE Fusion of a tetanus toxoid fragment and C-terminal of human CETP.

KW Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CETP;
 KW high-density lipoprotein-associated cholesterol; metabolism;
 KW low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
 KW cholesterol; atherosclerosis; heart disease.

OS Synthetic.

PN WO9920302-A1.

PD 29-APR-1999.

PF 20-OCT-1998; 98WO-US22145.

PR 20-OCT-1997; 97US-0954643.

PA (AVANT-) AVANT IMMUNOTHERAPEUTICS INC.

PI Rittershaus CW, Thomas LJ;

DR WPI; 1999-302645/25.

PT Vaccine against cholesteryl ester transfer protein

PS Disclosure; Page 55; 61pp; English.

XX The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein

CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC was used in the course of the invention.
 CC
 SQ Sequence 31 AA;

Query Match 100.0%; Score 162; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CQYKANSKFIQTGEPPEHLVDFLOSLS 31
 |||||
 DB 1 cgyikanskfigitelfephlvdfiqsls 31

RESULT 3

AA06131
 ID AAM06131 standard; Peptide; 50 AA.

AC AAM06131;

DT 07-FEB-1997 (first entry)

DE Anti-cholesteryl ester transfer multivalent vaccine peptide.

KW Cholesteryl ester transfer protein; CETP; antigen; vaccine;
 KW cardiovascular disease; atherosclerosis.

OS Synthetic.

EH Key Location/Qualifiers

FT MISC-difference 1 /note= "C-terminal Cys residue is present for use
 FT in linking the peptide to itself or other
 FT molecules"

FT Region 2..15 /label= "T-cell epitope
 FT /note= "T-cell epitope comprises amino acids
 FT 830-843 of tetanus toxoid protein"

FT Region 16..34 /label= "B-cell epitope
 FT /note= "B-cell epitope comprises amino acids
 FT 349-367 of human CETP"

FT Region 35..50 /label= "B-cell epitope
 FT /note= "B-cell epitope comprises the C-terminal 16
 FT amino acids of human CETP, involved in
 FT neutral lipid binding or transfer activity"

PN WO9634888-A1.

PD 07-NOV-1996.

PF 01-MAY-1996; 96WO-US06147.

PR 01-MAY-1995; 95US-0432483.

PA (TCCL-) T CELL SCI INC.

PI Rittershaus CW, Thomas LJ;

DR WPI; 1996-506103/50.

PT Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CETP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.

```

PT  atherosclerosis
XX
XX  Disclosure: Page 7; 72pp; English.
XX
CC  A multivalent vaccine comprises an immunogenic helper T-cell
CC  epitope of tetanus toxoid protein covalently linked to the B-cell
CC  epitopes of human cholesteryl ester transfer protein (CETP) (see
CC  also AAW06127). The vaccine elicits an immune response against
CC  endogenous CETP activity, and is used to treat or prevent a
CC  cardiovascular disease, such as atherosclerosis.
XX
XX  Sequence 50 AA:

Query Match      88.0%; Score 142.5; DB 17; Length 50;
Best Local Similarity 62.0%; Pred. No. 8.5e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY  1 QYIKANSKFGITGTE-----FGPPEHLVDFLOSL 31
    |||||
DB  1 cgytkanskfigitelfrpdqghvayrfeedtfgfpehlvdfllqsls 50

RESULT 4
AAW06132
ID  AAW06132 standard; Peptide; 50 AA.
XX
AC  AAW06132:
XX
DT  07-FEB-1997 (first entry)
XX
DE  Anti-cholesteryl ester transfer multivalent vaccine peptide.
XX
KM  Cholesteryl ester transfer protein; CETP; antigen; vaccine;
KW  cardiovascular disease; atherosclerosis.
XX
OS  Synthetic.
XX
FH  Key
FT  Location/Qualifiers
    2..15
    /label= "T-cell epitope
    /note= "T-cell epitope comprises amino acids
    16..34
    /label= "B-cell epitope
    /note= "B-cell epitope comprises amino acids
    350-368 of rabbit CETP"
FT  Region
    35..50
    /label= "B-cell epitope
    /note= "B-cell epitope comprises the C-terminal 16
    amino acids of rabbit CETP, involved in
    neutral lipid binding or transfer activity"
XX
XX  WO9634888-A1.
XX
XX  07-NOV-1996.
XX
XX  01-MAY-1996; 96WO-US06147.
XX
XX  01-MAY-1995; 95US-0432483.
XX
XX  (TCEL-) T CELL SCI INC.
XX
XX  Rlterhaus CW, Thomas LJ;
XX
XX  WPI: 1996-506103/50.
XX
PT  Cholesteryl ester transfer protein B cell epitope linked to T cell
PT  epitope - used to generate vaccine to regulate CETP activity for
PT  decreasing the risk of developing a cardiovascular disease e.g.
XX  atherosclerosis
XX
XX  Disclosure: Page 7; 72pp; English.

```

```

XX
XX  A multivalent vaccine comprises an immunogenic helper T-cell
CC  epitope of tetanus toxoid protein covalently linked to the B-cell
CC  epitopes of rabbit cholesteryl ester transfer protein (CETP) (see
CC  also AAW06133). The vaccine elicits an immune response against
CC  endogenous CETP activity, and is used to treat or prevent a
CC  cardiovascular disease, such as atherosclerosis.
XX
XX  Sequence 50 AA:

Query Match      79.9%; Score 129.5; DB 17; Length 50;
Best Local Similarity 59.2%; Pred. No. 8.9e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY  2 QYIKANSKFGITGTE-----FGPPEHLVDFLOSL 31
    |||||
DB  2 qytkanskfigiterfrpdgreavayrfeedtfgfpehlvdfllqsls 50

RESULT 5
AAW46447
ID  AAW46447 standard; Peptide; 50 AA.
XX
AC  AAW46447:
XX
DT  18-MAY-1998 (first entry)
XX
DE  CETP B cell epitope/tetanus toxoid construct for a plasmid vaccine.
XX
KM  Cholesteryl ester transfer protein; CETP; cholesteryl ester;
KW  high density lipoprotein; HDL; very low density lipoprotein; VLDL;
KW  low density lipoprotein; LDL; atherosclerosis; neutral lipid binding;
KW  transfer activity; immunogenic; B cell epitope; antibody;
KW  DNA plasmid-based vaccine; broad range helper T cell epitope;
KW  treatment; cardiovascular disease; chimeric.
XX
XX
XX  Chimeric - Clostridium tetani.
OS  Chimeric - Oryctolagus sp.
XX
FH  Key
FT  Location/Qualifiers
    2..15
    /label= "tetanus toxoid broad range helper T cell
    16..34
    /note= "CETP epitope of amino acids 350-368 of
    AAW46445"
FT  Peptide
    35..50
    /note= "CETP epitope of amino acids 481-496 of
    AAW46445"
XX
XX  WO9741227-A1.
XX
XX  06-NOV-1997.
XX
XX  01-MAY-1997; 97WO-US07294.
XX
XX  21-FEB-1997; 97US-0802967.
XX
XX  01-MAY-1996; 96US-0640713.
XX
XX  (TCEL-) T CELL SCI INC.
XX
XX  Thomas LJ;
XX
XX  WPI: 1997-549731/50.
XX
XX  N-PSDB; AAW05128.
XX
PT  DNA plasmid-based vaccine encodes CETP B cell and helper T cell
PT  epitope(s) - used for elevating high density lipoprotein levels, and
PT  for treating cardiovascular disease
XX
XX  Claim 8; Page 22; 67pp; English.

```

XX The present sequence represents a construct containing a helper T cell
CC epitope from the toxoid teatus protein, and 2 B cell epitopes of rabbit
CC mature cholesteryl ester transfer protein (CETP). CETPs mediate the
CC transfer of cholesteryl esters from high density lipoprotein (HDL) to
CC very low density lipoprotein (VLDL) and low density lipoprotein (LDL),
CC and vice versa. An increased CETP activity produces an atherogenic
CC lipoprotein profile and induces atherosclerosis. A 13 amino acid stretch
CC in the rabbit CETP (AAW46445) (Phe483 to Ieu495) is important for
CC neutral lipid binding and transfer activity. This region has been shown
CC to be immunogenic as a B cell epitope of CETP. A second B cell epitope
CC is defined by Arg350 to Ile368. Antibodies to this second epitope would
CC allow the formation of immune complexes involving CETP, and promote
CC the removal of the complexed CETP. The present sequence is encoded by a
CC DNA plasmid-based vaccine which comprises sequences encoding at least 1
CC B cell epitope of CETP linked in frame with at least one segment
CC encoding a broad range helper T cell epitope. The vaccines can be used to
CC elevate the ratio of circulating HDL to circulating LDL, VLDL, or total
CC cholesterol in a human. It can also be used for decreasing the level of
CC endogenous CETP activity in a human. The vaccine can be used to produce
CC anti-CETP antibodies in vivo and for treating cardiovascular disease.

SO Sequence 50 AA;

Query Match 79.9%; Score 129.5; DB 18; Length 50;
Best Local Similarity 59.2%; Pred. No. 8.9e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

OY 2 OYIANSKFIGITE-----RGPPEHLVDFQSLIS 31
Db 2 qylkanskfigiterprdpdgreavayrfeedifgrphllvdfqls 50
|||||

RESULT 6
AAV91236 standard; peptide; 35 AA.

AAV91236;

22-MAY-2000 (first entry)

Modified HBV surface Ag/CETP peptide, SEQ ID NO:114.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin-6 releasing hormone; IL6R; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antitumor; PMDV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

OS Chimeric - Hepatitis B virus.
OS Chimeric - Homo sapiens.

PN WO966957-A2.

XX 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
DT or human immune deficiency virus
XX

P5 Claim 11; Page 106; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC and peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunosuppression; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAV91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAV91122-Y91142,
CC AAV91226 and AAV91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AAV91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAV91156-Y91196, AAV91227 and AAV91242-Y91244 are antigenic peptides.
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAV91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAV91200 is somatostatin, and AAV91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAV91208 is a
CC human CD4-CDR2-like domain antigenic site, and AAV91209-Y90211 are MVH Th
CC epitope/CD4-CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAV90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAV90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAV91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAV91221-Y91222 comprise this peptide and a Th
CC epitope. AAV91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAV91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AAV91228-Y91231 represent
CC CETP-derived peptides and AAV91232-Y91241 are immunogens comprising a
CC Th epitope and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAV91247 and AAV91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAV91248-Y91251 and
CC AAV91256-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAV91198 and AAV91199 are respectively an immunostimulatory invasion
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

SO Sequence 35 AA;

Query Match 53.7%; Score 87; DB 21; Length 35;
Best Local Similarity 89.5%; Pred. No. 2.3e-06;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 13 ITRGPEHLVDFQSLIS 31
Db 17 idkfgpehlvdfqls 35
|:|||||

RESULT 7

AAV13815 standard; peptide; 22 AA.

AAV13815;

08-JUL-1999 (first entry)

DE Rabbit CERP immunogenic fragment.
 XX CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Oryctolagus sp.
 XX
 XX W09915655-A1.
 PN 01-APR-1999.
 XX
 PF 17-SEP-1998; 98MO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI: 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 XX
 PS Disclosure: Page 75; 99pp: English.
 XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an atherogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 SO Sequence 22 AA:
 QY 15 EFGFPEHLVDFLQSLG 31
 :|||||
 Db 6 dfgfpehlvdfllqsls 22

Query Match 52.5%; Score 85; DB 20; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 AAY13821
 ID AAY13821 standard; peptide: 22 AA.
 XX
 AC AAY13821;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Human CERP immunogenic fragment.
 XX
 KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Homo sapiens.
 XX
 PN W09915655-A1.
 XX
 PD 01-APR-1999.
 XX

PF 17-SEP-1998; 98MO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI: 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 XX
 PS Disclosure: Page 88; 99pp: English.
 XX
 CC This sequence represents an immunogenic fragment of the human
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an atherogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 SO Sequence 22 AA:
 QY 15 EFGFPEHLVDFLQSLG 31
 :|||||
 Db 6 dfgfpehlvdfllqsls 22

Query Match 52.5%; Score 85; DB 20; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 AAW06128
 ID AAW06128 standard; Peptide; 26 AA.
 XX
 AC AAW06128;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Human cholesteryl ester transfer protein C-terminal B-cell epitope.
 XX
 KW Cholesteryl ester transfer protein; CERP; antigen; vaccine;
 KW cardiovascular disease; atherosclerosis; B-cell epitope.
 XX
 OS Homo sapiens.
 XX
 PN W09634888-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 01-MAY-1996; 96MO-US06147.
 XX
 PR 01-MAY-1995; 95US-0432483.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI: 1996-506103/50.
 XX
 PT Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CERP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX

PS Claim 5; Page 41; 72pp; English.

XX A B-cell epitope (AAW06128) comprising the C-terminal 26 amino acids
 CC of human liver mature cholesteryl ester transfer protein (CETP)
 CC (see also AAW06127) is involved in a neutral lipid binding or a
 CC transfer activity of CETP. It can be linked to a universal or a
 CC broad range immunogenic T-cell epitope, such as that found at amino
 CC acids 830-843 of tetanus toxoid protein, to produce a synthetic
 CC vaccine (see also AAW06129) that elicits an immune response against
 CC endogenous CETP activity, thereby treating or preventing
 CC cardiovascular disease, such as atherosclerosis. It may also be
 CC incorporated into a multivalent vaccine (see also AAW06131)
 CC including another CETP B-cell epitope.

XX Sequence 26 AA:

SO

Query Match 52.5%; Score 85; DB 17; Length 26;
 Best Local Similarity 94.1%; Pred. No. 3.4e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 ERGPEHLVDFQSLS 31
 Db 10 dfgpehlvdfqsls 26
 :|||||

RESULT 10
 AAY13801
 ID AAY13801 standard; peptide; 26 AA.
 XX AAY13801;
 AC
 XX 08-JUL-1999 (first entry)
 DT
 XX Rabbit CETP immunogenic fragment.
 DE
 XX CETP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Oryctolagus sp.
 XX
 XX WO9915655-A1.
 PN
 XX 01-APR-1999.
 PD
 XX 17-SEP-1998; 98WO-US19366.
 PE
 XX 19-SEP-1997; 97US-0934367.
 PR
 XX (MONS) MONSANTO CO.
 PA
 XX Glenn K, Needleman P;
 PI WPI; 1999-276984/23.
 DR
 XX New recombinant DNA vaccines
 PT
 XX Claim 15; Page 85; 99pp; English.

XX This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CETP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CETP, which can be used for producing antitoxins to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenous immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CETP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX Sequence 26 AA:

SO

Query Match 52.5%; Score 85; DB 20; Length 26;
 Best Local Similarity 94.1%; Pred. No. 3.4e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 ERGPEHLVDFQSLS 31
 Db 10 dfgpehlvdfqsls 26
 :|||||

RESULT 11
 AAY91228
 ID AAY91228 standard; peptide; 26 AA.
 XX AAY91228;
 AC
 XX 22-MAY-2000 (first entry)
 DT
 XX Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:106.
 DE
 XX Promiscuous T-cell epitope; measles virus F protein; WVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin hormone releasing hormone; IHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumporozoite; antimalarial; CETP;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 XX WO9966957-A2.
 PN
 XX 29-DEC-1999.
 PD
 XX 21-JUN-1999; 99WO-US13975.
 PE
 XX 20-JUN-1998; 98US-0100412.
 PR
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA
 XX Wang CY;
 PI WPI; 2000-160564/14.
 DR
 XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 PS
 XX Claim 10; Page 49; 129pp; English.

XX The invention relates to novel, promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (IHRH) for contraception, treatment of hormone-
 CC dependent cancer; prevention of boar taint in meat; and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (WVF) protein and sequences AAY91122-V91142,

AAV91226 and AAV91245-Y91246 represent synthetic Th epitopes based on the MVE Th epitope. Sequence AAV91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAV91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAV91156-Y91196, AAV91227 and AAV91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAV91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAV91200 is somatostatin, and AAV91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAV91208 is a human CD4 CD8-like domain antigenic site, and AAV91209-Y90211 are MVE Th epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV infection of T cells. AAV90212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AAV90213-Y90219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AAV91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAV91221-Y91222 comprise this peptide and a Th epitope. AAV91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAV91224-Y91225 comprise the CS antigen and an MVE Th epitope and may be used in a malaria vaccine. AAV91228-Y91231 represent CEMP-derived peptides and AAV91232-Y91241 are immunogens comprising a CEMP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAV91247 and AAV91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAV91248-Y91251 and AAV91258-Y91273 are antigenic peptides comprising MVE Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAV91199 and AAV91199 are respectively an immunostimulatory invasion protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. Note: Sequence AAV91227 is also designated SEQ ID NO:106 in the specification.

SQ Sequence 26 AA;

Query Match	52.58;	Score 85;	DB 21;	Length 26;
Best Local Similarity	94.18;	Pred. NO. 3.4e-06;		
Matches 16;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY 15 EFGFPEHLLVDLQSL 31
      :|||||
Db 10 dfgfpehllvdflqsl 26
```

```
Db 10 dfgfpehl1vdf1qsls 26
```

RESULT 12

ID AY91232 standard; peptide; 46 AA.

AC AAY91232;

DT 22-MAY-2000 (first entry)

DE Modified MVE Th epitope/CETP peptide, SEQ ID NO:110.

KW Promiscuous T-cell epitope; measles virus F protein; NVF;

KW Inteinising hormone releasing hormone; LHRH; contraceptive; anticancer

KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;

KW cholesterol ester transport protein; anti-arteriosclerotic.

OS Chimeric - measles virus.

XX
XX
XXXXXXX

20-DEC-1 0000
XX
XX

XX
PE 21-TIN-1000. 0000-1101307E

XX
PR 20-TTN-1998. 98RTS-0100412

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY:

DR WPI; 2000-160564/14

PT New artificial T helper cell epitope and derived immunogens with target

PT or human immune deficiency virus -

PS Claim 11; page 104; 129pp; English.

CC The invention relates to novel prom

and immunogenic peptides comprising one or more of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CTRP) or HIV epitopes, but more generally against any pathogen. Immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of lutealising hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AA911121 represents a promiscuous T helper epitope from the measles virus F (VWF) protein and sequences AA911122-AA911142, AA911226 and AA911245-911246 represent synthetic Th epitopes based on the VWF Th epitope. Sequence AA911143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AA911144-911155 are synthetic epitopes derived from this HBV epitope. AA911156-911196, AA911227 and AA911242-911244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AA911197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AA911200 is somatostatin, and AA911201-911209 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AA911208 is a human CD4 CDR2-like domain antigenic site, and AA911209-911211 are MHC Th epitopes/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AA912012 is a modified version of a human IGE (immunoglobulin E) CH3 domain, and AA912013-912019 are Th epitopes/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AA911220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AA911221-911222 comprise this peptide and a Th epitope. AA911223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AA911224-911225 comprise the CS antigen and an MWF Th epitope and may be used in a malaria vaccine. AA911228-911231 represent CTRP-derived peptides and AA911232-911241 are immunogens comprising a CTRP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AA911248-911251 and AA911258-911273 are antigenic peptides comprising MHC Th and HIV-1-B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AA911198 and AA911199 are respectively an immunostimulatory invasive protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

Sequence 46 AA;

Query Match	52.5%	Score 85;	DB 21;	Length 46;
Best Local Similarity	94.1%;	Pred. No. 6.6e-06;		
Matches 16; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

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QY 15 EFGFPEHLLVDFQSL 31
      :|||||
Db 30 dfgfpehllvdflqsl 46
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Db 30 dfgfpehlvdflqsls 46

RESULT 13
 AAY91233
 ID AAY91233 standard; peptide: 46 AA.
 XX
 AC AAY91233;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Modified MWF Th epitope/CERP peptide, SEQ ID NO:111.
 XX
 KM Promiscuous T-cell epitope; measles virus F protein; MWF;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMOV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 PN MO966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-0513975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBL-) UNITED BIOMEDICAL, INC.
 XX
 PI Wang CY;
 XX
 DR WPI: 2000-160564/14.
 XX
 FT New artificial T helper cell epitope and derived immunogens with target
 FT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 FT or human immune deficiency virus
 XX
 PS Claim 11: Page 104-105; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals, and
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MWF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin, and AAY91201-Y91207 are antigenic
 CC immunogens may be used to promote growth in livestock. AAY91208 is a

CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MWF Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MWF Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC Th epitope and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MWF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasion
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 CC
 XX
 SQ Sequence 46 AA:
 XX
 Query Match 52.5%; Score 85; DB 21; Length 46;
 Best Local Similarity 94.1%; Pred. No. 6.6e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 15 EFGFPEHLVDLFLQSLS 31
 :|||||
 DB 30 dfgfpehlvdflqsls 46
 XX
 RESULT 14
 AAM06127
 ID AAM06127 standard; Protein: 476 AA.
 XX
 AC AAM06127;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Human cholesterol ester transfer protein.
 XX
 KM Cholesteryl ester transfer protein; CETP; antigen; vaccine;
 KM cardiovascular disease; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 349..367
 FT /label= B-cell_epitope
 FT Region 461..476
 FT /label= B-cell_epitope
 FT /note= "C-terminal epitope involved in neutral
 FT lipid binding or a transfer activity of
 FT CETP (Claim 5)"
 XX
 PN MO9634888-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 01-MAY-1996; 96WO-US06147.
 XX
 PR 01-MAY-1995; 95US-0432483.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI: 1996-506103/50.
 XX
 FT Cholesteryl ester transfer protein B cell epitope linked to T cell
 FT epitope - used to generate vaccine to regulate CETP activity for

PT decreasing the risk of developing a cardiovascular disease e.g. atherosclerosis

XX Claim 2; Page 44-47; 72pp; English.

XX Human liver mature cholesterol ester transfer protein (CETP) (AA06127)

CC plays a role in altering the relative profile of circulating lipoproteins to one associated with an increased risk of cardiovascular disease. B-cell epitopes (see also AA06128) of CETP can be used in novel peptide vaccines (see also AA06129; AA06131) that elicit an immune response against endogenous CETP activity, thereby treating or preventing cardiovascular disease, such as atherosclerosis.

CC Sequence 476 AA;

SQ

Query Match 52.5%; Score 85; DB 17; Length 476;
 Best Local Similarity 94.1%; Pred. No. 9.7e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPPEHLVDFLOSLS 31
 :|||||
 Db 460 dfgfpehlvdfllqsls 476

RESULT 15
 AA06446
 ID AA06446 standard; Peptide: 476 AA.
 AC AA06446;
 XX 18-MAY-1998 (first entry)
 DT
 XX Human mature cholesterol ester transfer protein (CETP).
 DE
 XX Cholesterol ester transfer protein; CETP; cholesterol ester; high density lipoprotein; HDL; very low density lipoprotein; VLDL; low density lipoprotein; LDL; atherosclerosis; neutral lipid binding; transfer activity; immunogenic; B cell epitope; antibody; TP2; DNA plasmid-based vaccine; broad range helper T cell epitope; treatment; cardiovascular disease.
 KW
 XX Homo sapiens.
 OS
 XX MO9741227-A1.
 PN
 XX 06-NOV-1997.
 PD
 XX 01-MAY-1997; 97MO-0507294.
 PF
 XX 21-FEB-1997; 97US-0802967.
 PR
 XX 01-MAY-1996; 96US-0640713.
 XX
 PA (TCCEL-) T CELL SCI INC.
 XX
 PT Thomas LJ;
 XX
 DR WPI: 1997-549731/50.
 DR N-PSDB: AAV05127.
 XX
 PT DNA plasmid-based vaccine encodes CETP B cell and helper T cell epitope(s) - used for elevating high density lipoprotein levels, and for treating cardiovascular disease
 XX
 PS Claim 6; Pages 36-38; 67pp; English.
 XX
 CC The present sequence represents a human mature cholesterol ester transfer protein (CETP). CETPs mediate the transfer of cholesterol esters from high density lipoprotein (HDL) to very low density lipoprotein (VLDL) and low density lipoprotein (LDL). An increased CETP activity produces an atherogenic lipoprotein profile and induces atherosclerosis. A 13 amino acid stretch in the human CETP (Phe463 to Leu475), and also

CC possibly Asp460, are particularly important for neutral lipid binding and transfer activity. This region has been shown to be immunogenic as a B cell epitope of CETP, and a monoclonal antibody (TP2) directed at this region has been shown to inhibit neutral lipid transfer. A second B cell epitope is defined by Arg349 to Ile367. Antibodies to this second epitope would allow the formation of immune complexes involving CETP, and promote the removal of the complexed CETP. This peptide region was selected for its potential antigenicity and high possibility for surface expression on native CETP. Sequences encoding these 2 epitopes can be used in a DNA plasmid-based vaccine which comprises sequences encoding at least 1 B cell epitope of CETP linked in frame with at least one segment encoding a broad range helper T cell epitope. The vaccines can be used to elevate the ratio of circulating HDL to circulating LDL, VLDL or total cholesterol in a human. It can also be used for decreasing the level of endogenous CETP activity in a human. The vaccine can be used to produce anti-CETP antibodies in vivo and for treating cardiovascular disease.

CC Sequence 476 AA;

SQ

Query Match 52.5%; Score 85; DB 18; Length 476;
 Best Local Similarity 94.1%; Pred. No. 9.7e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPPEHLVDFLOSLS 31
 :|||||
 Db 460 dfgfpehlvdfllqsls 476

Search completed: June 18, 2002, 08:08:27
 Job time: 156 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:11:59 / Search time 205.61 seconds
(without alignments)

53,068 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYIKANSFKTGTETFGPEHLVDFLQSL 31

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	31	US-08-432-483-2	Sequence 2, Appl1
2	162	100.0	31	US-08-432-483A-2	Sequence 2, Appl1
3	162	100.0	31	US-08-943-548-2	Sequence 2, Appl1
4	162	100.0	31	US-08-943-548-7	Sequence 2, Appl1
5	162	100.0	31	US-09-529-762-2	Sequence 7, Appl1
6	162	100.0	31	US-09-943-334-2	Sequence 2, Appl1
7	162	100.0	31	US-09-943-548-2	Sequence 2, Appl1

8	142.5	88.0	50	13	US-08-945-289-8	Sequence 8, Appl1
9	142.5	88.0	50	23	US-09-943-334-8	Sequence 8, Appl1
10	142.5	88.0	50	23	US-09-943-548-8	Sequence 8, Appl1
11	129.5	79.9	50	10	US-08-640-713-7	Sequence 7, Appl1
12	129.5	79.9	50	12	US-08-802-967A-7	Sequence 7, Appl1
13	129.5	79.9	50	13	US-08-945-289-9	Sequence 9, Appl1
14	129.5	79.9	50	23	US-09-943-334-9	Sequence 9, Appl1
15	129.5	79.9	50	23	US-09-943-548-9	Sequence 9, Appl1
16	87	53.7	35	1	PCT-US99-139758-114	Sequence 114, App
17	87	53.7	35	21	US-09-701-588-114	Sequence 114, App
18	85	52.5	22	11	US-08-785-997-10	Sequence 10, Appl
19	85	52.5	22	11	US-08-785-997-34	Sequence 34, Appl
20	85	52.5	22	11	US-08-788-882-10	Sequence 10, Appl
21	85	52.5	22	11	US-08-788-882-34	Sequence 34, Appl
22	85	52.5	22	13	US-08-934-367-10	Sequence 10, Appl
23	85	52.5	22	13	US-08-934-367-34	Sequence 34, Appl
24	85	52.5	22	17	US-09-386-591-10	Sequence 10, Appl
25	85	52.5	22	17	US-09-386-591-34	Sequence 34, Appl
26	85	52.5	22	17	US-09-387-340-10	Sequence 10, Appl
27	85	52.5	22	17	US-09-387-340-34	Sequence 34, Appl
28	85	52.5	26	1	PCT-US99-139758-106	Sequence 106, App
29	85	52.5	26	8	US-08-432-483-1	Sequence 1, Appl1
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39	85	52.5	26	23	US-09-943-548-1	Sequence 1, Appl1
40	85	52.5	46	1	PCT-US99-139758-110	Sequence 110, App
41	85	52.5	46	1	US-09-701-588-110	Sequence 110, App
42	85	52.5	46	21	US-09-701-588-111	Sequence 111, App
43	85	52.5	46	21	US-09-701-588-111	Sequence 111, App
44	85	52.5	470	19	US-09-518-598-114	Sequence 14, Appl
45	85	52.5	470	22	US-09-872-128-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-432-483-2
Sequence 2, Appl1
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSPORT PROTEIN (CEP) ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179/(PCS-95179)

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-432-483-2

Query Match          100.0%; Score 162; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 COYIKANSKFTGTFEGFPEHLVDFLOSLS 31
       11111111111111111111111111111111
Db      1 COYIKANSKFTGTFEGFPEHLVDFLOSLS 31

RESULT 2
US-08-432-483A-2
; Sequence 2, Application US/08432483A
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483A
; FILING DATE: 1-May-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-432-483A-2

Query Match          100.0%; Score 162; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 COYIKANSKFTGTFEGFPEHLVDFLOSLS 31
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Db      1 COYIKANSKFTGTFEGFPEHLVDFLOSLS 31

RESULT 3
US-08-945-289-2
; Sequence 2, Application US/08945289
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,289
; FILING DATE: October 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/432,483
; FILING DATE: May 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-411.1P US
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-945-289-2

Query Match          100.0%; Score 162; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-08-954-643-7
; Sequence 7, Application US/08954643
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: XENOTGENIC CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) FOR MODULATION OF CETP ACTIVITY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: MA
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COUNTRY: U.S.A.
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,643
FILING DATE: concurrently herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-420.0 US
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-954-643-7
```

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Query Match          100.0%; Score 162; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
```

```
RESULT 5
US-09-529-762-7
; Sequence 7, Application US/09529762
; GENERAL INFORMATION:
; APPLICANT: AVANT Immunotherapeutics, Inc.
; APPLICANT: Rittershaus, Charles
; APPLICANT: Thomas, Lawrence
; TITLE OF INVENTION: Xenogeneic Cholesteryl Ester Transfer Protein (CETP) for
; FILE REFERENCE: sequence listing for TCS-420.1 PCT
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US/09/529,762
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fusion protein containing tetanus toxoid segment
; OTHER INFORMATION: linked to human CETP C-terminus
US-09-529-762-7
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Query Match          100.0%; Score 162; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
```

RESULT 6

```
US-09-943-334-2
; Sequence 2, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US/09/943,334
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-334-2
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Query Match          100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
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RESULT 7
US-09-943-548-2
; Sequence 2, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-2
```

```
Query Match          100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
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RESULT 8
US-08-945-289-8

```
Sequence 8, Application US/08945289
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
NUMBER OF INVENTIONS: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,289
FILING DATE: October 17, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/432,483
FILING DATE: May 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-411.1P US
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY:
LOCATION:
US-08-945-289-8

Query Match      88.0% Score 142.5; DB 13; Length 50;
Best Local Similarity 62.0%; Pred. No. 6.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 CQYKANSKFIGITE-----FGPEHLVDPLQSL 31
Db 1 CQYKANSKFIGITELEFPRPDQHSVAYTFEEDIFGPEHLVDPLQSL 50

RESULT 9
US-09-943-334-8
Sequence 8, Application US/09943314
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,334
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 50
```

```
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: vaccine peptide of the Invention
US-09-943-334-8

Query Match      88.0% Score 142.5; DB 23; Length 50;
Best Local Similarity 62.0%; Pred. No. 6.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 CQYKANSKFIGITE-----FGPEHLVDPLQSL 31
Db 1 CQYKANSKFIGITELEFPRPDQHSVAYTFEEDIFGPEHLVDPLQSL 50

RESULT 10
US-09-943-548-8
Sequence 8, Application US/09943548
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,548
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 50
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: vaccine peptide of the Invention
US-09-943-548-8

Query Match      88.0% Score 142.5; DB 23; Length 50;
Best Local Similarity 62.0%; Pred. No. 6.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 CQYKANSKFIGITE-----FGPEHLVDPLQSL 31
Db 1 CQYKANSKFIGITELEFPRPDQHSVAYTFEEDIFGPEHLVDPLQSL 50

RESULT 11
US-08-640-713-7
Sequence 7, Application US/08640713
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMIN-BASED VACCINE FOR TREATING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/640,713
FILING DATE: May 1, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,1102(TCS-205-999)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE: amino acid sequence of peptide encoded by
FEATURE: bases 10 to 159 of SEQ ID NO:5
NAME/KEY:
LOCATION:
US-08-640-713-7

Query Match 79.9%; Score 129.5; DB 10; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 2 QYKANSKFIGITE-----FGPPEHLVDPLQSL 31
DB 2 QYKANSKFIGITERPPDGRAVAVRFEEDIFGPKHLVDPLQSL 50

RESULT 12
US-08-967A-7
Sequence 7, Application US/08802967A
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMIID-BASED VACCINE FOR
NUMBER OF INVENTION: TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: word 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,967A
FILING DATE: 21-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 US
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:

NAME/KEY: amino acid sequence of peptide encoded
NAME/KEY: by bases 10 to 159 of SEQ ID NO:5
LOCATION:
US-08-802-967A-7

Query Match 79.9%; Score 129.5; DB 12; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 2 QYKANSKFIGITE-----FGPPEHLVDPLQSL 31
DB 2 QYKANSKFIGITERPPDGRAVAVRFEEDIFGPKHLVDPLQSL 50

RESULT 13
US-08-945-289-9
Sequence 9, Application US/08945289

GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,289
FILING DATE: October 17, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/432,483
FILING DATE: May 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-411.1P US
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY:
LOCATION:
US-08-945-289-9

Query Match 79.9%; Score 129.5; DB 13; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 2 QYKANSKFIGITE-----FGPPEHLVDPLQSL 31
DB 2 QYKANSKFIGITERPPDGRAVAVRFEEDIFGPKHLVDPLQSL 50

RESULT 14
US-09-943-334-9
Sequence 9, Application US/09943334

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; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; PRIORITY FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-334-9

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```

Query Match          79.9%; Score 129.5; DB 23; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

```

```

QY 2 QYKANSKFIGITE-----FGFPHLVDPLQSLIS 31
   |||||
DB 2 QYKANSKFIGITERFPPDGRBAVAYRFEEDI FGFPHLVDPLQSLIS 50

```

```

RESULT 15
US-09-943-548-9
; Sequence 9, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; PRIORITY FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-9

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```

Query Match          79.9%; Score 129.5; DB 23; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

```

```

QY 2 QYKANSKFIGITE-----FGFPHLVDPLQSLIS 31
   |||||
DB 2 QYKANSKFIGITERFPPDGRBAVAYRFEEDI FGFPHLVDPLQSLIS 50

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Search completed: June 18, 2002, 08:11:59
 Job time: 368 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 08:07:29 ; Search time 26.25 Seconds
(without alignments)
99.954 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 CQYKANSKRTGTERGPEHLVDLQSLUS 31

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 257105 seqs, 84670655 residues

Total number of hits satisfying chosen parameters: 257105

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

Pending Patents_AA-New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	52.5	470	5	US-09-446-415B-6
2	78.5	48.5	24	6	US-10-128-711-110
3	71.5	44.1	27	6	US-10-076-674-7
4	71.5	44.1	27	6	US-10-076-674-7
5	70	43.2	14	5	US-09-707-738-5
6	70	43.2	14	5	US-09-543-608A-38
7	70	43.2	14	5	US-09-709-774-5
8	70	43.2	14	5	US-09-942-052-710
9	70	43.2	14	5	US-09-260-714B-1
10	70	43.2	14	6	US-10-128-711-95
11	70	43.2	14	6	US-10-001-469-1403
12	70	43.2	15	5	US-09-413-186A-11
13	70	43.2	17	1	PCT-US02-10293-3
14	70	43.2	25	5	US-09-413-186A-14
15	70	43.2	25	5	US-09-413-186A-15
16	70	43.2	25	5	US-09-413-186A-16
17	70	43.2	27	6	US-10-128-711-111
18	70	43.2	27	6	US-10-128-711-112
19	70	43.2	1315	6	US-10-018-997-1
20	53	32.7	11	5	US-09-523-033A-3
21	51	31.5	348	7	US-60-360-039-850
22	49	30.2	80	5	US-09-620-393B-4183
23	49	30.2	80	5	US-09-620-393B-8965
24	49	30.2	99	5	US-09-620-393B-4182
25	49	30.2	99	5	US-09-620-393B-8964
26	49	30.2	120	5	US-09-620-393B-4181

27	49	30.2	120	5	US-09-620-393B-8963	Sequence 8963, Ap
28	48.5	29.9	735	6	US-10-032-361-2	Sequence 2, Appl1
29	48.5	29.9	826	1	PCT-US02-08886-10	Sequence 10, Appl
30	48.5	29.9	826	1	PCT-US02-08864-6	Sequence 6, Appl1
31	48.5	29.9	826	1	PCT-US02-08946-2	Sequence 2, Appl1
32	48.5	29.9	826	1	PCT-US02-08946-5	Sequence 5, Appl1
33	48.5	29.9	826	1	PCT-US02-08946-6	Sequence 6, Appl1
34	48.5	29.9	826	1	PCT-US02-08946-7	Sequence 7, Appl1
35	48.5	29.9	826	5	US-09-555-362-10	Sequence 10, Appl
36	48.5	29.9	826	6	US-10-032-361-1	Sequence 1, Appl1
37	48.5	29.9	826	6	US-10-113-872-330	Sequence 330, App
38	48.5	29.9	826	6	US-10-028-158-23	Sequence 23, Appl
39	48.5	29.9	826	6	US-10-007-255-4	Sequence 4, Appl1
40	47	29.0	331	6	US-09-540-209B-8239	Sequence 8239, App
41	47	29.0	335	6	US-10-102-806-729	Sequence 729, App
42	47	29.0	538	1	PCT-US02-11152-5	Sequence 5, Appl1
43	46	28.4	555	6	US-10-104-047-2011	Sequence 2011, Ap
44	46	28.4	1038	5	US-09-935-625-16165	Sequence 16166, A
45	46	28.4	1124	5	US-09-935-625-22443	Sequence 22443, A

ALIGNMENTS

```

RESULT 1
US-09-446-415B-6
; Sequence 6, Application US/09446415B
; GENERAL INFORMATION:
; APPLICANT: Beamer, Lesa J.
; APPLICANT: Eisenberg, David
; TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
; TITLE OF INVENTION: STRUCTURALIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
; TITLE OF INVENTION: MOLECULAR MODELING OF RELATED PROTEINS
; FILE REFERENCE: 11034US02
; CURRENT APPLICATION NUMBER: US/09/446,415B
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 08/879,565
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: Cholesteryl ester transfer protein (CETP) (Figure
US-09-446-415B-6
;

Query Match          52.5%; Score 85; DB 5; Length 470;
Best local similarity 94.1%; Pred. No. 5e+05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EGFPEHLVDLQSLUS 31
Db 454 DFEFPEHLVDLQSLUS 470

RESULT 2
US-10-128-711-110
; Sequence 110, Application US/10128711
; GENERAL INFORMATION:
; APPLICANT: VITTILO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esben
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-128-711-110

Query Match 48.5%; Score 78.5; DB 6; Length 24;
Best local similarity 65.5%; Pred. No. 1.8e-05;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY 2 OYIKANSKFIGITGEGPEHLDVDELSL 30
DB 1 OYIKANSKFIGITGEGPEHLDVDELSL 24

RESULT 3
US-10-076-674-7
Sequence 7, Application US/10076674
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent version 3.1
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Human
US-10-076-674-7

Query Match 44.1%; Score 71.5; DB 6; Length 27;

Best Local Similarity 80.0%; Pred. No. 0.00024;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 2 OYIKANSKFIGITGEGPEH 21
DB 3 OYIKANSKFIGITGEL---EH 19

RESULT 4
US-10-076-674A-7
Sequence 7, Application US/10076674A
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674A
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent version 3.1
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Human
US-10-076-674A-7

Query Match 44.1%; Score 71.5; DB 6; Length 27;
Best local similarity 80.0%; Pred. No. 0.00024;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 2 OYIKANSKFIGITGEGPEH 21
DB 3 OYIKANSKFIGITGEL---EH 19

RESULT 5
US-09-707-738-5
Sequence 5, Application US/09707738
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffery L.
TITLE OF INVENTION: Induction of Immune Response Against
FILE REFERENCE: 018623-006250US
CURRENT APPLICATION NUMBER: US/09/707,738
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 08/121,101
PRIOR FILING DATE: 1993-09-14
PRIOR APPLICATION NUMBER: US 08/305,871
PRIOR FILING DATE: 1994-09-14
PRIOR APPLICATION NUMBER: US 08/485,218
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 60/010,510
PRIOR FILING DATE: 1996-01-24
PRIOR APPLICATION NUMBER: US 08/788,822
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/310,462
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tet Tox 830-843, T-helper epitope from tetanus
OTHER INFORMATION: toxin p2, peptide 553-01
US-09-707-738-5

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Query Match      43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 OYKANSKFIGITE 15
DB      1 OYKANSKFIGITE 14

RESULT      6
US-09-543-608A-38
; Sequence 38, Application US/09543608A
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Vaccine Compositions
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tetanus toxoid positions 830-843, Standard Peptide
US-09-543-608A-38

Query Match      43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 OYKANSKFIGITE 15
DB      1 OYKANSKFIGITE 14

RESULT      7
US-09-709-774-5
; Sequence 5, Application US/09709774
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffery L.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan DR-Binding
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 018623-006240US
; CURRENT APPLICATION NUMBER: US/09/709,774
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 08/121,101
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: US 08/305,871
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: US 60/010,510
; PRIOR FILING DATE: 1996-01-24
; PRIOR APPLICATION NUMBER: US 08/788,822
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tet Tox 830-843
US-09-709-774-5

Query Match      43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 OYKANSKFIGITE 15
DB      1 OYKANSKFIGITE 14

RESULT      8
US-09-942-052-710
; Sequence 710, Application US/09942052
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afari, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Chailita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tetanus toxoid
US-09-942-052-710

Query Match      43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 OYKANSKFIGITE 15
DB      1 OYKANSKFIGITE 14

RESULT      9
US-09-260-714B-1
; Sequence 1, Application US/09260714B
; GENERAL INFORMATION:
; APPLICANT: EpiImmune Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chesnut, Robert
; APPLICANT: Sidney, John
; TITLE OF INVENTION: PEPTIDES WITH INCREASED BINDING AFFINITY
; TITLE OF INVENTION: FOR HLA A3 SUPERTYPE MOLECULES
; FILE REFERENCE: 39963-20028.00
; CURRENT APPLICATION NUMBER: US/09/260,714B
; CURRENT FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
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TYPE: PRT
ORGANISM: Tetanus toxoid
US-09-260-714B-1

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
DB 1 OYIKANSKFIGITE 14

RESULT 10
US-10-128-711-95
Sequence 95, Application US/10128711
GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.
CHESTNUT, Robert W.
SETTE, Alessandro D.
CEUS, Estdan
GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..14

OTHER INFORMATION: /note= "Tetanus toxoid 830-843"

US-10-128-711-95

Query Match 43.2%; Score 70; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
DB 1 OYIKANSKFIGITE 14

RESULT 11
US-10-001-469-1403

Sequence 1403, Application US/10001469
GENERAL INFORMATION:

APPLICANT: JAKOBOWITS, AVA
APPLICANT: RATTANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: SAFRAN, DOUGLAS
APPLICANT: HUBERT, RENE
APPLICANT: PARIS, MARY

APPLICANT: CHALLITA-EID, PIA

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

FILE REFERENCE: 51158-20024.20

CURRENT APPLICATION NUMBER: US/10/001,469

CURRENT FILING DATE: 2002-05-20

PRIOR APPLICATION NUMBER: 60/157,902

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/291,118

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 09/680,728

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 2868

SOFTWARE: Patentln Ver. 2.1

SEQ ID NO 1403

LENGTH: 14

TYPE: PRT

ORGANISM: Clostridium sp.

US-10-001-469-1403

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
DB 1 OYIKANSKFIGITE 14

RESULT 12
US-09-413-186A-11

Sequence 11, Application US/09413186A
GENERAL INFORMATION:

APPLICANT: Steinna, Lucilla
APPLICANT: Moutilsen, Soren
APPLICANT: Gautam, Anand
APPLICANT: Haaning, Jesper
APPLICANT: Dalum, Iben
APPLICANT: Birk, Peter
APPLICANT: Leach, Dana

APPLICANT: Nielsen, Klaus

APPLICANT: Karlsson, Gunilla

TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION

FILE REFERENCE: 3631-0115P

CURRENT APPLICATION NUMBER: US/09/413,186A

CURRENT FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/105,011

PRIOR FILING DATE: 1998-10-20

PRIOR APPLICATION NUMBER: PA 1998 01261

PRIOR FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 36

US-09-413-186A-11

```

; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-413-186A-11

```

```

Query Match      43.2%; Score 70; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 QYKANSKFIGITE 15
        |||||
Db       1 QYKANSKFIGITE 14

```

```

RESULT 13
PCT-US02-10293-3

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```

; Sequence 3, Application PC/TUS0210293
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: PCT/US02/10293
; CURRENT FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Clostridium tetani
PCT-US02-10293-3

```

```

Query Match      43.2%; Score 70; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 QYKANSKFIGITE 15
        |||||
Db       3 QYKANSKFIGITE 16

```

```

RESULT 14

```

```

US-09-413-186A-14
; Sequence 14, Application US/09413186A
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gaustam, Amand
; APPLICANT: Haaning, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 3631-0115P
; CURRENT APPLICATION NUMBER: US/09-413,186A
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
US-09-413-186A-14

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```

Query Match      43.2%; Score 70; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 QYKANSKFIGITE 15
        |||||
Db       6 QYKANSKFIGITE 19

```

```

RESULT 15

```

```

US-09-413-186A-15
; Sequence 15, Application US/09413186A
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gaustam, Amand
; APPLICANT: Haaning, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 3631-0115P
; CURRENT APPLICATION NUMBER: US/09-413,186A
; CURRENT FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
US-09-413-186A-15

```

```

Query Match      43.2%; Score 70; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 QYKANSKFIGITE 15
        |||||
Db       6 QYKANSKFIGITE 19

```

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Search completed: June 18, 2002, 08:07:29
Job time: 98 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 08:06:56 ; Search time 21.87 seconds
(Without alignments)
34.666 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162

Sequence: 1 COYIKANSKRFITGFEPGPHLVDFLOSLIS 31

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129.5	79.9	50	4	US-09-171-969-7
2	85	52.5	470	3	US-08-879-565-14
3	85	52.5	476	4	US-09-171-969-4
4	81	50.0	496	4	US-09-171-969-2
5	78.5	48.5	24	5	PCT-US92-07218-25
6	78.5	48.5	24	5	PCT-US95-02121-110
7	78.5	48.5	27	5	PCT-US95-02121-110
8	77.5	47.8	37	2	US-08-446-692-63
9	77.5	47.8	37	2	US-08-446-692-63
10	76.5	47.2	47	1	US-08-446-692-35
11	76.5	47.2	47	2	US-08-446-692-35
12	76	46.9	37	2	US-08-446-692-57
13	76	46.9	37	2	US-08-446-692-57
14	71.5	44.1	27	1	US-08-446-692-13
15	71.5	44.1	27	2	US-08-446-692-13
16	70	43.2	14	1	US-08-186-266-5
17	70	43.2	14	1	US-08-305-871A-5
18	70	43.2	14	1	US-08-465-167A-18
19	70	43.2	14	5	US-08-817-933A-9
20	70	43.2	14	5	PCT-US92-07218-15
21	70	43.2	14	5	PCT-US92-07218-30
22	70	43.2	14	5	PCT-US95-02121-95
23	70	43.2	15	2	US-08-319-704-10
24	70	43.2	15	2	US-08-661-052-6
25	70	43.2	15	2	US-08-460-502-7
26	70	43.2	15	4	US-09-046-373-2
27	70	43.2	15	4	US-09-188-082-6

28	70	43.2	15	5	PCT-US93-11703-69	Sequence 69, Appl
29	70	43.2	16	4	US-09-248-588-55	Sequence 55, Appl
30	70	43.2	17	1	US-08-446-692-4	Sequence 4, Appl
31	70	43.2	17	2	US-08-488-351A-4	Sequence 4, Appl
32	70	43.2	17	5	US-09-100-409A-40	Sequence 23, Appl
33	70	43.2	17	5	PCT-US95-08596-23	Sequence 23, Appl
34	70	43.2	17	5	PCT-US95-13841-7	Sequence 7, Appl
35	70	43.2	24	5	PCT-US92-07218-31	Sequence 31, Appl
36	70	43.2	27	5	PCT-US92-07218-26	Sequence 26, Appl
37	70	43.2	27	5	PCT-US92-07218-27	Sequence 27, Appl
38	70	43.2	27	5	PCT-US92-07218-28	Sequence 28, Appl
39	70	43.2	27	5	PCT-US95-02121-111	Sequence 111, App
40	70	43.2	27	5	PCT-US95-02121-112	Sequence 112, App
41	70	43.2	29	3	US-09-075-257A-13	Sequence 13, Appl
42	70	43.2	29	3	US-09-075-257A-14	Sequence 14, Appl
43	70	43.2	29	4	US-09-534-639-13	Sequence 13, Appl
44	70	43.2	29	4	US-09-534-639-14	Sequence 14, Appl
45	70	43.2	30	5	PCT-US92-07218-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-171-969-7
Sequence 7, Appl
Patent No. 628453
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Mitcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL:
NAME/KEY:
FEATURE: amino acid sequence of peptide encoded
FEATURE: by bases 10 to 159 of SEQ ID NO:5
LOCATION:
US-09-171-969-7
Query Match 79.9%; Score 129.5; DB 4; Length 50;

Best Local Similarity 59.2%; Pred. No. 2.2e-14;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

OY 2 OYKANSKFIGITE-----FGFPHLVDFLOSIS 31
|||||
Db 2 OYKANSKFIGITERPPRDPGRVAVAREEDIFGFPHLVDFLOSIS 50

RESULT 2
US-08-879-565-14

; Sequence 14, Application US/08879565A
; Patent No. 6093573

; GENERAL INFORMATION:
; APPLICANT: Beamer, Lesa J.

; APPLICANT: Carroll, Stephen F.
; APPLICANT: Eisenberg, David

; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF
; TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN

; FILE REFERENCE: 1103/11034US01
; CURRENT APPLICATION NUMBER: US/08/879,565A

; CURRENT FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14

; LENGTH: 470
; TYPE: PRT

; ORGANISM: Human
; FEATURE:

; OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure
; OTHER INFORMATION: 5)

US-08-879-565-14

Query Match 52.5%; Score 85; DB 3; Length 470;
Best Local Similarity 94.1%; Pred. No. 6.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPHLVDFLOSIS 31
:|||||

Db 454 DFGFPHLVDFLOSIS 470

RESULT 3
US-09-171-969-4

; Sequence 4, Application US/09171969
; Patent No. 6284533

; GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.

; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.

; STREET: 75 State Street, Suite 2300
; CITY: Boston

; STATE: Massachusetts
; COUNTRY: USA

; ZIP: 02109-1807
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,969

; FILING DATE: 01 May 1997 (01.05.97)
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,713

; FILING DATE: 01 May 1996 (01.05.96)
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/802,967
; FILING DATE: 21 February 1997 (21.02.97)

; ATTORNEY/AGENT INFORMATION:
; ATTORNEY/AGENT INFORMATION:

NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYDROTHERICAL:
ANTI-SENSE:

FEATURE:

NAME/KEY: Amino acid sequence of mature human
NAME/KEY: CETP
LOCATION:

PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.

TITLE: Cloning and sequencing of human
TITLE: cholesterol ester transfer cDNA

JOURNAL: Nature
VOLUME: 327

ISSUE:
PAGES: 632 - 634

DATE: 18-JUN-1987
; RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476

US-09-171-969-4

Query Match 52.5%; Score 85; DB 4; Length 476;
Best Local Similarity 94.1%; Pred. No. 6.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPHLVDFLOSIS 31
:|||||

Db 460 DFGFPHLVDFLOSIS 476

RESULT 4
US-09-171-969-2

; Sequence 2, Application US/09171969
; Patent No. 6284533

; GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.

; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.

; STREET: 75 State Street, Suite 2300
; CITY: Boston

; STATE: Massachusetts
; COUNTRY: USA

; ZIP: 02109-1807
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,969

; FILING DATE: 01 May 1997 (01.05.97)
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,713

; FILING DATE: 01 May 1996 (01.05.96)
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/802,967
; FILING DATE: 21 February 1997 (21.02.97)

; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich

; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)

; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence for mature
NAME/KEY: rabbit CERP protein.
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Nagashima, Mariko, et al.
TITLE: Cloning and mRNA tissue
TITLE: distribution of rabbit
TITLE: cholesterol ester transfer
TITLE: protein
JOURNAL: J. Lipid Res.
VOLUME: 29
ISSUE:
PAGES: 1643 - 1649
DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 496
US-09-171-969-2

Query Match 50.0%; Score 81; DB 4; Length 496;
Best Local Similarity 88.2%; Pred. No. 3.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 15 EFGPEHLVDLQSL 31
:|||||
Db 480 DFGPKHLVDLQSL 496

RESULT 5
PCT-US92-07218-25
Sequence 25, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitiello, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPITOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-07218-25

Query Match 48.5%; Score 78.5; DB 5; Length 24;
Best Local Similarity 65.5%; Pred. No. 2.2e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

Qy 2 QYTKANSFGITGEPPEHLVDLQSL 30
:|||||
Db 1 QYTKANSFGITGEP-----LPSPFFPSV 24

RESULT 6
PCT-US95-02121-110
Sequence 110, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-110

Query Match 48.5%; Score 78.5; DB 5; Length 24;
Best Local Similarity 65.5%; Pred. No. 2.2e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

```
OY      2 OYKANSKFITGTERGPEHLVDFLOSL 30
Db      1 OYKANSKFITGTER-----LPSDFPSV 24

RESULT 7
PCT-US92-07218-32
; Sequence 32, Application PC/TUS9207218
; GENERAL INFORMATION:
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Chesnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPTOPES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07218
; FILING DATE: 19920826
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,423
; REFERENCE/DOCKET NUMBER: 14137-26-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-5043
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-07218-32

Query Match      48.5%; Score 78.5; DB 5; Length 27;
Best Local Similarity 65.5%; Pred. No. 2.6e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY      2 OYKANSKFITGTERGPEHLVDFLOSL 30
Db      4 OYKANSKFITGTER-----LPSDFPSV 27

RESULT 8
US-08-446-692-63
; Sequence 63, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
;

OY      2 OYKANSKFITGTERG-----FPEH 21
Db      5 OYKANSKFITGTERLGTAKSKKPPSY 31

Query Match      47.8%; Score 77.5; DB 1; Length 37;
Best Local Similarity 63.0%; Pred. No. 5.5e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

RESULT 9
US-08-488-351A-63
; Sequence 63, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-63

Query Match 47.8%; Score 77.5; DB 2; Length 37;
Best Local Similarity 63.0%; Pred. No. 5.5e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 2 QYIANSKFIGITRGFG-----PPEH 21
DB 5 QYIANSKFIGITRGFGTRAKSKKFPY 31

RESULT 10
US-08-446-692-35
; Sequence 35, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
```

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-35
```

```

Query Match 47.2%; Score 76.5; DB 1; Length 47;
Best Local Similarity 85.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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QY 2 QYIANSKFIGITRGFGPPEH 21
DB 21 QYIANSKFIGITRGFG-GRH 39
```

```

RESULT 11
US-08-488-351A-35
; Sequence 35, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Y1
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-35
```

```

Query Match 47.2%; Score 76.5; DB 2; Length 47;
Best Local Similarity 85.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
```

OY 2 OYKANSKFITGTEFGPEH 21
 ||||| 11
 Db 21 OYKANSKFITGTEFG-GEH 39

RESULT 12

US-08-446-692-57
 Sequence 57, Application US/08446692
 Patent No. 5759551

GENERAL INFORMATION:
 APPLICANT: Ladd, Anna
 APPLICANT: Wang, Chang Y1
 APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C.H. Lin
 REGISTRATION NUMBER: 29,323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)415-8745
 TELEFAX: (516)751-6849
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-446-692-57

Query Match 46.9%; Score 76; DB 1; Length 37;
 Best Local Similarity 93.8%; Pred. No. 9.7e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 OYKANSKFITGTEFG 17
 ||||| 11
 Db 21 OYKANSKFITGTEFG 36

RESULT 13

US-08-488-351A-57
 Sequence 57, Application US/08488351A
 Patent No. 5843446

GENERAL INFORMATION:
 APPLICANT: Ladd, Anna
 APPLICANT: Wang, Chang Y1
 APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York

STATE: NY
 COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,351A
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,692
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/229,275
 FILING DATE: 14-APR-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/057,166
 FILING DATE: 27-APR-1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Maria C.H. Lin
 REGISTRATION NUMBER: 29,323
 REFERENCE/DOCKET NUMBER: 1151-4146 US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)415-8745
 TELEFAX: (516)751-6849
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-488-351A-57

Query Match 46.9%; Score 76; DB 2; Length 37;
 Best Local Similarity 93.8%; Pred. No. 9.7e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 OYKANSKFITGTEFG 17
 ||||| 11
 Db 21 OYKANSKFITGTEFG 36

RESULT 14

US-08-446-692-13
 Sequence 13, Application US/08446692
 Patent No. 5759551

GENERAL INFORMATION:
 APPLICANT: Ladd, Anna
 APPLICANT: Wang, Chang Y1
 APPLICANT: Zamb, Timothy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Maria C.H. Lin
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-692-13

Query Match 44.1%; Score 71.5; DB 1; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 QYKANSKFIGITFGGPEH 21
|||||
DB 3 QYKANSKFIGITEL--EH 19

RESULT 15
US-08-488-351A-13
Sequence 13, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulants for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745

TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-13

Query Match 44.1%; Score 71.5; DB 2; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 QYKANSKFIGITFGGPEH 21
|||||
DB 3 QYKANSKFIGITEL--EH 19

Search completed: June 10, 2002, 08:06:57
Job time: 66 sec

4
5
6

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:08:31 ; Search time 14.11 Seconds

(without alignments)
177,060 Million cell updates/sec

Title: US-09-943-334-1

Sequence: 1 RDGFLLQMDGFPPEHLVDFLQSL 26

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 5201

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	20.9	19	2 A39504	octamer-binding pr
2	28	20.9	24	2 A24417	interphotoreceptor
3	28	20.9	26	2 B59018	MOC1 enhancer bind
4	27	20.1	21	2 A32521	hexokinase (EC 2.7
5	27	20.1	23	2 S43632	cytochrome-c oxida
6	27	20.1	26	2 S78374	hypothetical prote
7	26.5	19.8	20	2 A54077	cytochrome b558 -
8	26	19.4	15	2 S59492	formate dehydrogen
9	26	19.4	25	2 B24417	interphotoreceptor
10	26	19.4	26	2 C85947	hypothetical prote
11	25	18.7	15	2 S71306	heat shock protein
12	25	18.7	16	2 T44936	calmodulin kinase
13	25	18.7	16	2 C49048	T-cell receptor be
14	25	18.7	17	2 PH1607	Ig H chain V-D-J r
15	25	18.7	20	2 S77989	cytochrome-c oxida
16	25	18.7	23	2 PC4030	rRNA endonuclease
17	25	18.7	25	2 A60502	myonectin - norther
18	24.5	18.3	14	2 B61597	cytochrome P450 AL
19	24	17.9	13	2 S03879	6-phosphofructokin
20	24	17.9	14	2 A01250	angiotensin precur
21	24	17.9	15	2 A60834	angiotensin I prec
22	24	17.9	17	2 B31769	T-cell receptor de
23	24	17.9	18	2 FN0175	glutathione transf
24	24	17.9	18	2 H75063	hypothetical prote
25	24	17.9	20	2 A60822	cytochrome P450 PB
26	24	17.9	20	2 A37984	ADP-ATP carrier pr
27	23	17.2	7	2 S36662	dermorphin (lys-7)
28	23	17.2	14	2 PA0015	seed storage prote
29	23	17.2	17	2 S71864	glutathione transf

30	23	17.2	19	2 I46654	T-cell receptor de
31	23	17.2	21	2 T07683	protease inhibit
32	23	17.2	23	2 I39681	exeg protein - Aer
33	23	17.2	24	2 PC2199	alicyclic amine N-
34	23	17.2	24	2 T42257	phosphoprotein pho
35	23	17.2	24	2 A53357	neurotoxin Bc-II -
36	23	17.2	25	2 S35926	T-cell receptor ga
37	23	17.2	26	2 J70965	cytochrome-c oxida
38	23	17.2	26	2 M42218	early protein Sx1
39	23	16.4	7	1 A61324	dermorphin - Rohde
40	22	16.4	11	2 PT0250	19 heavy chain CRD
41	22	16.4	12	2 C36201	19 heavy chain CRD
42	22	16.4	14	2 A61002	photosystem II oxy
43	22	16.4	19	2 B60822	cytochrome P450 UT
44	22	16.4	20	2 S72501	protein kinase C 1
45	22	16.4	20	2 A31049	calsequestrin, fas

ALIGNMENTS

RESULT 1

1n, Ku-like, 72K chain - human (fragment)
ns (man)
sequence, revision 30-Dec-1991 #text_change 30-Sep-1993

: Gould, H.
J52-3059, 1991
and characterization of Ku-2, an octamer-binding protein relate
19504; MUID:91131605

1n

Query Match 20.9%; Score 28; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 LQMDGFP 13
|||
DB 11 LQMDGFP 17

RESULT 2
A24417
interphotoreceptor retinoid-binding protein - sheep (fragment)

N: Alternate names: Interstitial retinol-binding protein
C: Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C: Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
C: Accession: A24417

R: Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
FEBS Lett. 205, 309-312, 1986

A: Title: N-terminal sequence homologues in interstitial retinol-binding proteins from
A: Reference number: A91365; MUID: 86301171

A: Accession: A24417

A: Molecule type: protein

A: Residues: 1-24 <FON>
C: Superfamily: Interphotoreceptor retinoid-binding protein

Query Match 20.9%; Score 28; DB 2; Length 24;
Best Local Similarity 35.0%; Pred. No. 6.5e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 6; Gaps 1;

OY 5 LLLQMDGFPPEHL 18
|||
DB 5 LVLDMAQVLDNYTFPEPLM 24

RESULT 3
B59018
MUC1 enhancer binding protein 85K chain MUC1EBP-85 - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C:Accession: B59018
R:Abbe, M.; Smith, C.J.; Larson, C.J.
A:Submitted to the Protein Sequence Database, May 1998
A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a pro-
A:Reference number: A59018
A:Accession: B59018
A:Molecule type: protein
A:Residues: 1-171;18-26 <ABE>
A:Experimental source: breast cancer cell line MCF-7
C:Keywords: DNA binding; heterodimer

Query Match 20.9%; Score 28; DB 2; Length 26;
Best Local Similarity 37.5%; Pred. No. 7;1e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 LLQMDGCFPEHLVD 20
||| ||| ||| |||
Db 9 VVLMADYGFILPLIE 24

RESULT 4
A32521
hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995
C:Accession: A32521
R:Schlitch, D.M.; Wilson, J.E.
Arch. Biochem. Biophys. 257, 1-12, 1987
A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding site
A:Reference number: A90080; MUID:87324917
A:Accession: A32521
A:Molecule type: protein
A:Residues: 1-21 <SCH>
A:Superfamily: human hexokinase I; hexokinase homology
C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 20.1%; Score 27; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 LQMDGCFPEHL 16
| | | | |
Db 3 LGTFEFPXH 12

RESULT 5
S43632
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C:Accession: S43632
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochr
A:Reference number: S43624; MUID:94237150
A:Accession: S43632
A:Molecule type: protein
A:Residues: 1-23 <FRE>
A:Note: the source is designated as Salmo gairdneri
C:Genetics:
A:Genome: nuclear
C:Superfamily: mammalian cytochrome-c oxidase chain VIIa
C:Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.1%; Score 27; DB 2; Length 23;

Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 LLQMDGCFPEHL 17
| | | | |
Db 11 LFOAXNGIPIVHL 22

RESULT 6
S78374
hypothetical protein 26b - Odontella sinensis chloroplast
C:Species: chloroplast Odontella sinensis
C>Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 24-Apr-1998
C:Accession: S78374
R:Kowalik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A:Title: The Chloroplast Genome of a Chlorophyll a+c- containing Alga, Odontella sine
A:Reference number: S78238
A:Accession: S78374
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-26 <KOM>
A:Cross-references: EMBL:Z67753; NID:q1185127; PID:e211900; PID:q1185264
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 20.1%; Score 27; DB 2; Length 26;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 6; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 2 DGFL--LLQMDGCF 13
||| | |
Db 11 DGFIECLMINIKF 24

RESULT 7
A54077
cytochrome b558 - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A54077
R:Escrivou, V.; Laporte, F.; Garin, J.; Brandolin, G.; Vignals, P.V.
J. Biol. Chem. 269, 14007-14014, 1994
A:Title: Purification and physical properties of a novel type of cytochrome b from ra
A:Reference number: A54077; MUID:94245717
A:Accession: A54077
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <ESC>
A:Experimental source: peritoneal neutrophils
A:Note: sequence extracted from NCBI backbone (NCBIP:148739)

Query Match 19.8%; Score 26.5; DB 2; Length 20;
Best Local Similarity 45.0%; Pred. No. 9e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

QY 3 GFLLQMDGCFPEHLVDL 22
||| | |
Db 6 GFLVILV-----SALLVQFL 20

RESULT 8
S59492
formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)
C:Species: Alcaligenes eutrophus
C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S59492
R:Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.
Biol. Chem. Hoppe-Seyler 376, 561-568, 1995

A:Title: Structural and immunological studies on the soluble formate dehydrogenase from
 A:Reference number: S59492; MUID:96145736
 A:Accession: S59492
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <FRI>

Query Match 19.4%; Score 26; DB 2; Length 25;
 Best Local Similarity 57.1%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 OMDCFP 14
 DB 6 EIDGCP 12

RESULT 9
 B24417
 Interphotoreceptor retinoid-binding protein - pig (fragment)
 N:Alternate names: Interstitial retinol-binding protein
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
 C:Accession: B24417
 R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Hlou, G.L.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A:Title: N-terminal sequence homologues in interstitial retinol-binding proteins from 10
 A:Reference number: A91365; MUID:86301171
 A:Accession: B24417
 A:Molecule type: protein
 A:Residues: 1-25 <FON>
 C:Superfamily: Interphotoreceptor retinoid-binding protein
 C:Keywords: duplication

Query Match 19.4%; Score 26; DB 2; Length 25;
 Best Local Similarity 38.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 6 LLOMDFCPHLL 18
 DB 12 ILDMYTFPESLM 24

RESULT 10
 C85947
 Hypothetical protein 24250 (Imported) - Escherichia coli (strain O157:H7, substrain EDL93
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: C85947
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grothbeck, E.J.; Davis, N.W.; Llave, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: AB5480; MUID:21074935; PMID:11206551
 A:Accession: C85947
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-26 <STO>
 A:Cross-references: GB:AE005174; MID:q12517442; PIDN:AA658039 1; GSPDB:GN00145; UMGF:242
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 24250

Query Match 19.4%; Score 26; DB 2; Length 26;
 Best Local Similarity 38.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 14 PEHLVDPLQSL 26
 DB 14 PRALIDVDPL 26

RESULT 11

S71306
 heat shock protein 90 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
 C:Accession: S71306
 R:Conconi, M.; Szewda, L.I.; Levine, R.L.; Stademan, E.R.; Friguetti, B.
 Arch. Biochem. Biophys. 331, 232-240, 1996
 A:Title: Age-related decline of rat liver multicatalytic proteinase activity and prot
 A:Reference number: S71306; MUID:9629287
 A:Accession: S71306
 A:Molecule type: protein
 A:Residues: 1-15 <CON>
 A:Experimental source: liver
 C:Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 18.7%; Score 25; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 14 PEHLVDPLQ 23
 DB 6 PDHPIVETLR 15

RESULT 12
 T44936
 calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
 C:Accession: T44936
 R:Alamy, V.; Allque, R.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: 222873
 A:Accession: T44936
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-16 <ALE>
 A:Cross-references: EMBL:U57982; PIDN:AA09466.1

Query Match 18.7%; Score 25; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGPP 14
 DB 5 FGPP 8

RESULT 13
 C49048
 T-cell receptor beta chain V region (CD83 junction, clone Vbeta20.1) - human (fragmen
 C:Species: Homo sapiens (man)
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C:Accession: C49048
 R:Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
 Eur. J. Immunol. 22, 2413-2418, 1992
 A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juven
 A:Reference number: A49048; MUID:92387250
 A:Accession: C49048
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-16 <SIO>
 A:Experimental source: patient EV, IL-2R+ synovial T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:113265)
 C:Keywords: T-cell receptor

Query Match 18.7%; Score 25; DB 2; Length 16;
 Best Local Similarity 54.5%; Pred. No. 1.2e+03;

	Matches	6; Conservative	1; Mismatches	4; Indels	0; Gaps
OY	3	GFLLIOMDFG 13	11	11	1;
Db	3	GFYLLGSPGX 13			

RESULT 14
PH1607
Ig H chain V-D-J region (wild-type clone 333) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1607
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 311-319, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MCID:93301609
A:Accession: PH1607
A:Molecule type: DNA
A:Residues: 1-17 <LEV>
C:Experimental source: bone marrow pre-B lymphocyte
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: Immunoglobulin

Query Match	18.7%;	Score 25;	DB 2;	Length 17;
Best Local Similarity	40.0%;	Pred. No. 1.3e+03;		
Matches	4;	Conservative	2;	Mismatches 4; Indels 0; Gaps 0;

RESULT 15
S77989
cytochrome-c oxidase (EC 1.9.3.1) chain VIIb - biyege tuna (fragment)
C:Species: Thunnus obesus (biyege tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #next_change 30-Jan-1998
R:Accession: S77989
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77989
A:Molecule type: protein
A:Residues: 1-20 <ARN>
A:Experimental source: heart
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: oxidative phosphorylation; respiratory chain
A:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match	18.7%	Score 25;	DB 2;	Length 20;
Best Local Similarity	46.2%	Pred. No.	1.6e+03;	
Matches	6;	Conservative	0;	Mismatches 7; Indels 0; Caps 0;
QY	4 ELLLDMDGFPFH	16		
Db	8 FHLETDNDMPVH	20		

Search completed: June 18, 2002, 08:13:49
Job time: 318 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 18, 2002, 08:13:32 ; Search time 10.19 seconds

(without alignments)
98.794 Million cell updates/sec

Title: US-09-943-334-1

Sequence: 1 RDGFLLQMDFGPEHLLVDPLQSL 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 155:

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	33	24.6	24	1	COXJ_SHEEP
2	28	20.9	24	1	IRBP_SHEEP
3	27	20.1	23	1	COXJ_ONCOM
4	27	20.1	24	1	CCAA_STRT
5	27	20.1	26	1	YCND_ODOSI
6	26	19.4	25	1	AUSJ_LITRA
7	26	19.4	25	1	IRBP_PIG
8	25	18.7	16	1	ARCD_PSEPU
9	25	18.7	20	1	COXN_THUOB
10	25	18.7	23	1	COXK_CANFA
11	24	17.9	14	1	ANGT_HORSE
12	24	17.9	20	1	TL22_SPILO
13	23	17.2	18	1	MUJ1_LITGE
14	23	17.2	24	1	SCX2_MESTA
15	23	17.2	35	1	UCOJ_MALIZ
16	22	16.4	18	1	UCOJ_MALIZ
17	22	16.4	20	1	CAQS_RAT
18	22	16.4	20	1	MIF_PIG
19	22	16.4	24	1	FIBG_CANFA
20	22	16.4	24	1	KPYK_CLOPA
21	22	16.4	26	1	CATG_RAT
22	22	16.4	26	1	CT21_LITCI
23	21.5	16.0	25	1	ALR_PSEFL
24	21	15.7	9	1	FARD_CALVO
25	21	15.7	9	1	SAMP_MUSCA
26	21	15.7	25	1	AMP3_MELGA
27	21	15.7	25	1	PTM_SKECO
28	20	14.9	10	1	TEMK_BANTE
29	20	14.9	11	1	CA31_LITCI
30	20	14.9	11	1	CA32_LITCI
31	20	14.9	14	1	DCMK_PSECP
32	20	14.9	16	1	MDH_STRTA
33	20	14.9	21	1	ATPB_PHTPA

34	20	14.9	23	1	SODM_RANCA
35	20	14.9	25	1	AUSJ_LITRA
36	19.5	14.6	19	1	NUO6_SOLRU
37	19.5	14.6	25	1	METE_CANAL
38	19	14.2	12	1	V23K_WSSV
39	19	14.2	19	1	OXLA_OPBHA
40	19	14.2	19	1	UP21_UPEIN
41	19	14.2	19	1	UP25_UPEIN
42	19	14.2	20	1	ITRA_ALBUB
43	19	14.2	20	1	SUCB_CANFA
44	19	14.2	21	1	DCMS_PSECA
45	19	14.2	21	1	SP13_SOLRU

ALIGNMENTS

RESULT 1	COXJ_SHEEP	STANDARD:	PRT: 24 AA.
ID	COXJ_SHEEP		
AC	DEPR30:		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Cytochrome c oxidase polypeptide V1a-liver/heart, mitochondrial		
DE	(EC 1.9.3.1) (Cytochrome c oxidase subunit V1a-l) (Fragment).		
GN	COX7A2 OR COX7AL.		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Liver, and Heart;		
RC	MEDLINE=96092035; PubMed=8529022;		
RA	Linder D, Freund R, Kadenbach B ;		
RT	*Species-specific expression of cytochrome c oxidase isozymes.*;		
RL	Comp. Biochem. Physiol. 112B:461-469(1995).		
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE		
CC	CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN		
CC	-1- CATALYTIC ACTIVITY: 4 ferri-cytochrome c + O(2) = 4 ferri-cytochrome		
CC	c + 2 H(2)O.		
CC	-1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.		
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE V1A FAMILY.		
KW	Oxidoreductase; Inner membrane; Mitochondrion.		
FT	NON_TER 24		
SO	SEQUENCE 24 AA; 2795 MW; DA9D27C03B61F803 CRC64;		
Query Match	24.6%;	Score 33;	DB 1;
Best Local Similarity	58.3%;	Pred. No. 56;	
Matches 7;	Conservative 0;	Mismatches 5;	Indels 0;
Gaps 0;			
QY	6 LQMDFGPEHL 17		
DB	11 LFQDNGIPVHL 22		
RESULT 2	IRBP_SHEEP	STANDARD:	PRT: 24 AA.
ID	IRBP_SHEEP		
AC	P12653:		
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-OCT-1989 (Rel. 12, Last sequence update)		
DT	01-FEB-1996 (Rel. 33, Last annotation update)		
DE	Interphotoreceptor retinoid-binding protein (IRBP) (interstitial		
DE	retinol-binding protein) (Fragment).		
GN	IRBP.		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		

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OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=99940;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
RA Bridges C.D.B.;
RT "N-terminal sequence homologues in interstitial retinol-binding
RT proteins from 10 vertebrate species.";
RL FEBS Lett. 205:309-312(1986).
CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOLIDS BETWEEN
CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
CC EPITHELIUM CELLS.
DR PIR: A24417; A24417.
KW Vitamin A; Transport.
FT NON_TER 24
SQ SEQUENCE 24 AA: 2799 MW; 02EDBB61ABE4523 CRC64;

Query Match 20.9%; Score 28; DB 1; Length 24;
Best Local Similarity 35.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 6; Gaps 1;

OY 5 LLLQW-----DFGPPPHL 18
DB 5 LVLDMAQVLLDNYTPENLM 24

RESULT 3
COX1_CONCMY
ID COX1_CONCMY STANDARD; PRT; 23 AA.
AC P80333;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIa-Liver (EC 1.9.3.1) (VIIC)
DS (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferrocyclochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR: S43637; S43632.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 23
SQ SEQUENCE 23 AA: 2635 MW; BCBED43PBAD9C509 CRC64;

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Query Match 20.1%; Score 27; DB 1; Length 23;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 LLLQWDFGPPPHL 17
DB 11 LFOAXNGITPVHL 22

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RESULT 4
CCAA_STRTI
ID CCAA_STRTI STANDARD; PRT; 24 AA.
AC P80436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Chinoxalin-2-carboxylic acid activating enzyme (Fragment).
OS Streptomyces triostinicus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=45399;
RN [1]
RP SEQUENCE.
RA Pahl A., Schlumbohm M., Keller U.;
RL Submitted (MAR-1995) to the SWISS-PROT data bank.
CC -1- FUNCTION: INVOLVED IN TRIOSTIN BIOSYNTHESIS.
KW Antibiotic biosynthesis.
FT NON_TER 24
SQ SEQUENCE 24 AA: 2900 MW; 91C222B57CEB6D1 CRC64;

Query Match 20.1%; Score 27; DB 1; Length 24;
Best Local Similarity 30.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 6; Gaps 1;

OY 2 DGFLLQWDFGPPPHL 21
DB 3 DGFV-----PMPDHLADRY 16

RESULT 5
YCXD_ODOSI
ID YCXD_ODOSI STANDARD; PRT; 26 AA.
AC P49839;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 3.2 kDa protein in RPOC2-RP52 intergenic region (ORF20B).
DS Odontella sinensis.
OS Odontella sinensis.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Bidulophycidae; Eupodiscaceae; Odontella.
OX NCBI_TaxID=2839;
RN [1]
RP SEQUENCE FROM N.A.
RA Kowallik K.V., Stroebe B., Schaffran I., Kroth-Pancic P., Freier U.;
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
RT Odontella sinensis.";
RL Plant Mol. Biol. Rep. 13:336-342(1995).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z67753; CAA91747.1;
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 26 AA: 3137 MW; 8305B587C0A30B36 CRC64;

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Query Match 20.1%; Score 27; DB 1; Length 26;
Best Local Similarity 42.9%; Pred. No. 5.3e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

OY 2 DGFLLQWDFGPPPHL 13
DB 11 DGFTECHLMLNRYF 24

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:13:12 ; Search time 23.95 Seconds

(without alignments)
187.724 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134

Sequence: 1 RDGFLQLQMDRCFRENLLVDPLQSL 26

Scoring table: BIOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 9143

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORNITHINE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	23.1	19	6	Q9TRR6
2	30.5	22.8	17	4	Q9UJH1
3	30	22.4	21	2	P70861
4	29	21.6	20	5	Q9TWH5
5	28	20.9	23	11	Q9JIN0
6	27	20.1	12	4	Q9UCS1
7	27	20.1	14	6	Q9TRQ7
8	27	20.1	22	10	Q9S8E1
9	27	20.1	26	11	Q9S8E1
10	26.5	19.8	20	6	Q9TRC2
11	26.5	19.8	21	2	Q9ZG55
12	26	19.4	9	4	Q9KPF6
13	26	19.4	12	2	Q9K3B4
14	26	19.4	12	2	Q9L8H5
15	26	19.4	12	2	Q9L8H5
16	26	19.4	22	6	O02830

17	26	19.4	23	4	Q9GCD6	Q9GCD6 homo sapien
18	26	19.4	24	2	Q46081	Q46081 clostridium
19	26	19.4	25	13	P82401	P82401 litorea ran
20	25	18.7	16	3	Q94554	Q94554 schizosacch
21	25	18.7	19	13	Q9P570	Q9P570 gallus gall
22	25	18.7	20	10	Q9S878	Q9S878 petunia hyb
23	25	18.7	21	12	Q93044	Q93044 maize strea
24	25	18.7	21	12	Q93046	Q93046 maize strea
25	25	18.7	21	12	Q93047	Q93047 maize strea
26	25	18.7	21	12	Q93047	Q93047 maize strea
27	25	18.7	24	2	Q933P6	Q933P6 helicobacte
28	25	18.7	24	4	Q13651	Q13651 homo sapien
29	24.5	18.3	22	13	Q9P542	Q9P542 human herpe
30	24.5	18.3	22	12	Q9P542	Q9P542 gallus gall
31	24.5	18.3	25	13	Q9P541	Q9P541 influenza a
32	24.5	18.3	26	11	Q9P541	Q9P541 gallus gall
33	24	17.9	13	2	Q34622	Q34622 mus musculu
34	24	17.9	13	2	Q34622	Q34622 borrelia bu
35	24	17.9	13	2	Q31364	Q31364 borrelia ga
36	24	17.9	18	17	Q9UYK7	Q9UYK7 pyrococcus
37	24	17.9	20	6	Q9TTC3	Q9TTC3 ateles belz
38	24	17.9	21	2	Q9X3D0	Q9X3D0 prochloroco
39	24	17.9	21	12	Q93050	Q93050 maize strea
40	24	17.9	22	4	Q9UQ31	Q9UQ31 homo sapien
41	24	17.9	22	5	Q9SNW7	Q9SNW7 helicobact
42	24	17.9	22	6	Q9XTA7	Q9XTA7 cericophilic
43	24	17.9	22	6	Q9XTA6	Q9XTA6 canis fami
44	24	17.9	22	11	Q9WVT2	Q9WVT2 cricetus
45	24	17.9	22	11	Q9WVT1	Q9WVT1 felis nory

ALIGNMENTS

RESULT 1
Q9TRR6 PRELIMINARY; PRT; 19 AA.
AC Q9TRR6;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)
DE CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CAL2/PHOSPHOLIPID-BINDING PROTEIN
DE L-14 FRAGMENT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP MEDLINE=9250478; PubMed=1533622;
RX Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hatake H.;
RT "A calyculin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924(1992).
SQ SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;

Query Match 23.1%; Score 31; DB 6; Length 19;
Best Local Similarity 43.8%; Pred. No. 4,1e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY 11 FGPEHLVDPLQSL 26
DB 2 FGTEQAIDIXLSRS 17
RESULT 2
Q9UJH1 PRELIMINARY; PRT; 17 AA.
AC Q9UJH1;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)

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DE D0436M1.2 (RETINOSCHISIS (X-LINKED, JUVENILE) 1 (XLRIS1))
DE (FRAGMENT).
GN RSL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606.
RN [1]
RP SEQUENCE FROM N.A.
RA Grafham D.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; 294056; CAB40073.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2029 MW; 810E1B78C52C7FB CRC64;

Query Match 22.8%; Score 30.5; DB 4; Length 17;
Best Local Similarity 58.3%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 2 DGFLLQMDFFGF 13
   :| | | | : | |
Db 6 EGFLLLL-FCY 16

RESULT 3
ID P70861 PRELIMINARY; PRT; 21 AA.
AC P70861;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE THDP (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=212;
RX MEDLINE=97312006; Pubmed=9168617;
RA Ge Y., Old I.G., Girons I.S., Charon N.W.;
RT "The flag motility operon of Borrelia burgdorferi is initiated by a
RT sigma 70-like promoter."
RL Microbiology 143:1681-1690(1997).
DR EMBL; U62901; AAB62742.1; -.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5B33 CRC64;

Query Match 22.4%; Score 30; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 MDGFPPEHL 18
   :| | | | : |
Db 7 IEDFPEGL 16

RESULT 4
ID 09TWH5 PRELIMINARY; PRT; 20 AA.
AC 09TWH5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 40 KDA GAP JUNCTION PROTEIN (FRAGMENT).
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Metazoa; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5B33 CRC64;

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RX MEDLINE=95347000; Pubmed=7621522;
RA Ryerse J.S.;
RT "Immunocytochemical, electrophoresis, and immunoblot analysis of
RT Heliothis virescens gap junctions isolated in the presence and absence
RT of protease inhibitors."
RL Cell Tissue Res. 281:179-186(1995).
SQ SEQUENCE 20 AA; 2304 MW; A298D3EB3E89586B CRC64;

Query Match 21.6%; Score 29; DB 5; Length 20;
Best Local Similarity 35.3%; Pred. No. 8.9e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 LLLQMDGFPPEHLVDF 21
   :| | :| | | |
Db 3 VIFNIDGYLEFLTRDF 19

RESULT 5
ID 09JIN0 PRELIMINARY; PRT; 23 AA.
AC 09JIN0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAP JUNCTION SUBUNIT PROTEIN CONNEXIN37 (FRAGMENT).
CN GJA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=20461860; Pubmed=11004519;
RA "Mouse connexin37: gene structure and promoter analysis."
RT Biochim. Biophys. Acta 1492:499-504(2000).
DR EMBL; AF216831; AAF51222.1; -.
FR MGD; MG1:95715; Gja4.
FT NON_TER 23
SQ SEQUENCE 23 AA; 2617 MW; 2E879CA19105F7F8 CRC64;

Query Match 20.9%; Score 28; DB 11; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 DFGFPPEHL 18
   :| | | | |
Db 3 DMGFLEKLL 11

RESULT 6
ID 09UGS1 PRELIMINARY; PRT; 12 AA.
AC 09UGS1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE D1796117.4 (NOVEL PROTEIN SIMILAR TO GS2) (FRAGMENT).
CN D1796117.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035398; CAB63074.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69A6 CRC64;

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Query Match 20.1%; Score 27; DB 4; Length 12;
 Best Local Similarity 44.4%; Pred. No. 1e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 LLLQMDFGF 13
 : : : : :
 DB 1 MLEMDMSF 9

RESULT 7
 ID 09TR07 PRELIMINARY; PRT; 14 AA.
 AC 09TR07;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CALCICLIN-ASSOCIATED PROTEIN PEPTIDE L-8, CAP-50-ANNEXIN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92317074; PubMed=161851;
 RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
 RA Kobayashi R., Hidaka H.;
 RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
 RT fibroblasts. 311 cells.";
 RL J. Biol. Chem. 267:13498-13504(1992).
 SQ SEQUENCE 14 AA; 1446 MW; C8322E896DD9C6C6 CRC64;

Query Match 20.1%; Score 27; DB 6; Length 14;
 Best Local Similarity 41.7%; Pred. No. 1.2e+03;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 11 FGPEHLVDFL 22
 : : : : :
 DB 2 FGTEQALIDXL 13

RESULT 8
 ID 09SBE1 PRELIMINARY; PRT; 22 AA.
 AC 09SBE1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE ANNEXIN (FRAGMENT).
 OS Capsicum annuum (Bell pepper).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eumasterids I; Solanales; Solanaceae; Capsicum.
 ON NCBI_TaxID=4072;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95353219; PubMed=7627125;
 RA Hoshino T., Mizutani A., Chida M., Hidaka H., Mizutani J.;
 RT "Plant annexin form homodimer during Ca(2+)-dependent liposome
 RT aggregation.";
 RL Biochem. Mol. Biol. Int. 35:749-755(1995).
 SQ SEQUENCE 22 AA; 2465 MW; A36D1A1FE311F0F CRC64;

Query Match 20.1%; Score 27; DB 10; Length 22;
 Best Local Similarity 41.7%; Pred. No. 2e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 11 FGPEHLVDFL 22
 : : : : :
 DB 11 FGPEHLVDFL 22

DB 3 WGTDEKLIIDIL 14

RESULT 9
 ID 099JW8 PRELIMINARY; PRT; 26 AA.
 AC 099JW8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 3.1 KDA PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005613; AA005613.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 26 AA; 3090 MW; 4759778C1D32AC98 CRC64;

Query Match 20.1%; Score 27; DB 11; Length 26;
 Best Local Similarity 41.7%; Pred. No. 2.4e+03;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 DGFLLQMDFGF 13
 : : : : :
 DB 4 DSFLMLMLRAAF 15

RESULT 10
 ID 09TRC2 PRELIMINARY; PRT; 20 AA.
 AC 09TRC2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HEMOPROTEIN P-30 (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94245717; PubMed=8188680;
 RA Escarion V., Laporte F., Garin J., Brandolin G., Vignais P.V.;
 RT "Purification and physical properties of a novel type of cytochrome b
 RT from rabbit peritoneal neutrophils.";
 RL J. Biol. Chem. 269:14007-14014(1994).
 SQ SEQUENCE 20 AA; 2198 MW; 2301B616163DMA19 CRC64;

Query Match 19.8%; Score 26.5; DB 6; Length 20;
 Best Local Similarity 45.0%; Pred. No. 2.2e+03;
 Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

OY 3 GFLLQMDFGPEHLVDFL 22
 : : : : :
 DB 6 GFVLVLFV-----SALLVGLF 20

RESULT 11
 ID 09ZG55 PRELIMINARY; PRT; 21 AA.
 AC 09ZG55;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ATP-BINDING PROTEIN (FRAGMENT).
 RN RECF.

```

OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-L2 434B:
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT *Gene identification of Chlamydia trachomatis by random DNA
RL sequencing.
DR EMBL; AF087306; AAD04082.1; -.
KW ATP-binding.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2336 MW; 0185D9AC428276D9 CRC64;

Query Match 19.4%; Score 26.5; DB 2; Length 21;
Best Local Similarity 41.7%; Pred. No. 2.3e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 6 L10MDFGFEHL 17
DB 8 ILQL-TSPKHI 18

RESULT 12
O96KF6 PRELIMINARY; PRT; 9 AA.
ID O96KF6;
AC O96KF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STEAROYL-COA DESATURASE (FRAGMENT).
GN SCD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KEFARINOCYTES, LIVER, HAIR FOLLICULE, AND BRAIN;
RA Zhang L., Ge L., Tran T., Steen K., Protuy S.M.;
RT *Isolation and characterization of the Human Stearoyl-CoA Desaturase
RT Gene Promoter: Requirement of a Conserved CCAAT cis-Element.
RL Biochem. J. 0.0-0(2001).
DR EMBL; AF320307; AAK54510.1; -.
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1039 MW; 3593B6D72721EDC7 CRC64;

Query Match 19.4%; Score 26; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 PHLHVD 20
DB 2 PAHLLOD 8

RESULT 13
O9K3B4 PRELIMINARY; PRT; 12 AA.
ID O9K3B4;
AC O9K3B4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 1.5 KDA PROTEIN (FRAGMENT).
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1352;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS; TRANSPOSON-TN5382;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Koekenes T.P., Olsvik O., Sundsfjord A.;
RT *Genetic linkage of the vanB2 gene cluster to TN5382 in vancomycin
RT resistant enterococci and characterization of two novel insertion
RT sequences.
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF203417; AAF70584.1; -.
DR EMBL; AF203405; AAF70560.1; -.
DR EMBL; AF203405; AAF70562.1; -.
DR EMBL; AF203409; AAF70564.1; -.
DR EMBL; AF203412; AAF70574.1; -.
DR EMBL; AF203413; AAF70576.1; -.
DR EMBL; AF203414; AAF70578.1; -.
DR EMBL; AF203415; AAF70580.1; -.
DR EMBL; AF203416; AAF70582.1; -.
KW Hypothetical protein.
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1476 MW; 1613207414DIEAB CRC64;

Query Match 19.4%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 16 HLVDVF 21
DB 7 HALIDF 12

RESULT 14
O9L8H6 PRELIMINARY; PRT; 12 AA.
ID O9L8H6;
AC O9L8H6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 1.5 KDA PROTEIN (FRAGMENT).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUH7-54, TUH4-67, AND TUH1-75; TRANSPOSON-TN5382;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Koekenes T.P., Olsvik O., Sundsfjord A.;
RT *Genetic linkage of the vanB2 gene cluster to TN5382 in vancomycin
RT resistant enterococci and characterization of two novel insertion
RT sequences.
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF203411; AAF70572.1; -.
DR EMBL; AF203408; AAF70566.1; -.
DR EMBL; AF203404; AAF70558.1; -.
KW Hypothetical protein.
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1476 MW; 1613207414DIEAB CRC64;

Query Match 19.4%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 16 HLVDVF 21
DB 7 HALIDF 12

RESULT 15
O9L8H8 PRELIMINARY; PRT; 12 AA.
ID O9L8H8;
AC O9L8H8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 1.5 KDA PROTEIN (FRAGMENT).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]

```

AC Q9L8H8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 1.5 KDA PROTEIN (FRAGMENT).
OS Enterococcus gallinarum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1353;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TJH7-16; TRANSPOSON-TN5382;
RX MEDLINE-20307504; PubMed-10846225;
RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin
RT resistant enterococci and characterization of two novel insertion
RT sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL: AF203410; AAF70570.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 12 AA: 1476 MW: 1613207414DIEAB CRC64;

Query Match 19.4%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 16 HLVDYF 21
| | | | |
Db 7 HALIDF 12

Search completed: June 18, 2002, 08:16:29
Job time: 197 sec

1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 08:13:52 ; Search time 29.43 Seconds

(without alignments)
98,128 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134

Sequence: 1 RDGFLLQMDRFPPEHLVDFLGSLIS 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 258094

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :
A.Geneseq_032802:*

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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	134	100.0	26 17	AAW06128 Human cholesteryl
2	134	100.0	26 21	AAV13801 Rabbit CETP immuno
3	134	100.0	26 21	AAV91228 Human cholesteryl
4	117	87.3	26 20	AAV13802 Rabbit CETP immuno
5	117	87.3	26 21	AAV91231 Human cholesteryl
6	111	82.8	22 20	AAV13815 Rabbit CETP immuno
7	111	82.8	22 20	AAV13821 Human CETP immuno
8	107	79.9	22 20	AAV13809 Rabbit CETP immuno
9	83	61.9	16 21	AAV91229 Human cholesteryl
10	79	59.0	16 21	AAV91230 Human cholesteryl
11	53	39.6	11 18	AAW24294 Human/Rabbit CETP

Result No.	Score	Query Match Length	ID	Description
12	34	25.4	22 22	AAW64886 Human secreted pro
13	34	25.4	25 20	AAV12067 Human 5' EST seque
14	33	24.6	12 4	AAV30225 Sequence of Interf
15	33	24.6	12 9	AAV80053 Sequence of human
16	33	24.6	14 20	AAV27814 Human secreted pro
17	33	24.6	21 18	AAW38080 Peppy motif contai
18	33	24.6	22 22	AAV14445 Interferon- α 2
19	33	24.6	24 18	AAW22196 Endogenous TCR α
20	32.5	24.3	22 22	AAW89172 HIV gp120 protein
21	32	23.9	21 19	AAW65690 Fibrinectin bindin
22	32	23.9	22 20	AAV19066 Lecithin:cholester
23	32	23.9	22 20	AAV18812 Lecithin:cholester
24	32	23.9	22 20	AAV18549 Lecithin:cholester
25	32	23.9	22 20	AAV19320 Lecithin:cholester
26	31.5	23.5	26 21	AAV36931 Human IL-1 recepto
27	31	23.1	12 20	AAV32796 Mammalian prolact
28	31	23.1	21 19	AAW55666 Fibrinectin bindin
29	31	23.1	22 19	AAW65669 Peptide #13. Synt
30	30	22.4	17 21	AAV68335 Amyotrophic latera
31	30	22.4	19 22	ABW41585 Peptide #9091 enco
32	30	22.4	19 22	AAW62456 Human brain expres
33	30	22.4	19 22	AAW75265 Peptide #9414 enco
34	30	22.4	20 15	AAW51377 Transactivating pr
35	30	22.4	20 15	AAW61276 Tax protein fragme
36	30	22.4	20 19	AAW11290 Peptide #4689 enco
37	30	22.4	22 17	AAW35899 Protein #4870 enco
38	30	22.4	25 22	ABW32318 Murine muscle-spec
39	30	22.4	26 22	AAW19853 SH2 domain bindin
40	30	22.4	10 19	AAW78506 Interleukin-2 rece
41	29	21.6	11 20	AAW94442 Peptide exhibiting
42	29	21.6	11 21	AAW82915 Target-receptor-bi
43	29	21.6	11 22	AAW12095 MAb anti-HBsAg bin
44	29	21.6	11 22	AAW10883
45	29	21.6	13 18	AAW10883

ALIGNMENTS

RESULT 1

AAW06128 standard; Peptide: 26 AA.

ID AAW06128;

AC AAW06128;

XX 07-FEB-1997 (first entry)

DT 07-FEB-1997 (first entry)

XX Human cholesteryl ester transfer protein C-terminal B-cell epitope.

DE Cholesteryl ester transfer protein; CETP; antigen; vaccine;

XX Cholesteryl ester transfer protein; CETP; antigen; vaccine;

KW cardiovascular disease; atherosclerosis; B-cell epitope.

XX Homo sapiens.

OS Homo sapiens.

XX MO9634888-A1.

PN MO9634888-A1.

XX 07-NOV-1996.

PD 07-NOV-1996.

PF 01-MAY-1996; 96MO-US06147.

XX 01-MAY-1996; 96MO-US06147.

PR 01-MAY-1995; 95US-0432483.

XX (TCEL-) T CELL SCI INC.

PA Rittershaus CW, Thomas LJ;

XX WPI: 1996-506103/50.

DR Cholesteryl ester transfer protein B cell epitope linked to T cell

PT epitope - used to generate vaccine to regulate CETP activity for

PT decreasing the risk of developing a cardiovascular disease e.g.

PT atherosclerosis

XX

XX	Sequence	26 AA:	100.0%;	Score 134;	DB 20;	Length 26;
SO	Query Match		100.0%;	Pred. No. 1.2e-13;		
	Best Local Similarity		100.0%;	Pred. No. 1.2e-13;		
	Matches	26;	Conservative	0;	Mismatches	0;
OY	1	RDGFLLQMDFGPEHLVDFIQSIS	26			
Db	1	rdgfillqmdfgpehlvdfiqs	26			
RESULT	3					
ID	AAV91228	standard; peptide; 26 AA.				
XX	AAV91228					
AC	AAV91228;					
XX						
DT	22-MAY-2000	(first entry)				
XX						
DE	Human cholesterol transport protein (CEMP) peptide, SEQ ID NO:106.					
XX						
KW	Promiscuous T-cell epitope; measles virus F protein; MWP;					
KW	hepatitis B virus surface antigen; HBV; Immunogenic; B-cell epitope;					
KW	luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;					
KW	somatostatin; growth promotion; CD4 receptor; HIV-1; antitumor; FMDV;					
KW	foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;					
KW	plasmodium falciparum; circumsporozoite; antimalarial; CEMP;					
KW	cholesterol ester transport protein; anti-arteriosclerotic.					
XX						
OS	Homo sapiens.					
PN	WO9966957-A2.					
XX						
PD	29-DEC-1999.					
XX						
PF	21-JUN-1999; 99WO-US133975.					
XX						
PR	20-JUN-1998; 98US-0100412.					
XX						
PA	(UNBFI-) UNITED BIOMEDICAL INC.					
PI	Wang CY;					
XX						
DR	WPI; 2000-160564/14.					
XX						
PT	New artificial T helper cell epitope and derived immunogens with target					
XX	antigenic site, for immunization against e.g. malaria, arteriosclerosis					
PT	or human immune deficiency virus					
XX						
PS	Claim 10; Page 49; 129pp; English.					
XX						
CC	The invention relates to novel promiscuous T helper cell epitopes (Th),					
CC	and immunogenic peptides comprising the Th epitopes of the invention					
CC	along with B cell epitopes. The Th epitopes and peptide immunogens					
CC	containing them, are used to induce a T helper cell response,					
CC	specifically against plasmodium falciparum, cholesterol ester transport					
CC	protein (CEMP) or HIV epitopes, but more generally against any pathogen,					
CC	immunoreactive self-antigen or tumour antigen. The Th epitopes and					
CC	peptide immunogens may be used for prevention and/or treatment of					
CC	infections (HIV, foot-and-mouth disease or malaria); for cancer					
CC	immunotherapy; for inhibition of the action of luteinizing hormone					
CC	releasing hormone (LHRH) for contraception, treatment of hormone-					
CC	independent cancer, prevention of boar taint in meat, and					
CC	immunocastration); for promoting the growth of animals; or for					
CC	treating allergies or arteriosclerosis. Incorporation of a promiscuous					
CC	Th (functional in genetically diverse subjects) into an immunogen					
CC	improves capacity to induce a strong T helper cell-mediated immune					
CC	response, resulting in production of antibodies against a target					
CC	antigen. Th can replace carrier proteins and pathogen-derived T helper					
CC	epitopes. Sequence AAV91121 represents a promiscuous T helper epitope					
CC	from the measles virus F (MVP) protein and sequences AAV91122-V91142,					

CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration), for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CD82-like domain antigenic site, and AAY91209-Y91211 are MVN Th
 CC epitope/CD4 CDR antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90215 are Th epitopes/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVN Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasion
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 26 AA:

Query Match 87.3%; Score 117; DB 21; Length 26;
 Best Local Similarity 92.0%; Pred. No. 4,8e-11;
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DQFLLQMDFGFPHLLVDFLOSL 26
 DB 2 DQFLLQMDFGFPHLLVDFLOSL 26

RESULT 6
 AAY13815
 ID AAY13815 standard; peptide; 22 AA.

XX AAY13815;

XX 08-JUL-1999 (first entry)

XX Rabbit CETP immunogenic fragment.

DE CETP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 XX antibody production; cholesterol ester transfer; therapy;
 KW

3

KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.

XX Oryctolagus sp.

XX W09915655-A1.

XX 01-APR-1999.

XX 17-SEP-1998; 98WO-US19366.

XX 19-SEP-1997; 97US-0934367.

XX (MONS) MONSANTO CO.

XX Glenn K, Needleman P;

XX WPI; 1999-276984/23.

XX New recombinant DNA vaccines

XX Disclosure: Page 75; 99pp; English.

XX This sequence represents an immunogenic fragment of the rabbit

XX cholesteryl ester transferase protein (CETP).

XX The invention relates to recombinant DNA vaccines that contain DNA

XX encoding CETP, which can be used for producing antibodies to lessen the

XX transfer of cholesterol esters from high density lipoprotein (HDL). The

XX method can provide an autogenic immunological process for lessening the

XX transfer of cholesterol esters from HDL particles and for increasing the

XX HDL cholesterol concentration of a mammal whose blood also contains

XX CETP. The method may be useful in treating human pro-atherogenic

XX dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The

XX method can have an effect that lasts for months as compared to the

XX short-term effects of the small molecule drugs now available.

SO Sequence 22 AA:

Query Match 82.8%; Score 111; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGFPHLLVDFLOSL 26
 DB 1 LLLQMDFGFPHLLVDFLOSL 22

RESULT 7
 AAY13821
 ID AAY13821 standard; peptide; 22 AA.

XX AAY13821;

XX 08-JUL-1999 (first entry)

XX Human CETP immunogenic fragment.

DE CETP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 XX antibody production; cholesterol ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.

XX Homo sapiens.

XX W09915655-A1.

XX 01-APR-1999.

XX 17-SEP-1998; 98WO-US19366.

XX 19-SEP-1997; 97US-0934367.

XX

PA (MONS) MONSANTO CO.
XX
XX Glenn K, Needleman P;
XX
XX WPI: 1999-276984/23.
DR
XX
XX New recombinant DNA vaccines
XX
XX Disclosure; Page 88; 99pp; English.
XX
XX This sequence represents an immunogenic fragment of the human
XX cholesterol ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesterol esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesterol esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
XX
XX Sequence 22 AA;
SQ

Query Match 82.8%; Score 111; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPFHHLVDFLOSLS 26
Db 1 LLLQMDGFPFHHLVDFLOSLS 22
|||||

RESULT 8
AA013809
ID AAY13809 standard; peptide: 22 AA.
XX
XX AAY13809;
AC
XX
XX 08-JUL-1999 (first entry)
DT
XX
XX Rabbit CETP immunogenic fragment.
DE
XX
XX CETP: cholesterol-ester transfer protein; recombinant DNA vaccine; HDL;
KM antibody production; cholesterol ester transfer; therapy;
KM high density lipoprotein; HDL cholesterol concentration;
KM pro-atherogenic dyslipoproteinaemia.
XX
XX Oryctolagus sp.
OS
XX
XX WO915655-A1.
PN
XX
XX 01-APR-1999.
PD
XX
XX 17-SEP-1998; 98WO-US19366.
PF
XX
XX 19-SEP-1997; 97US-0934367.
PR
XX
XX (MONS) MONSANTO CO.
PA
XX
XX Glenn K, Needleman P;
PI
XX
XX WPI: 1999-276984/23.
DR
XX
XX New recombinant DNA vaccines
PT
XX
XX Example 1; Page 73; 99pp; English.
PS
XX
XX This sequence represents an immunogenic fragment of the rabbit
CC cholesterol ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA

CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesterol esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesterol esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
XX
XX Sequence 22 AA;
SQ

Query Match 79.9%; Score 107; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e-09;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPFHHLVDFLOSLS 26
Db 1 LLLQMDGFPFHHLVDFLOSLS 22
|||||

RESULT 9
AA01229
ID AAY91229 standard; peptide: 16 AA.
XX
XX AAY91229;
AC
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Human cholesterol transport protein (CETP) peptide, SEQ ID NO:107.
DE
XX
XX Promiscuous T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; EMV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KM cholesterol ester transport protein; anti-arteriosclerotic.
XX
XX Homo sapiens.
OS
XX
XX WO966957-A2.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 21-JUN-1999; 99WO-US13975.
PF
XX
XX 20-JUN-1998; 98US-0100412.
PR
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
PA
XX
XX Wang CY;
PI
XX
XX WPI: 2000-160564/14.
DR
XX
XX New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
PT
XX
XX Claim 10; Page 50; 129pp; English.
PS
XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response.
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-

Query Match 59.0%; Score 79; DB 21; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.9e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGPEHLVDFLOSLS 26
 DB 1 fgfphllvdflosls 16

RESULT 11
 AAW24294
 ID AAW24294 standard; peptide: 11 AA.
 AC AAW24294:
 XX
 DT 17-OCT-1997 (first entry)
 XX
 DE Human/Rabbit CERP common peptide.
 XX
 KW Immune response; high density lipoprotein; HDL; cholesterol; human;
 KM serum; epitope; cholesterol ester transfer protein; CERP; rabbit.
 XX
 OS Oryctolagus cuniculus.
 XX Homo sapiens.
 XX WO9639168-A1.
 XX 12-DEC-1996.
 XX 05-JUN-1996; 96MO-US09143.
 XX 06-JUN-1995; 95US-0482454.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Brostoff SM, Carlo DJ, Kwon DY;
 XX
 DR WPI: 1997-042849/04.
 XX
 PT Stimulating an immune response to increase high density lipoprotein
 PT - avoids repeated administration of toxic drugs to lower cholesterol
 PT ester transfer protein levels
 XX
 PS Claim 5; Page 16; 26pp; English.
 XX
 CC The sequences given in AAW24292-94 were used in the method of the
 CC invention to stimulate an immune response to increase high density
 CC lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of
 CC serum HDL. These peptides represent immunogenic epitopes of
 CC cholesterol ester transfer protein (CERP). The method utilizes
 CC the body's own immune system to lower CERP levels, thereby increasing
 CC the level of beneficial HDL cholesterol, preferably in serum. The
 CC method avoids the problems associated with the repeated administration
 CC of drugs which have undesirable side effects. This peptide represents
 CC a region of CERP which is common to both human and rabbit proteins.
 XX
 SO Sequence 11 AA;

Query Match 39.6%; Score 53; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HTLVDFLOSLS 26
 DB 1 hllvdflosls 11

RESULT 12
 AAB64886
 ID AAB64886 standard; Protein: 22 AA.
 AC AAB64886;

XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 5 SEQ ID NO:64.
 XX
 KW Human; secreted protein; diagnosis; immunomodulatory; anti-sclerotic;
 KM dermatological; immunosuppressive; anti-inflammatory; anti-HIV;
 KW immunostimulant; cytoskeletal; cardiac; vascular; anti-angiogenic;
 KW ophthalmological; neuroprotectant; nootropic; anticonvulsant; vulnary;
 KW antialzheimers; antiparkinsonian; antimicrobial; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV; infection;
 KW hyperproliferative disorder; cancer; Gaucher's disease; wound healing;
 KW cardiovascular disease; Schmitzer syndrome; Chaga's cardiomyopathy;
 KW coronary arteriosclerosis; angiogenic disorder; diabetic retinopathy;
 KW corneal graft neovascularisation; neurological disorder; regeneration;
 KM Huntington's chorea; Alzheimer's disease; Parkinson's disease;
 XX infectious disease; chemotaxis; chromosome 1.
 XX
 OS Homo sapiens.
 XX
 PN WO200076530-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 01-JUN-2000; 2000MO-US14933.
 XX
 PR 11-JUN-1999; 99US-0138572.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Rosen CA, Ruben SM, Komatsu GA;
 XX
 DR WPI: 2001-071147/08.
 DR N-PSDB; AAF33217.
 XX
 PT Nucleic acids encoding 49 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 PS Claim 11; Page 486; 554pp; English.
 XX
 CC The polynucleotide sequences given in AAF33213 to AAF33261 encode the
 CC human secreted proteins given in AAB64882 to AAB64930. AAB64931 to
 CC AAB64991 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC immunomodulatory; anti-sclerotic; dermatological; immunosuppressive;
 CC anti-inflammatory; anti-HIV; immunostimulant; cytoskeletal; cardiac;
 CC vascular; antimicrobial; anti-angiogenic; ophthalmological;
 CC neuroprotectant; anticonvulsant; nootropic; antialzheimers;
 CC antiparkinsonian; and vulnary. The polynucleotides and polypeptides can
 CC be used in the prevention, diagnosis and treatment of diseases associated
 CC with inappropriate polypeptide expression. Disorders that may be
 CC prevented, diagnosed and/or treated by the above methods include immune
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
 CC human immuno-deficiency virus (HIV) infections), hyperproliferative
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
 CC (e.g. Schmitzer syndrome, Chaga's cardiomyopathy and coronary
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft
 CC neovascularisation) and diabetic retinopathy), neurological disorders
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),
 CC infectious diseases and/or for promoting wound healing, regeneration and
 CC /or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences
 CC used in the exemplification of the present invention.
 XX
 SO Sequence 22 AA;

Query Match 25.4%; Score 34; DB 22; Length 22;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GPEHILVDF 21
 ||| : |||
 Db 10 gfiyifvdf 19

RESULT 13

AA12067
 ID AA12067 standard; Protein: 25 AA.

AC AA12067;

DT 18-JUN-1999 (first entry)

DE Human 5' EST secreted protein SEQ ID NO: 380.

OS Homo sapiens.
 OS WO9906554-A2.
 PN 11-FEB-1999.
 PD 31-JUL-1998; 98WO-1H01238.
 PF 01-AUG-1997; 97US-0905134.
 PR (GEST) GENSET.
 PA Duglert A, Dumas Milne Edwards J, Lacroix B;
 PI WPI: 1999-153784/13.
 DR N-PSDB: AAX40900.
 XX New nucleic acids encoding human secreted proteins - obtained from
 PT cDNA libraries prepared from kidney, fetal kidney, dystrophic
 PT muscle, muscle and heart tissue
 XX

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KM forensic; gene therapy; chromosome mapping; signal peptide;
 KM upstream regulatory sequence; cytokine activity; cell proliferation;
 KM differentiation; haemopoiesis regulation; tissue growth regulation;
 KM reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KM thrombolytic; anti-inflammatory; tumour inhibition.
 XX

XX Homo sapiens.
 OS WO9906554-A2.
 PN 11-FEB-1999.
 PD 31-JUL-1998; 98WO-1H01238.
 PF 01-AUG-1997; 97US-0905134.
 PR (GEST) GENSET.
 PA Duglert A, Dumas Milne Edwards J, Lacroix B;
 PI WPI: 1999-153784/13.
 DR N-PSDB: AAX40900.
 XX New nucleic acids encoding human secreted proteins - obtained from
 PT cDNA libraries prepared from kidney, fetal kidney, dystrophic
 PT muscle, muscle and heart tissue
 XX
 PS Claim 34; Page 500-501; 622pp; English.

CC AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AA101602 and
 CC AA111994 to AA112260, respectively. The proteins given represent the
 CC signal peptide and an N-terminal fragment of a secreted protein. The
 CC nucleic acid sequences can be used for producing secreted human gene
 CC products. They can also be used to develop products for diagnosis and
 CC therapy. The proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used
 CC for directing extracellular secretion of a polypeptide or the insertion
 CC of a polypeptide into a membrane, or importing a polypeptide into
 CC a cell.
 CC
 XX Sequence 25 AA;

Query Match 25.4%; Score 34; DB 20; Length 25;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 2; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 9 MFGPEHILVDFLOSUS 26
 | | | : | | | | |
 Db 1 mgylaesficanflwys 18

RESULT 14

AA130225
 ID AAP30225 standard; Protein: 12 AA.

AC AAP30225;

DT 25-MAY-1992 (first entry)

DE Sequence of Interferon (HUIFN) -alpha-61A around amino acid 40.

KW Hybrid interferon: antiviral; therapy; cancer; tumour.

OS Homo sapiens.
 OS Key Location/Qualifiers
 FT Misc-difference 7 /label= AA No. 40
 FT
 XX

XX WO8302461-A.
 XX 21-JUL-1983.
 XX 18-JAN-1983; 83WO-0900607.
 XX 19-JAN-1982; 82US-0340782.
 XX 03-FEB-1983; 83US-0463574.
 XX 15-JUL-1985; 85US-0755265.
 XX (CETU-) CBTUS CORP.
 XX Mark DF, Creasey AA;
 XX WPI: 1983-723186/30.
 XX N-PSDB: AAN30158.
 XX Multi-class hybrid interferon poly(peptide(s) - with restricted
 XX antiviral and cell growth regulatory activities
 XX
 PS Example; Fig 17; 61pp; English.

CC The inventors claim a multiclass hybrid interferon polypeptide and a
 CC DNA unit having a nucleotide sequence which encodes it. Pref. the
 CC AA sequence consists of alpha and beta interferons. Pref. IF1 is
 CC (1) the 1-73 AA seq. of HUIFN-alpha-1 (and IF2 is the 74-166 AA seq. of
 CC HUIFN-beta-1) (see AAN30155, AAP30222) or (ii) the 1-41 AA seq. of
 CC HUIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HUIFN-beta-1) (see
 CC AAN30160, AAP30227). Alternatively IF1 is the amino terminal end of a
 CC beta-1F and IF2 is the carboxy terminal of an alpha-1F (esp. the
 CC 1-73 seq. of HUIFN-beta-1 and the 74-167 seq. of HUIFN-alpha-1
 CC resp.) (see AAN30156, AAP30223). In the examples plasmids pcw5 and
 CC pM101/ctp/beta-1 and p-alpha-61A were used (see AAN30151, AAN30152,
 CC AAN30157). HinfI was used to digest the DNA sequences in the region
 CC of significant handicaps (see AAN30153, AAN30154, AAN30158, AAN30159),
 CC and the restriction fragments were ligated to form hybrid DNA.
 CC
 XX Sequence 12 AA;

Query Match 24.6%; Score 33; DB 4; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPE 15
 ||||| :
 Db 2 dfgfpq 7

RESULT 15

Job time: 209 sec

```

AAP80053
ID AAP80053 standard; protein; 12 AA.
XX
AC AAP80053:
XX
XX 17-NOV-1990 (first entry)
XX
DE Sequence of human Interferon (huIFN) alpha-61A gene around AA 40.
XX
XX Alpha-beta hybrid Interferon; multi-class hybrid Interferon;
XX antitumour; antiviral; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 7
XX FT /note="Residue 40"
XX
XX US4758428-A.
XX
XX PD 19-JUL-1988.
XX
XX PF 15-JUL-1985; 85US-0755265.
XX
XX PR 15-JUL-1985; 85US-0755265.
XX PR 19-JAN-1983; 83CA-0419758.
XX
XX PA (CETU ) CETUS CORP.
XX
XX PI Mark DE, Creasey AA;
XX
XX DR WPI; 1988-219882/31.
XX DR N-PSDB: AAN80050.
XX
XX PT Multi-class hybrid Interferon polypeptide(s) -
XX PT having sequence from Interferon-alpha-1 and sequence from
XX PT Interferon-beta-1 for restricted activity
XX
XX PS Example; Fig 17; 24pp; English.
XX
CC Multi-class hybrid IFN polypeptides having an AA sequence composed
CC of 2 distinct subsequences are claimed. The plasmids used in the
CC construction of huIFN-alpha-61A-beta-1 hybrid are plasmids palpha61A and
CC pDM101/trp/beta-1. Assembly of the palpha61A plasmid involved replacing
CC the DNA fragment encoding the 23 AA signal polypeptide of preinterferon
CC with a 120BP EcoRI/Sau3A promoter fragment Eco11 trp promoter,
CC operator, and trp leader ribosome binding site preoperator, encoding an
CC ATG initiation codon and using HindIII site that was inserted, 59
CC nucleotides 3'-end of the TGA translational stop codon, to insert the
CC gene into the plasmid pDM11 (a deriv of pBR322 having a deletion between
CC the HindIII and PvuII sites). The complete DNA sequence of the promoter
CC and gene fragments inserted between the EcoRI and HindIII sites of pDM11
CC is shown in AAN80049. The hybrid gene was constructed by taking advantage
CC of the homologues between huIFN alpha 61A & huIFN beta-1 at around AA 40
CC of both proteins. The DNA sequence 5'-proximal to the DdeI restriction
CC enzyme cutting site of the huIFN alpha-61A DNA is ligated to the DNA
CC sequence 3'-proximal to the site of huIFN beta-1, to create a fusion of
CC the two genes while preserving the translational reading frame of both.
XX
SQ Sequence 12 AA:

```

Query Match 24.6%; Score 33; DB 9; Length 12;
 Best Local Similarity 83.3%; Pred. NO. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DRGPE 15
 |||||:
 Db 2 dfgfpq 7

Search completed: June 18, 2002, 08:17:21

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:12:01 ; Search time 102.57 Seconds

(Without alignments)
89,222 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134

Sequence: 1 RGFLLIOMRGFPFHLVDFLQSL S 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 2173486

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents, AA, Main:*

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2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*

3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*

4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*

5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*

6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*

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9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*

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11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*

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22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*

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24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*

25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*

26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134	100.0	26	1	PCT-US99-13975B-106
2	134	100.0	26	1	Sequence 106, App
3	134	100.0	26	8	US-08-432-463-1
4	134	100.0	26	11	US-08-432-483A-1
5	134	100.0	26	11	US-08-785-997-29
6	134	100.0	26	11	US-08-788-882-29
7	134	100.0	26	13	US-08-934-367-29
					Sequence 1, Appl1

8	134	100.0	26	17	US-09-386-591-29	Sequence 29, Appl1
9	134	100.0	26	17	US-09-387-340-29	Sequence 29, Appl1
10	134	100.0	26	21	US-09-701-588-106	Sequence 106, App
11	134	100.0	26	23	US-09-943-334-1	Sequence 1, Appl1
12	134	100.0	26	23	US-09-943-334-1	Sequence 1, Appl1
13	134	100.0	26	23	US-09-943-334-1	Sequence 1, Appl1
14	117	87.3	26	11	PCT-US99-13975B-109	Sequence 109, App
15	117	87.3	26	11	US-08-785-997-50	Sequence 50, Appl1
16	117	87.3	26	13	US-08-788-882-50	Sequence 50, Appl1
17	117	87.3	26	13	US-08-934-367-50	Sequence 50, Appl1
18	117	87.3	26	17	US-09-386-591-50	Sequence 50, Appl1
19	117	87.3	26	17	US-09-387-340-50	Sequence 50, Appl1
20	111	82.8	22	21	US-09-701-588-109	Sequence 109, Appl1
21	111	82.8	22	11	US-08-785-997-34	Sequence 10, Appl1
22	111	82.8	22	11	US-08-788-882-34	Sequence 34, Appl1
23	111	82.8	22	13	US-08-934-367-10	Sequence 10, Appl1
24	111	82.8	22	13	US-08-934-367-10	Sequence 34, Appl1
25	111	82.8	22	13	US-08-934-367-34	Sequence 34, Appl1
26	111	82.8	22	17	US-09-386-591-34	Sequence 34, Appl1
27	111	82.8	22	17	US-09-387-340-34	Sequence 34, Appl1
28	111	82.8	22	17	US-09-387-340-10	Sequence 10, Appl1
29	111	82.8	22	17	US-09-387-340-34	Sequence 34, Appl1
30	107	79.9	22	11	US-08-785-997-4	Sequence 4, Appl1
31	107	79.9	22	11	US-08-788-882-4	Sequence 4, Appl1
32	107	79.9	22	13	US-08-934-367-4	Sequence 4, Appl1
33	107	79.9	22	17	US-09-386-591-4	Sequence 4, Appl1
34	107	79.9	22	17	US-09-387-340-4	Sequence 4, Appl1
35	83	61.9	16	1	PCT-US99-13975B-107	Sequence 107, Appl1
36	83	61.9	16	21	US-09-701-588-107	Sequence 107, Appl1
37	79	59.0	16	1	PCT-US99-13975B-108	Sequence 108, Appl1
38	79	59.0	16	21	US-09-701-588-108	Sequence 108, Appl1
39	53	39.6	11	8	US-08-482-454-3	Sequence 3, Appl1
40	38	28.4	13	20	US-09-675-509-22	Sequence 22, Appl1
41	36.5	27.2	21	1	PCT-US01-14827-13017	Sequence 4506, App
42	36	26.9	21	1	PCT-US01-14827-13017	Sequence 13017, A
43	34	25.4	21	13	US-09-538-038-1267	Sequence 1267, App
44	34	25.4	21	23	US-09-950-083-4435	Sequence 4435, App
45	34	25.4	22	1	PCT-US00-14933-64	Sequence 64, Appl1

ALIGNMENTS

RESULT 1

PCT-US99-13975B-106

Sequence 106, Application PC/TUS9913975B

GENERAL INFORMATION:

APPLICANT: UNITED BIOMEDICAL INC., ET AL.

TITLE OF INVENTION: ARTIFICIAL T HELPER CELL

TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC

NUMBER OF SEQUENCES: 151

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US99/13975B

FILING DATE: 21-JUNE-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/100,412

FILING DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158PCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-106

Query Match 100.0%; Score 134; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLIQMDGFPFHLVDFLOSL 26
DB 1 RDGFLIQMDGFPFHLVDFLOSL 26

RESULT 2
US-08-432-483-1

Sequence 1, Application US/08432483
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino acids of
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
TITLE: cholesterol ester transfer CDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634

DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-432-483-1

Query Match 100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLIQMDGFPFHLVDFLOSL 26
DB 1 RDGFLIQMDGFPFHLVDFLOSL 26

RESULT 3
US-08-432-483A-1

Sequence 1, Application US/08432483A
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,483A
FILING DATE: 1-May-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino acids of
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
TITLE: cholesterol ester transfer CDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-432-483A-1

Query Match 100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDPLQSL 26
Db 1 RDGFLLLQMDGFPPEHLVDPLQSL 26

RESULT 4
US-08-785-997-29
; Sequence 29, Application US/08785997
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process for Increasing
; TITLE OF INVENTION: the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,997
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Swenson, T. L.
; JOURNAL: J. Biol. Chem.
; VOLUME: 264
; PAGES: 14318-14326
; DATE: 1989
US-08-785-997-29

Query Match 100.0%; Score 134; DB 11; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDPLQSL 26
Db 1 RDGFLLLQMDGFPPEHLVDPLQSL 26

RESULT 5
US-08-788-882-29
; Sequence 29, Application US/08788882
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamson, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs

; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,882
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Swenson, T. L.
; JOURNAL: J. Biol. Chem.
; VOLUME: 264
; PAGES: 14318-14326
; DATE: 1989
US-08-788-882-29

Query Match 100.0%; Score 134; DB 11; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPPEHLVDPLQSL 26
Db 1 RDGFLLLQMDGFPPEHLVDPLQSL 26

RESULT 6
US-08-934-367-29
; Sequence 29, Application US/08934367
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,367
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-08-934-367-29

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLQMDFGFPEHLVDPLQSL 26
DB 1 RDGFLLQMDFGFPEHLVDPLQSL 26

RESULT 7
US-08-945-289-1
; Sequence 1, Application US/08945289
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,289
; FILING DATE: October 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/432,483
; FILING DATE: May 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-411.1P US
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino
NAME/KEY: acids of human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-945-289-1

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLQMDFGFPEHLVDPLQSL 26
DB 1 RDGFLLQMDFGFPEHLVDPLQSL 26

RESULT 8
US-09-386-591-29
; Sequence 29, Application US/09386591
; GENERAL INFORMATION:
; APPLICANT: Needleman, Phillip
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/386,591
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Swenson, T. L.
; JOURNAL: J. Biol. Chem.
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VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-386-591-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPFPHLLVDFLOSLS 26
DB 1 RDGFLLQMDGFPFPHLLVDFLOSLS 26

RESULT 9
US-09-387-340-29
Sequence 29, Application US/09387340
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Ktul, Elaine
APPLICANT: Gamson, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-387-340-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPFPHLLVDFLOSLS 26
DB 1 RDGFLLQMDGFPFPHLLVDFLOSLS 26

RESULT 10
US-09-701-588-106
Sequence 106, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: NOVEL LRRH PEPTIDE
IMMUNOGENS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-Nov-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-158US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 106
US-09-701-588-106

Query Match 100.0%; Score 134; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPFPHLLVDFLOSLS 26
DB 1 RDGFLLQMDGFPFPHLLVDFLOSLS 26

RESULT 11
US-09-943-334-1
Sequence 1, Application US/09943334
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
FILE REFERENCE: TGS-411.1P US-1; TGS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,334
PRIOR FILING DATE: 2001-08-30
CURRENT APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1

SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
US-09-943-334-1

Query Match 100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26
DB 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26

RESULT 12
US-09-943-548-1
Sequence 1, Application US/0943548
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
US-09-943-548-1

Query Match 100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26
DB 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26

RESULT 13
PCT-US99-13975B-109
Sequence 109, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
TITLE OF INVENTION: EPITOPE AS IMMUNE STIMULATORS FOR SYNTHETIC
TITLE OF INVENTION: PEPTIDE IMMUNOGENS
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Flunegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158Pc1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-109

Query Match 87.3%; Score 117; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 5,4e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGCILLQMDGFPFPHLLVDFLOSL 26
DB 2 DGCILLQMDGFPFPHLLVDFLOSL 26

RESULT 14
US-08-785-997-50
Sequence 50, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process for Increasing
TITLE OF INVENTION: the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ganson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-785-997-50

Query Match 87.3%, Score 117, DB 11, Length 26;
Best Local Similarity 92.0%; Pred. No. 5.4e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGFLLQMDGFPFPHLLVDFLOSLS 26
DB 2 DGFLLQMDGFPFPHLLVDFLOSLS 26

RESULT 15

US-08-788-882-50
; Sequence 50, Application US/08788882
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gansson, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788.882
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gansson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/59242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-788-882-50

Query Match 87.3%, Score 117, DB 11, Length 26;
Best Local Similarity 92.0%; Pred. No. 5.4e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGFLLQMDGFPFPHLLVDFLOSLS 26
DB 2 DGFLLQMDGFPFPHLLVDFLOSLS 26

Search completed: June 18, 2002, 08:15:36
Job time: 215 sec

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OH protein - protein search, using sw model

Run on: June 18, 2002, 08:12:57 ; Search time 13.54 seconds

(without alignments)
162,588 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134
Sequence: 1 RDGFLLQMDPGRFPHLLVDFLOSLS 26

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 257105 seqs, 84670655 residues

Total number of hits satisfying chosen parameters: 44311

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_MA_New:*
1: /cgn2-6/ptodata/1/paa/PC/PC/NEW_COMB.pep:*
2: /cgn2-6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2-6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2-6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2-6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2-6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2-6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	39.5	11	5	US-09-523-033A-3
2	34	25.4	21	1	PCT-US02-09257-427
3	34	25.4	21	1	PCT-US02-09370-671
4	34	25.4	21	1	US-10-105-299-5439
5	32.5	24.3	12	6	US-10-145-415-68
6	32	23.9	22	5	US-09-453-834-133
7	32	23.9	22	5	US-09-453-834-133
8	32	23.9	22	6	US-10-099-574A-133
9	32	23.9	22	6	US-10-147-849-133
10	32	23.9	22	6	US-10-147-993-133
11	30	22.4	9	6	US-10-014-340-19
12	30	22.4	16	5	US-09-050-359B-135
13	30	22.4	16	5	US-09-069-827A-136
14	30	22.4	16	5	US-10-000-236A-110
15	29.5	22.0	22	6	US-09-721-505-280
16	29.5	22.0	22	6	US-10-105-299-4564
17	29	21.6	21	6	US-10-016-349A-215
18	28.5	21.3	15	1	PCT-US02-13200-5
19	28.5	21.3	15	6	US-10-132-100-5
20	28	20.9	16	5	US-10-105-232-72
21	28	20.9	16	5	US-09-547-938B-61
22	28	20.9	17	5	US-09-547-938B-59
23	28	20.9	17	6	US-10-105-232-374
24	28	20.9	17	6	US-10-105-232-377
25	28	20.9	18	6	US-10-105-232-333
26	28	20.9	19	6	US-10-105-232-326

27	28	20.9	22	1	PCT-US02-09188-487	Sequence 487, App
28	28	20.9	22	1	PCT-US02-09370-505	Sequence 505, App
29	28	20.9	22	5	US-09-453-834-134	Sequence 134, App
30	28	20.9	22	5	US-09-453-834-134	Sequence 134, App
31	28	20.9	22	6	US-10-099-574A-134	Sequence 134, App
32	28	20.9	22	6	US-10-099-574A-134	Sequence 134, App
33	28	20.9	22	6	US-10-147-849-134	Sequence 134, App
34	28	20.9	22	6	US-10-147-849-134	Sequence 134, App
35	27	20.1	9	6	US-10-089-783-10	Sequence 10, App
36	27	20.1	9	6	US-10-089-783-10	Sequence 10, App
37	27	20.1	10	6	US-10-089-783-23	Sequence 23, App
38	27	20.1	10	6	US-10-089-783-24	Sequence 24, App
39	27	20.1	13	1	PCT-US02-09135-151	Sequence 151, App
40	27	20.1	13	1	PCT-US02-09105-221	Sequence 221, App
41	27	20.1	13	1	PCT-US02-09257-299	Sequence 299, App
42	27	20.1	13	1	PCT-US02-09922-285	Sequence 285, App
43	27	20.1	13	6	US-10-105-299-3814	Sequence 3814, App
44	27	20.1	20	1	PCT-US02-01109-141	Sequence 141, App
45	27	20.1	22	6	US-10-115-123-516	Sequence 516, App

ALIGNMENTS

RESULT 1
US-09-523-033A-3
Sequence 3, Application US/09523033A
GENERAL INFORMATION:
APPLICANT: Kwosh, Deborah Y.
APPLICANT: Brostoff, Steven W.
TITLE OF INVENTION: METHOD FOR INCREASING HDL CHOLESTEROL LEVEL
FILE REFERENCE: TCS-428.0 US-1
CURRENT APPLICATION NUMBER: US/09/523-033A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 08/482,454
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-523-033A-3

Query Match 39.6% Score 53; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 HLLVDFLOSLS 26
DB 1 HLLVDFLOSLS 11
RESULT 2
PCT-US02-09257-427
Sequence 427, Application PC/TUS0209257
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS957PCT
CURRENT APPLICATION NUMBER: PCT/US02/09257
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 994
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 427

LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09257-427

Query Match 25.4%; Score 34; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GPEHLYVDF 21
||| : |||
DB 10 GPEYFEVDF 19

RESULT 3
PCT-US02-09370-671
Sequence 671, Application PC/TUS0209370
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS954PCT
CURRENT APPLICATION NUMBER: PCT/US02/09370
CURRENT FILING DATE: 2002-03-26
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
NUMBER OF SEQ ID NOS: 1834
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 671
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09370-671

Query Match 25.4%; Score 34; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GPEHLYVDF 21
||| : |||
DB 10 GPEYFEVDF 19

RESULT 4
US-10-105-299-5439
Sequence 5439, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - see file Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5439
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-10-105-299-5439

Query Match 25.4%; Score 34; DB 6; Length 21;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GPEHLYVDF 21
||| : |||

DB 10 GPEYFEVDF 19

RESULT 5
US-10-145-415-68
Sequence 68, Application US/10145415
GENERAL INFORMATION:
APPLICANT: Buckel, Thomas Gunter
APPLICANT: Hammer, Philip Eugene
APPLICANT: Hill, Dwight Steven
APPLICANT: Ligon, James Madison
APPLICANT: Molnar, Istvan
APPLICANT: Pachlatko, Johannes Paul
TITLE OF INVENTION: Methods and Compositions for Making Enamectin
FILE REFERENCE: SYN-117 109846.312
CURRENT APPLICATION NUMBER: US/10/145,415
CURRENT FILING DATE: 2002-05-14
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 12
TYPE: PRT
ORGANISM: Streptomyces tubercidicus
US-10-145-415-68

Query Match 24.3%; Score 32.5; DB 6; Length 12;
Best Local Similarity 58.3%; Pred. No. 92;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 6 LIDWDFGPEHL 17
||| : |||
DB 1 LMEK-LGLPHEL 11

RESULT 6
US-09-453-834-133
Sequence 133, Application US/09453834
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Melz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: ABOLIPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DISLIPIDMIC DISORDERS
NUMBER OF SEQUENCES: 238
CORRESPONDENCE ADDRESS:
ADDRESSEE: pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
US-09-453-834-133

Query Match 23.9%; Score 32; DB 5; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLYVDFLOSUS 26
DB 7 EHLEEDLQALN 18

RESULT 7
US-09-453-841-133
Sequence 133, Application US/09453841
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453, 841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940, 095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
US-09-453-841-133

Query Match 23.9%; Score 32; DB 5; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 15 EHLYVDFLOSUS 26
DB 7 EHLEEDLQALN 18

RESULT 8
US-10-099-574A-133
Sequence 133, Application US/10099574A
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099, 574A
FILING DATE: 29-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
US-10-099-574A-133

Query Match 23.9%; Score 32; DB 6; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 15 EHLYVDFLOSUS 26
DB 7 EHLEEDLQALN 18

RESULT 9
US-10-147-849-133
Sequence 133, Application US/10147849
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/147,849
FILING DATE: 29-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
US-10-147-849-133

Query Match 23.9%; Score 32; DB 6; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLYDFLOSLS 26
DB 7 ERLEDDLDALN 18

RESULT 10
US-10-147-993-133
Sequence 133, Application US/10147993
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/147,993
FILING DATE: 29-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
US-10-147-993-133

Query Match 23.9%; Score 32; DB 6; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLYDFLOSLS 26
DB 7 ERLEDDLDALN 18

RESULT 11
US-10-014-340-19
Sequence 19, Application US/10014340
GENERAL INFORMATION:
APPLICANT: Herath, et al
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, includ
FILE REFERENCE: 9195-078
CURRENT APPLICATION NUMBER: US/10/014,340
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-340-19

Query Match 22.4%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPHL 17
DB 2 PPHL 6

RESULT 12
US-09-050-359B-136
Sequence 136, Application US/09050359B
GENERAL INFORMATION:
APPLICANT: FOWLES, Dana M
KAY, Brian K
FREILINGER, Jeffrey A

HYDE-DEWUSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,359H
FILING DATE: 31-Mar-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-Oct-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOWLES-4B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-050-359B-136
Query Match 22.4%; Score 30; DB 5; Length 16;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 14 PEHLVDFLO 23
DB 5 PESTLVRLLO 14
RESULT 13
US-09-069-827A-136
Sequence 136, Application US/09069827A
GENERAL INFORMATION:
APPLICANT: FOWLES, Dana M
KAY, Brian K
FREILINGER, Jeffrey A
HYDE-DEWUSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,827A
FILING DATE: 30-Apr-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/050,359
FILING DATE: 31-Mar-1998
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-Oct-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOWLES-4C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-069-827A-136
Query Match 22.4%; Score 30; DB 5; Length 16;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 14 PEHLVDFLO 23
DB 5 PESTLVRLLO 14
RESULT 14
US-10-000-256A-210
Sequence 210, Application US/10000256A
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chonghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes
FILE REFERENCE: DER-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/244,782
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn version 3.1
SEQ ID NO 210
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-256A-210
Query Match 22.4%; Score 30; DB 6; Length 18;
Best Local Similarity 43.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 3 GFLLQMDGPEPHL 18
DB 2 GYGLGIMAGFEREYV 17
RESULT 15

US-09-721-506-290
; Sequence 290, Application US/09721506
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; Lindegar, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,506
; FILING DATE: 22-Nov-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: NO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: NO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /note="motif C peptide from human
; telomerase core protein 1 (TICP1)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 290:
US-09-721-506-290

Best Local Similarity 40.9%; Pred. No. 4.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 9; Gaps 1;
OY 1 RDGFLLQMDFGFPPEHLVDFL 22
||| | : |
||| | : |
DB 2 RDGILLRLVD-----DFL 14

Search completed: June 18, 2002, 08:15:57
Job time: 180 sec

Query Match 22.0%; Score 29.5; DB 5; Length 22;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:07:31 ; Search time 12.84 Seconds
(without alignments)
49,460 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDCFLQLQMDGFEPLHLVDLQSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters: 136340

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	23.9	22	3	US-08-940-095-133
2	32	23.9	22	3	US-08-940-093-133
3	32	23.9	22	3	US-08-940-096-133
4	32	23.9	22	4	US-09-465-719-133
5	32	23.9	22	4	US-09-453-605-133
6	32	23.9	26	5	PCT-US91-02942-98
7	31	23.1	23	4	US-09-183-217-8
8	30	22.4	20	1	US-08-199-608-2
9	29.5	22.0	22	3	US-08-851-843A-170
10	29.5	22.0	22	4	US-08-974-549A-290
11	29.5	22.0	22	4	US-08-854-050-170
12	29.5	22.0	22	4	US-09-430-323-170
13	29	21.6	11	4	US-09-128-572-15
14	29	21.6	19	1	US-08-359-696-85
15	29	21.6	20	2	US-08-484-530-22
16	29	21.6	20	2	US-08-468-540B-3
17	29	21.6	20	2	US-08-827-618A-22
18	29	21.6	20	3	US-08-483-952A-22
19	29	21.6	24	4	US-08-905-223-337
20	29	21.6	25	4	US-08-424-881-3
21	29	21.6	25	2	US-08-874-763-3
22	29	21.6	25	4	US-09-370-867-3
23	28	20.9	10	3	US-08-159-339A-401
24	28	20.9	10	5	PCT-US91-02942-88
25	28	20.9	22	3	US-08-940-095-134
26	28	20.9	22	3	US-08-940-093-134
27	28	20.9	22	3	US-08-940-096-134

28	28	20.9	22	4	US-09-465-719-134	Sequence 134, App
29	28	20.9	22	4	US-09-453-605-134	Sequence 134, App
30	28	20.9	26	2	US-08-482-142-22	Sequence 22, Appl
31	28	20.9	26	2	US-08-482-142-37	Sequence 37, Appl
32	28	20.9	26	2	US-08-482-142-134	Sequence 168, App
33	28	20.9	26	2	US-08-482-142-168	Sequence 22, Appl
34	28	20.9	26	2	US-08-478-572-22	Sequence 37, Appl
35	28	20.9	26	2	US-08-478-572-37	Sequence 168, App
36	28	20.9	26	2	US-08-478-572-134	Sequence 134, App
37	28	20.9	26	2	US-08-478-572-168	Sequence 168, App
38	28	20.9	26	4	US-08-484-286-22	Sequence 22, Appl
39	28	20.9	26	4	US-08-484-286-37	Sequence 37, Appl
40	28	20.9	26	4	US-08-484-286-134	Sequence 134, App
41	28	20.9	26	4	US-08-484-286-168	Sequence 168, App
42	28	20.9	26	5	PCT-US95-04481-13	Sequence 30, Appl
43	28	20.9	26	5	PCT-US95-04481-30	Sequence 83, Appl
44	27	20.1	9	2	US-08-765-783A-83	Sequence 83, Appl
45	27	20.1	9	4	US-09-416-557-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-08-940-095-133
Sequence 133, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-133

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Query Match      23.9%: Score 32; DB 3; Length 22;
Best Local Similarity 58.3%: Pred. No. 66;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDPLQSL 26
  ||| |||:
  7 ERLLEDLQALN 18

RESULT 2
US-08-940-093-133
; Sequence 133, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-133

Query Match      23.9%: Score 32; DB 3; Length 22;
Best Local Similarity 58.3%: Pred. No. 66;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDPLQSL 26
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  7 ERLLEDLQALN 18

RESULT 3
US-08-940-096-133
; Sequence 133, Application US/08940096
; Patent No. 6046166

GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-133

Query Match      23.9%: Score 32; DB 3; Length 22;
Best Local Similarity 58.3%: Pred. No. 66;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDPLQSL 26
  ||| |||:
  7 ERLLEDLQALN 18

RESULT 4
US-09-465-719-133
; Sequence 133, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
```

COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
US-09-465-719-133

Query Match 23.9%; Score 32; DB 4; Length 22;
Best Local Similarity 58.3%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDPLQSL 26
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DB 7 ERLLEDLQALN 18

RESULT 5
US-09-453-605-133
Sequence 133 Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
APPLICANT: Dassaux, Jean-Louis
Sekul, Renate
Butner, Klaus
Cornut, Isabelle
Meitz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NO. 6329341-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-09-453-605-133

Query Match 23.9%; Score 32; DB 4; Length 22;
Best Local Similarity 58.3%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDPLQSL 26
| | | | | | | | | |
DB 7 ERLLEDLQALN 18

RESULT 6
PCT-US91-02942-98
Sequence 98 Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADNAIR, JOHN R
APPLICANT: ATHMAL, DILJEET S
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011,0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US91-02942-98

Query Match 23.98; Score 32; DB 5; Length 26;
Best Local Similarity 54.58; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RDGFLLQMDP 11
1 1 1 1 1 1
DB 16 RCGWLLSFYD 26

RESULT 7

US-09-183-217-8
Sequence 8, Application US/09183217A
Patent No. 6153194
GENERAL INFORMATION:
APPLICANT: Skare, Jonathan T.
APPLICANT: Shang, Ellen S.
APPLICANT: Champion, Cheryl I.
APPLICANT: Blanco, David R.
APPLICANT: Miller, James N.
APPLICANT: Lovett, Michael A.
APPLICANT: Mizabekov, Tajib A.
APPLICANT: Kagan, Bruce L.
APPLICANT: Tempst, Paul
APPLICANT: Foley, Denise M.
TITLE OF INVENTION: BORRELIA BURGORDFERI OUTER MEMBRANE PROTEINS
FILE REFERENCE: UC Case No. 6153194 96-059-3/Skare et al.
CURRENT FILING DATE: 1998-10-29
PRIOR FILING DATE: 1997-01-22
PRIORITY FILING DATE: 1997-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 23
TYPE: PRT
ORGANISM: Borrelia burgdorferi
US-09-183-217-8

Query Match 23.18; Score 31; DB 4; Length 23;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

OY 1 RDGFLLQMDP 12
1 1 1 1 1 1
DB 4 KNTYLLIQMGTFD 17

RESULT 8

US-08-199-508-2
Sequence 2, Application US/08199508
Patent No. 5717058
GENERAL INFORMATION:
APPLICANT: Matthews, Maure-Ann H.
APPLICANT: Stettler, Gary L.
APPLICANT: Anthony-Cahill, Spencer J.
APPLICANT: Anderson, David C.
TITLE OF INVENTION: Modulators of Gene Expression
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 5797 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,508

FILING DATE: February 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,536
FILING DATE: February 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5717058ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 121 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-444-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
US-08-199-508-2

Query Match 22.48; Score 30; DB 1; Length 20;
Best Local Similarity 38.58; Pred. No. 1.2e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 11 FGPEHLVDPEQ 23
1 1 1 1 1 1
DB 1 FGPEYVVFEGCQV 13

RESULT 9

US-08-851-843A-170
Sequence 170, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:

1
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..22
OTHER INFORMATION: /note="motif C peptide from human
OTHER INFORMATION: telomerase core protein 1 (TCPI)"
US-08-851-843A-170

Query Match 22.0%; Score 29.5; DB 3; Length 22;
Best Local Similarity 40.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY 1 RDGFLLLQMDGFPFPHLVDFL 22
||| || : |||
Db 2 RDGILLRLVLD-----DPL 14

RESULT 10
US-08-974-549A-290
Sequence 290, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00261005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 290:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..22
OTHER INFORMATION: /note="motif C peptide from human
OTHER INFORMATION: telomerase core protein 1 (TCPI)"
US-08-974-549A-290

Query Match 22.0%; Score 29.5; DB 4; Length 22;
Best Local Similarity 40.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY 1 RDGFLLLQMDGFPFPHLVDFL 22
||| || : |||
Db 2 RDGILLRLVLD-----DPL 14

RESULT 11
US-08-854-050-170
Sequence 170, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..22
OTHER INFORMATION: /note="motif C peptide from human
telomerase core protein 1 (TcP1)"
US-08-854-050-170

Query Match      22.0%; Score 29.5; DB 4; Length 22;
Best Local Similarity 40.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY 1 RDGFLLMDFGFFPHLLVDFL 22
   |||||:|
Db 2 RDGLLRIVD-----DFL 14

RESULT 12
US-09-430-323-170
; Sequence 170, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
;               Molin, Gregg B.
;               Harley, Calvin
;               Andrews, William H.
; TITLE OF INVENTION: NO. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..22
OTHER INFORMATION: /note="motif C peptide from human
telomerase core protein 1 (TcP1)"
US-09-430-323-170

Query Match      22.0%; Score 29.5; DB 4; Length 22;
Best Local Similarity 40.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY 1 RDGFLLMDFGFFPHLLVDFL 22
   |||||:|
Db 2 RDGLLRIVD-----DFL 14

RESULT 13
US-09-128-572-15
; Sequence 15, Application US/09128572
; Patent No. 6251866
; GENERAL INFORMATION:
; APPLICANT: Prakash, Ramesh K.
; TITLE OF INVENTION: Conjugates Targeted to the Interleukin-2 Receptor
; FILE REFERENCE: T5181.CIP
; CURRENT APPLICATION NUMBER: US/09/128,572
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: US 08/914,042
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Wordperfect 8.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exhibits sequence similarity to a portion of human IL-2.
```

US-09-128-572-15

Query Match 21.6%; Score 29; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 15 EHLVDFL 22
| | | | | |
DB 3 EHLIDGL 10

RESULT 14
US-08-399-696-85
; Sequence 85, Application US/08399696
; Patent No. 5756669
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: P53-BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 126
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,696
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,671
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15522-000710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-399-696-85

Query Match 21.6%; Score 29; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 15 EHLVDFL 22
| | | | | |
DB 12 EHLIDGL 19

RESULT 15
US-08-484-530-22
; Sequence 22, Application US/08484530
; Patent No. 5846740
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J.
; APPLICANT: Kaufman, Mark G.
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pfeiffer, Hobbach, West, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco

STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-398-3249
TELEFAX: 415-781-1989
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-22

Query Match 21.6%; Score 29; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 MDGPEHLL 18
| | | | | |
DB 9 IDHHPNELL 18

Search completed: June 18, 2002, 08:13:27
Job time: 356 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:16:32 ; Search time 14.14 Seconds
(without alignments)
210.663 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162

Sequence: 1 COYIKANSKFIGITEFGFEPHLLVDFLOSLIS 31

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 6607

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR-71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	19.1	23	2	homeotic protein S
2	31	19.1	24	2	thymidine phosphor
3	31	19.1	28	2	protein kinase 4 (
4	30	18.5	20	2	translation elonga
5	29	17.9	30	2	fibrinogen beta ch
6	29	17.9	31	2	hypothetical prote
7	28	17.6	21	2	hexokinase (EC 2.7
8	28	17.3	21	2	nitrite hydratase
9	28	17.3	24	2	glyceroldehyde-3-P
10	27	17.0	27	2	chitinase (EC 3.2.
11	27	16.7	24	2	interphotoreceptor
12	26	16.0	19	2	wd-repeat protein
13	26	16.0	22	2	polygalacturonase
14	26	16.0	26	2	C85947
15	26	16.0	27	2	hypothetical prote
16	26	16.0	27	2	hypothetical prote
17	26	16.0	27	2	stp protein (Baker
18	26	16.0	27	2	hypothetical prote
19	26	16.0	28	2	hypothetical prote
20	26	16.0	30	2	hypothetical prote
21	25	15.4	15	2	heat shock protein
22	25	15.4	16	2	calmodulin kinase
23	25	15.4	22	2	glyceroldehyde-3-P
24	25	15.4	23	2	PC4030
25	25	15.4	25	2	RNA endonuclease
26	25	15.4	25	2	myonexin - norther
27	25	15.4	25	2	interphotoreceptor
28	25	15.4	28	4	fringe shifted PKM1
29	25	15.4	30	2	proteinase inhibit
30	25	15.4	31	2	G-alpha-1 protein

30	24.5	15.1	24	2	S69080	GDNF receptor alph
31	24.5	15.1	28	2	S64701	hypothetical prote
32	24.5	15.1	29	2	A60717	hypothetical prote
33	24	14.8	10	2	PT0230	Ig heavy chain CDR
34	24	14.8	14	2	A01250	angiotensin I prec
35	24	14.8	15	2	A60834	angiotensin I prec
36	24	14.8	20	2	A37984	ADP,ATP carrier pr
37	24	14.8	22	2	C46285	formaldehyde dehyd
38	24	14.8	23	2	S51188	aldehyde dehydroge
39	24	14.8	24	2	S10618	superoxide dismuta
40	24	14.8	26	2	JM0965	cytochrome-c oxida
41	24	14.8	26	2	B54257	deoxynucleoside ki
42	24	14.8	30	2	A48299	taurine transporte
43	24	14.8	30	2	E71264	hypothetical prote
44	23.5	14.5	25	2	PH1717	Ig heavy chain V r
45	23	14.2	7	2	S36662	dermorphin (Lys-7)

ALIGNMENTS

RESULT 1
S45030
homeotic protein SPOX H1 - Halictona sp. (fragment)
C:Species: Halictona sp.
C:Date: 06-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 15-Oct-1999
C:Accession: S45030
R:Degan, B.M.; Degan, S.M.; Glust, A.; Morse, D.E.
Submitted to the EMBL Data Library, May 1994
A:Description: A Hox homeobox gene in sponges.
A:Reference number: S45030
A:Accession: S45030
A:Molecule type: DNA
A:Residues: 1-23 <DEG>
A:Cross-references: EMBL:X79263; NID:G488754; PIDN:CAA55850.1; PID:G488755
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 19.1%; Score 31; DB 2; Length 23;
Best Local Similarity 35.3%; Pred. No. 4.3e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 7 NSKFIGITEFGFEPHLL 23
DB 1 SKRYLSTERSHAHL 17

RESULT 2
S11384
thymidine phosphorylase (EC 2.4.2.4) - Lactobacillus casei (fragment)
M:Alternate names: pyrimidine phosphorylase
C:Species: Lactobacillus casei
C:Date: 19-Mar-1997 #sequence_revision 26-Feb-1998 #text_change 21-Nov-1998
C:Accession: S11384
R:Avraham, Y.; Grossowicz, N.; Yashpe, J.
Biochim. Biophys. Acta 1040, 287-293, 1990
A:Title: Purification and characterization of uridine and thymidine phosphorylase fro
A:Reference number: S11383; WUID:90381286
A:Accession: S11384
A:Molecule type: protein
A:Residues: 1-24 <AVR>
A:Experimental source: strain ATCC 7469
A:Note: This protein was shown to possess thymidine phosphorylase activity and not gl
C:Superfamily: glyceroldehyde-3-phosphate dehydrogenase
C:Keywords: glycosyltransferase; homodimer; pentosyltransferase

Query Match 19.1%; Score 31; DB 2; Length 24;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 IGITEFG 17

Db 5 IGINFEG 11

RESULT 3

D38578

protein kinase 4 (EC 2.7.1.-) - slime mold (Dictyostellium discoideum) (fragment)

C:Species: Dictyostellium discoideum

C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 23-Feb-1997

C:Accession: D38578

R:Haribabu, B.; Dotin, R.P.

A:Title: Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991

A:Reference: Identification of a protein kinase multigene family of Dictyostellium discoideum

A:Accession: D38578; MUID:91142122

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-28 <HAR>

A:Cross-references: GB:M59747

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine

Query Match

Best Local Similarity 19.1%; Score 31; DB 2; Length 28;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 11 IGINFEGPEHL 22

Db 9 IKIDFGFAKRI 20

RESULT 4

S57286

translation elongation factor aEF-1 beta - Sulfolobus solfataricus (fragments)

C:Species: Sulfolobus solfataricus

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999

C:Accession: S57286

R:Arcari, P.; Raimo, G.; Iannicelli, G.; Gallo, M.; Bocchini, V.

A:Title: Biochem. Biophys. Acta 1263, 86-88, 1995

A:Reference: The first nucleotide sequence of an archaeal elongation factor 1-beta gene.

A:Accession: S57286

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <ARC>

Query Match

Best Local Similarity 18.5%; Score 30; DB 2; Length 20;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 11 IGINFEGP 18

Db 13 VGIIRLGF 20

RESULT 5

A34622

fibrinogen beta chain - California spiny lobster (fragment)

C:Species: Panulirus interruptus (California spiny lobster)

C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 26-Jan-1996

C:Accession: A34622

R:Doallittle, R.F.; Riley, M.

A:Title: Biochem. Biophys. Res. Commun. 167, 16-19, 1990

A:Reference: The amino-terminal sequence of lobster fibrinogen reveals common ancestry with

A:Accession: A34622; MUID:90179743

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-30 <DOO>

C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match

Best Local Similarity 17.9%; Score 29; DB 2; Length 30;

Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 9 KFIGITEFGPEH 21

Db 10 KYHGIVAGLIPST 22

RESULT 6

A70219

hypothetical protein BB21 - Lyme disease spirochete plasmid B/cp26

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000

C:Accession: A70219

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh

son, D.; Peterson, J.; Kellavag, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943

A:Accession: A70219

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-31 <KLE>

A:Cross-references: GB:AE000792; MUID:93253098; PIDN:AAC66340.1; PID:92669909; TIGR:BB

A:Experimental source: strain B31

C:Genetics:

A:Genome: plasmid

Query Match

Best Local Similarity 17.9%; Score 29; DB 2; Length 31;

Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 QYIKANSKFTG 12

Db 19 QYIKDNSFFFG 29

RESULT 7

A32521

hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995

C:Accession: A12521

R:Schirch, D.M.; Wilson, J.E.

A:Title: Biochem. Biophys. 257, 1-12, 1987

A:Reference number: A80080; MUID:67324917

A:Accession: A12521

A:Molecule type: protein

A:Residues: 1-21 <SCH>

C:Superfamily: human hexokinase I; hexokinase homology

C:Keywords: ATP; glycolysis; phosphotransferase

Query Match

Best Local Similarity 17.6%; Score 28.5; DB 2; Length 21;

Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

OY 11 IGINFEGPEH 21

Db 3 LGFT-FSPFXH 12

RESULT 8

JU0386

nitrile hydratase (EC 4.2.1.84) - Acinetobacter sp. (fragment)

C:Alternate names: nitrilase

C:Species: Acinetobacter sp.

```

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999
C/Accession: J00386
R:Yamamoto, K.; Komatsu, K.
Agric. Biol. Chem. 55, 1459-1466, 1991
A>Title: Purification and characterization of nitrilase responsible for the enantioselect
A/Reference number: J00386; MUID:91345837
A/Accession: J00386
A:Molecule type: protein
A:Residues: 1-21 <YAM>
A:Experimental source: strain AK226
C/Comment: The enzyme prefers S-(-)-2-(4'-isobutylphenyl)-propanionitrile to R-(+)-2-(4'-i
C/Keywords: carbon-oxygen lyase, hydro-lyase

Query Match      17.3%; Score 28; DB 2; Length 21;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 IKANSKFICIT 14
: |||||
DB 1 VSYNSKFLAAT 11

RESULT 9
PN0163
glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - fungus (Fusarium sporotrichoid
C/Species: Fusarium sporotrichoides
C/Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 22-Apr-1995
C/Accession: PN0163
R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A/Reference number: PN0160
A/Accession: PN0163
A:Molecule type: protein
A:Residues: 1-24 <FUK>
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C/Keywords: oxidoreductase

Query Match      17.3%; Score 28; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 KFIGITFG 17
: |||||
DB 3 KIVGNGFG 11

RESULT 10
C44908
chitinase (EC 3.2.1.14), 47K - Streptomyces olivaceoviridis (fragment)
C/Species: Streptomyces olivaceoviridis
C/Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C/Accession: C44908
R:Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.
J. Bacteriol. 174, 3450-3454, 1992
A>Title: Chitinases of Streptomyces olivaceoviridis and significance of processing for m
A/Reference number: A44908; MUID:92276319
A/Accession: C44908
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-27 <ROM>
A:Experimental source: ATCC 11228
A>Note: sequence extracted from NCBI backbone (NCBI:P104591)
C:Superfamily: Streptomyces chitinase chi40
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      17.0%; Score 27.5; DB 2; Length 27;
Best Local Similarity 53.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

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QY 6 ANSKFICITFG 17
: |||||
DB 1 AGSKVGFTEFG 13

RESULT 11
A24417
Interphotoreceptor retinoid-binding protein - sheep (fragment)
N:Alternate names: Interstitial retinoid-binding protein
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
C/Accession: A24417
R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
FEBS Lett. 205, 309-312, 1986
A>Title: N-terminal sequence homologies in interstitial retinoid-binding proteins from
A/Reference number: A91365; MUID:86301171
A/Accession: A24417
A:Molecule type: protein
A:Residues: 1-24 <FON>
C:Superfamily: Interphotoreceptor retinoid-binding protein
C/Keywords: duplication

Query Match      16.7%; Score 27; DB 2; Length 24;
Best Local Similarity 36.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 13 ITFGFPEHLL 23
: |||||
DB 14 LDNYTFPEHLL 24

RESULT 12
T50329
Wd-repeat protein popl. [Imported] - fission yeast (Schizosaccharomyces pombe) (fragm
C/Species: Schizosaccharomyces pombe
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C/Accession: T50329
R:Lyne, M.; Rajadream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A/Reference number: 225062
A/Accession: T50329
A>Status: preliminary; translated from GB/EMBL/DDAJ
A:Molecule type: DNA
A:Residues: 1-19 <LYN>
A:Cross-references: EMBL:AL157874; PDB:CMR75991.1; GSPDB:GN00067; SPDB:SPBC1718.01
A:Experimental source: strain 972h(?); cosmid cl718
C/Genetics:
A:gene: SPBC262.18; SPDB:SPBC1718.01
A:Map position: 2

Query Match      16.0%; Score 26; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 2e+03;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 IKANSKFICITFG 17
: |||||
DB 1 LRNNRPIEVLDFG 14

RESULT 13
P00143
Polygalacturonase (EC 3.2.1.15) p26 - evening primrose (fragment)
C/Species: Oenothera organensis (evening primrose)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 06-Dec-1996
C/Accession: P00143
R:Brown, S.M.; Crouch, M.L.
Plant Cell 2, 263-274, 1990
A>Title: Characterization of a gene family abundantly expressed in Oenothera organensis
A/Reference number: J00992; MUID:93005658
A/Accession: P00143
A:Molecule type: mRNA

```

A:Residues: 1-22 <BRO>
 A:Experimental source: pollen
 C:Comment: This protein is specifically translated in the pollens.
 C:Comment: This protein functions by depolymerizing pectin in the cell walls of the pistil growing tube.
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Search completed: June 18, 2002, 08:18:37
 Job time: 125 sec

Query Match 16.0%; Score 26; DB 2; Length 22;
 Best Local Similarity 36.4%; Pred. No. 2.4e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 NSKFTGTERG 17
 ||| |||:
 Db 5 NNAQFDITKYG 15

RESULT 14

C85947
 hypothetical protein Z4250 [imported] - Escherichia coli (strain O157:H7, substrain EDLg)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: C85947
 R:Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grodzicki, E.O.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C85947
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-26 <STO>
 A:Cross-references: GB:AE005174; NID:g12517442; PIDN:AAG58039.1; GSPDB:GN00145; UWGP:Z42
 A:Experimental source: strain O157:H7, substrain EDLg933
 C:Genetics:
 A:Gene: Z4250

Query Match 16.0%; Score 26; DB 2; Length 26;
 Best Local Similarity 38.5%; Pred. No. 2.8e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 19 PEHLVDFLOSL 31
 | | | | |:
 Db 14 PRALIDIVDSLT 26

RESULT 15

A28391
 hypothetical protein 1 - Streptomyces albidoflavus (fragment)

C:Species: Streptomyces albidoflavus
 C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 11-Jan-2000
 C:Accession: A28391
 R:Long, C.M.; Virolle, M.J.; Chang, S.Y.; Chang, S.; Bibb, M.J.
 J. Bacteriol. 169, 5745-5754, 1987
 A:Title: Alpha-amylase gene of Streptomyces limosus: nucleotide sequence, expression not
 A:Reference number: A91856; MUID:88058792
 A:Accession: A28391
 A:Molecule type: DNA
 A:Residues: 1-27 <LON>
 A:Note: The source is designated as Streptomyces limosus
 C:Superfamily: lac repressor

Query Match 16.0%; Score 26; DB 2; Length 27;
 Best Local Similarity 54.5%; Pred. No. 2.9e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 14 TEPGPPEHLV 24
 ||| | |:
 Db 6 TEFVQPELV 16

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:18:17 ; Search time 10.15 Seconds
(without alignments)
118.257 Million cell updates/sec

Title: US-09-943-334-2

Sequence: 1 CQIRANSKFIGITGFGPEHLVDFLOSL 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 1969

Minimum DB seq length: 0

Maximum DB seq length: 31

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32.5	20.1	30	1	OTCX_STAEP
2	31	19.1	23	1	TYPH_LACCA
3	31	19.1	29	1	PK4_DICDI
4	30	18.5	22	1	PSP2_PHPA
5	29	17.9	30	1	FIBR_PANIN
6	28	17.3	21	1	NRLA_ACTIP
7	27.5	17.0	27	1	CHT2_STR01
8	27	16.7	24	1	IRBP_SHEEP
9	26	16.0	19	1	NS2_MCTU
10	26	16.0	28	1	GUN_SCHCO
11	25	15.4	22	1	CR33_LITCE
12	25	15.4	22	1	CR34_LITCE
13	25	15.4	25	1	IRBP_PIG
14	25	15.4	30	1	KAB5_OLDAP
15	24.5	15.1	25	1	AMP3_MELFA
16	24	14.8	11	1	TKC2_CAIVO
17	24	14.8	13	1	TEML_RANTE
18	24	14.8	14	1	ANGT_HORSE
19	24	14.8	20	1	TL22_SPIOL
20	24	14.8	24	1	SODC_RANCA
21	24	14.8	26	1	DMS5_PHYBI
22	24	14.8	30	1	CLPA_PINPS
23	24	14.8	30	1	PERN_NEPOL
24	24	14.8	30	1	Y932_TREPA
25	24	14.8	31	1	PERT_OENHO
26	23.5	14.5	31	1	TRR2_LEUMA
27	23	14.2	17	1	WZ21_LITGE
28	23	14.2	18	1	TRP3_LEUMA
29	23	14.2	19	1	TRP3_LEUMA
30	23	14.2	18	1	TRP3_LEUMA
31	23	14.2	24	1	COXJ_ONCMY
32	23	14.2	24	1	COXJ_ONCMY
33	23	14.2	24	1	COXJ_SHEEP

34	23	14.2	25	1	GBX1_MOUSE
35	23	14.2	29	1	COXK_SHEEP
36	23	14.2	30	1	CYH1_VIOHE
37	22.5	13.9	30	1	Y523_BORBU
38	22	13.6	13	1	PARB_ASCSU
39	22	13.6	20	1	AMP_FUSNU
40	22	13.6	20	1	CAOS_RAT
41	22	13.6	20	1	DNAR_CLOPA
42	22	13.6	21	1	DCMS_PSECA
43	22	13.6	24	1	KPYR_CLOPA
44	22	13.6	25	1	AVU1_LITRA
45	22	13.6	25	1	G3P2_JACOR

ALIGNMENTS

RESULT 1
OTCX_STAEP STANDARD: PRT: 30 AA.
AC P81682;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Probable ornithine carbamoyltransferase (EC 2.1.3.3) (OTCase) (Fragment).
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_Taxid=1282;
RN [1]
RP SEQUENCE.
RC SPRAIN-AB9;
RA Hussain M.S., Herrmann M., Chhatwal G.S., Peters G.;
RT A 42 kDa protein with broad affinity to bind several plasma and ECM-proteins in lithium chloride extract of Staphylococcus epidermidis is ornithine carbamoyltransferase.";
RL Submitted (FEB-1999) to the SWISS-PROT data bank.
CC -1- FUNCTION: HAS VITRONECTIN AND FIBRONECTIN-BINDING ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine -> phosphate + L-citrulline.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ATCASSES/OTCASES FAMILY.
DR InterPro: IPR002029; Cardmy/trans.asor.
DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW transferase.
FT NON_TER
SQ SEQUENCE 30 AA: 3629 MW: A78EE64FCA87A7D CRC64:
Query Match 20.1%; Score 32.5; DB 1; Length 30;
Best local Similarity 36.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
OY 7 NSKFIGITGFGPEHLVDFLOSL 31
Db 6 NRSFLTLDPSRQ--VEFLTSL 27
RESULT 2
TYPH_LACCA STANDARD: PRT: 23 AA.
AC P19653;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Thymidine phosphorylase (EC 2.4.2.4) (TDRPASE) (Fragment).
GN DEOA.
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus
OX NCBI_Taxid=1562;
RN [1]

RP SEQUENCE.
 RC STRAIN-ATCC 7469;
 RX MEDLINE-90381286; PubMed-2119230;
 RA Avraham Y., Grossowicz N., Yashphe J.;
 RT "Purification and characterization of uridine and thymidine
 RT phosphatase from *Lactobacillus casei*."
 RL Biochim Biophys Acta 1040:287-293(1990).
 CC -1- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLATION
 CC OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
 CC COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
 CC OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-
 CC ribose 1-phosphate.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
 CC PHOSPHORYLASES FAMILY.
 CC PIR: S11384; S11384.
 DR HSSP: P00357; 1GPD.
 DR InterPro: IPR000173; GAP_DH.
 DR InterPro: IPR000053; Thymid_phosphils.
 DR Pfam: PF00044; gpch; 1.
 DR PROSITE: PS00647; THYMID_PHOSPHORYLASE; PARTIAL.
 KM Transferrase; Glycosyltransferase.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2752 MW; 8705C9C4D82C1AD7 CRC64;

Query Match 19.1%; Score 31; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 11 IGTERFG 17
 ||| |||
 Db 4 IGNEFG 10

RESULT 3
 PK4_DICDI STANDARD; PRT; 29 AA.
 ID PK4_DICDI
 AC P34103;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein kinase 4 (EC 2.7.1.-) (Fragment).
 GN PKCD.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91142122; PubMed-1996312;
 RA Haribabu B., Dotlin R.P.;
 RT "Identification of a protein kinase multigene family of Dictyostelium
 RT discoideum: molecular cloning and expression of a cDNA encoding a
 RT developmentally regulated protein kinase."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1115-1119(1991).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL: M59747; AAA33189.1; .
 DR PIR: D38578; D38578.
 DR DictyDB: DD05049; PKGp.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; PARTIAL.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; PARTIAL.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT NON_TER 1 1
 FT DOMAIN <1 >29 PROTEIN KINASE.
 FT MOD_RES 27 27 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3358 MW; B12D4F42C4C110DA CRC64;

Query Match 19.1%; Score 31; DB 1; Length 29;
 Best Local Similarity 41.7%; Pred. No. 2.3e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 11 IGTERGPEHL 22
 | : | | | : :
 Db 10 IKLTDGFAKRI 21

RESULT 4
 PSP2_PHYPA STANDARD; PRT; 22 AA.
 ID PSP2_PHYPA
 AC P80661;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oxygen-evolving enhancer protein 2 (OEE2) (22 kDa subunit of oxygen
 DE evolving system of photosystem II) (Fragments).
 OS Physcomitrella patens (Moss).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 OX NCBI_TaxID=3218;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Protonema;
 RX MEDLINE-97275459; PubMed-9129336;
 RA Kasten B., Buck F., Nuske J., Reek R.;
 RT "Cytochrome affects nuclear- and plastome-encoded energy-converting
 RT plastid enzymes."
 RL Planta 201:261-272(1997).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF PHOTOSYSTEM II.
 CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
 CC with the photosystem II complex.
 CC -1- INDUCTION: BY LIGHT.
 CC -1- SIMILARITY: BELONGS TO THE PSBP FAMILY.
 CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
 KM Multigene family.
 KM NON_CONS 15 16
 FT NON_TER 22 22
 SQ SEQUENCE 22 AA; 2316 MW; E1553CC57C54B81 CRC64;

Query Match 18.5%; Score 30; DB 1; Length 22;
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 6 ANSKFETIEFG 17
 | : | | | : :
 Db 10 AGNFTYIEYG 21

RESULT 5
 FIBR_PANIN STANDARD; PRT; 30 AA.
 ID FIBR_PANIN
 AC P22775;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibrinogen (Fragment).
 OS Panulirus interruptus (California spiny lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;

OC Palnuroides; Palnuroides; Panulirus.
 OX NCBI_TaxID=6735;
 RN [1]
 RP MEDLINE=9019743; PubMed=2310387;
 RA Doolittle R.F., Riley M.;
 RT "The amino-terminal sequence of lobster fibrinogen reveals common
 RT ancestry with vitellogenins.";
 RL Blochem Biophys Res Commun. 167:16-19(1990).
 CC -1- FUNCTION: CLOTTING PROTEIN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SECRETED INTO THE HEMOLYMPH.
 CC -1- SIMILARITY: TO VITELLOGENINS.
 DR PIR: A34622; A34622.
 KM Glycoprotein; Lipid-binding; Hemolymph clotting.
 FT NON_TER 30
 SQ SEQUENCE 30 AA: 3572 MW: A4808AAFI8E0794C CRC64;

Query Match 17.9%; Score 29; DB 1; Length 30;
 Best Local Similarity 38.5%; Pred. No. 4.7e+02;
 Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 9 KFIGTEGSPFH 21
 DB 10 KYHGVALGIPSY 22

RESULT 6
 ID NR_1_ACI8P STANDARD: PRT: 21 AA.
 AC P33036;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Nitrilase (EC 3.5.3.1) (Fragment).
 OS Acinetobacter sp. (Strain AK226).
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 OX NCBI_TaxID=472;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91345837; PubMed=1369128;
 RA Yamamoto K., Komatsu K.;
 RT "Purification and characterization of nitrilase responsible for the
 RT enantioselective hydrolysis from Acinetobacter sp. AK 226.";
 RL Agric. Biol. Chem. 55:1459-1466(1991).
 CC -1- FUNCTION: ACTS ON MANY KINDS OF NITRILE COMPOUNDS SUCH AS
 CC ALIPHATIC, AROMATIC, AND HETEROCYCLIC MONONITRILES OR DINITRILES.
 CC PREPERS S-(+)-2-(4'-ISOBUTYLPHENYL)-PROPIONITRILE TO R-(+)-2-(4'-
 CC ISOBUTYLPHENYL)-PROPIONITRILE AS THE SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: A nitrile + H(2)O = a carboxylate + NH(3).
 CC -1- SIMILARITY: BELONGS TO THE NITRILASE FAMILY.
 DR PIR: J00386; J00386.
 DR InterPro: IPR000132; NITRIL_CYN_hydrolase.
 DR PROSITE: PS00920; NITRIL_CHT_1; PARTIAL.
 DR PROSITE: PS00921; NITRIL_CHT_2; PARTIAL.
 KW Hydrolase.
 FT NON_TER 21
 SQ SEQUENCE 21 AA: 2223 MW: 5FA741C41EAC619B CRC64;

Query Match 17.3%; Score 28; DB 1; Length 21;
 Best Local Similarity 45.5%; Pred. No. 4.6e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 IKANSKFIGIT 14
 DB 1 VSYNSKFLANT 11

RESULT 7

CH12_STROI
 ID CH12_STROI STANDARD: PRT: 27 AA.
 AC P29116;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Chitinase 47 kDa (EC 3.2.1.14) (Fragment)
 OS Streptomyces olivaceoviridis (Streptomyces corchorus11).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1921;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 11228;
 RX MEDLINE=92276319; PubMed=1592803;
 RA Romaguera A., Menge U., Breves R., Diekmann H.;
 RT "Chitinases of Streptomyces olivaceoviridis and significance of
 RT processing for multiplicity";
 RL J. Bacteriol. 174:3450-3454(1992).
 CC -1- FUNCTION: ABLE TO CLEAVE CHITIN OLIGOMERS FROM N-3 TO 6.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4'-beta-linkages of N-
 CC acetyl-D-glucosamine polymers of chitin.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES).
 DR PIR: C44908; C44908.
 DR InterPro: IPR001579; Chitinase-2.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR PROSITE: PS01095; CHITINASE_18; PARTIAL.
 KM Hydrolase; Glycosidase; Chitin degradation.
 FT NON_TER 27
 SQ SEQUENCE 27 AA: 3172 MW: E9549D5E273DDEE9 CRC64;

Query Match 17.0%; Score 27.5; DB 1; Length 27;
 Best Local Similarity 53.8%; Pred. No. 7.1e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 6 ANSKFIG-ITFEG 17
 DB 1 AGSKVGYEYEMG 13

RESULT 8
 ID IRBP_SHEEP STANDARD: PRT: 24 AA.
 AC P12663;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
 DE retinol-binding protein) (Fragment).
 GN RBP3.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86301171; PubMed=3743780;
 RA Fong S.L., Cook R.G., Alvarez R.A., Llou G.I., Landers R.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologues in interstitial retinol-binding
 RT proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHOOTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX LAYER OF PIGMENT
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.

DR PIR: A24417; A24417.
 KW Vitamin A; Transport.
 FT NON_TER 24
 SQ SEQUENCE 24 AA; 2799 MW; 02EDEBE61A8B4523 CRC64;

Query Match
 Best Local Similarity 36.4%; Score 27; DB 1; Length 24;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 13 ITFEGPEHL 23
 DB 14 LDNYTPENIM 24

RESULT 9
 NS2_MYCTU STANDARD; PRT; 19 AA.
 ID NS2_MYCTU
 AC P81136;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 2 (Fragment).
 OS Mycobacterium tuberculosis.
 OC Bacteria; Filumetes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=H37RV;
 RA Prasad H.K., Annapurna P.S.,
 RL Submitted (DEC 1997) to the SWISS-PROT data bank.
 CC -1 SIMILARITY: STRONG. TO PHE N-TERMINALS OF C.ELEGANS F20A1.4
 CC -1 AND H. INFLUENZAE HT0967.
 CC -1 CAUTION: We are unable to find this protein in the translation of
 CC the genome of strain H37RV.
 FT NON_TER 19
 FT SEQUENCE 19 AA; 2211 MW; A8C1854BF1F70 CRC64;

Query Match
 Best Local Similarity 57.1%; Score 26; DB 1; Length 19;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 12 GIVEGEF 18
 DB 10 GVAEFSF 16

RESULT 10
 GUN_SCHCO STANDARD; PRT; 28 AA.
 ID GUN_SCHCO
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Stereales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.,
 RT Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases.
 RL FEBS Lett. 414:359-361(1997).
 CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1 SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor

CC (Probable). BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC -1 SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR INTERPRO: IPR001547; GLYCO_HYDRO_F5.
 DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match
 Best Local Similarity 38.5%; Score 26; DB 1; Length 28;
 Matches 5; Conservative 6; Mismatches 0; Indels 2; Gaps 1;
 QY 2 QYKANSK--FIG 12
 DB 7 EMLKANNRGFLG 19

RESULT 11
 CR33_LITCE STANDARD; PRT; 22 AA.
 ID CR33_LITCE
 AC P56240;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 3.3.
 OS Litorea caerulea (Green tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litorea.
 OX NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland.
 RA Stone D.V.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 RT Litorea caerulea".
 RL J. Chem. Res. 138:910-936(1993).
 CC -1 FUNCTION: ANTIBACTERIAL. PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CC CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1 TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1 MASS SPECTROMETRY: MW=2424; METHOD=FAH.
 CC Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 22
 FT SEQUENCE 22 AA; 2427 MW; ID440B2200D4367C CRC64;

Query Match
 Best Local Similarity 54.5%; Score 25; DB 1; Length 22;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 KANSKFIGITE 15
 DB 9 KANLVSIGIVE 19

RESULT 12
 CR34_LITCE STANDARD; PRT; 22 AA.
 ID CR34_LITCE
 AC P56241;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 3.4.
 OS Litorea caerulea (Green tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litorea.

OK NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=Parotid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 RT *Litoria caerulea*.";
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE. THAT ADOPTS AN ALPHA HELICAL
 CC CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW=2452; METHOD=FAH.
 CC Antibiotic: Amphibian skin; Amlidation.
 FT MOD_RES 22
 FT SEQUENCE 22 AA; 2455 MW; 3AB40B2200D43663 CRC64;

Query Match 15.4%; Score 25; DB 1; Length 22;
 Best Local Similarity 54.5%; Pred. No. 1.4e+03;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 KANSKFGITE 15
 DB 9 KANELVSGIVE 19

RESULT 13
 IRBP_PIG STANDARD; PRT; 25 AA.
 AC P12662;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Interphotoreceptor retinoid-binding protein (IRBP) (interstitial
 DE retinoid binding protein) (fragment).
 GN RBP3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Theria; Cetartiodactyla; Suidae; Sus
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86301171; PubMed=3743780;
 RA Fong S.L., Cook R.G., Alvarez R.A., Llou G.I., Landers F.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologies in interstitial retinoid binding
 RT proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIAL CELLS.
 CC PIR: B24417; B24417.
 DR Vitamin A; Transport.
 FT NON_TER 25
 FT SEQUENCE 25 AA; 2813 MW; 4E751DF6A160231B7 CRC64;

Query Match 15.4%; Score 25; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 1.6e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 13 ITTGFEPFHL 23
 DB 14 LDNYTFPESLM 24

RESULT 14
 KAB5_OLDAP

ID KAB5_OLDAP STANDARD; PRT; 30 AA.
 AC P58456;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Kalata B5.
 OS Olenidania affinis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asceridae; Euastrales; Gentianales; Rubiaceae; Rubioidae;
 OC Spermocaceae; Olenidania.
 OX NCBI_TaxID=60225;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=20069951; PubMed=10600389;
 RA Craik D.J., Daly N.L., Bond T., Walne C.;
 RT "Plant cyclotides: a unique family of cyclic and knotted proteins that
 RT defines the cyclic cysteine knot structural motif.";
 RL J. Mol. Biol. 294:1327-1336(1999).
 CC -1- FUNCTION: Probably participates in a plant defense mechanism.
 CC -1- PMW: This is a cyclic peptide.
 CC -1- CAUTION: This peptide is cyclic. Its sequence was chosen to start
 CC at the position shown below by similarity to oak1 (kalata B1)
 CC whose DNA sequence is known.
 CC Multigene family.
 KW DISULFID 4 20
 FT DISULFID 8 22
 FT DISULFID 13 27
 FT SEQUENCE 30 AA; 3044 MW; CDA3C52FC0EB7A3 CRC64;

Query Match 15.4%; Score 25; DB 1; Length 30;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 COYKANSKFIG 12
 DB 8 CVYIPCSGVIG 19

RESULT 15
 AMP3_MELGA STANDARD; PRT; 25 AA.
 ID AMP3_MELGA
 AC P80393;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Antimicrobial peptide YRP3 (Turkey heterophil peptide 3) (fragment).
 DE *Melagris gallopavo* (common turkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Melagrididae; Melagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95053386; PubMed=7964174;
 RA Evans E.W., Beach G.G., Wunderlich J., Harmon B.G.;
 RT "Isolation of antimicrobial peptides from avian heterophils.";
 RL J. Leukoc. Biol. 56:661-665(1994).
 CC -1- FUNCTION: BACTERICIDAL ACTIVITY; INHIBITS STRAPHYLOCOCCUS AUREUS.
 CC Antibiotic.
 FT NON_TER 25
 FT SEQUENCE 25 AA; 2592 MW; 4AAB9AC193874035 CRC64;

Query Match 15.1%; Score 24.5; DB 1; Length 25;
 Best Local Similarity 46.2%; Pred. No. 1.6e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

OY 12 GITEFG-FPEHL 23
 DB 6 GTCHFGRCPSHLI 18

Wed Jun 19 10:20:12 2002

us-09-943-334-2.closed.rsp

Page 6

Search completed: June 18, 2002, 08:21:34
Job time: 197 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:18:02 ; Search time 23.85 seconds
(without alignments)
224.857 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYIKANSKFTGITEFGFPHLVDPLQSLSS 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 14118

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

```

1: SP_TREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeo:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	21.6	28	12	037279 hepatitis C
2	34	21.0	27	7	09GJPA gasterosten
3	32	19.8	21	2	P70861 borrelia bu
4	32	19.8	23	2	09H495 streptococ
5	32	19.8	30	2	09G227 chlamydia t
6	31	19.1	19	6	09TRR6 mycoplasma s
7	31	19.1	23	5	025161 haliclonas
8	31	19.1	28	7	09GJPA gasterosten
9	31	19.1	30	2	09G280 streptomyc
10	30	18.5	26	2	09ZAA4 mycoplasma
11	30	18.5	27	12	037180 hepatitis C
12	30	18.5	28	15	09JYV7 mycobacteri
13	30	18.5	28	15	09JYV7 mycobacteri
14	29.5	18.2	30	2	09R415 mycoplasma
15	29.5	18.2	30	2	09R415 mycoplasma
16	29	17.9	24	2	046081 clostridium

17	29	17.9	27	12	09YOR9	09YOR9 hepatitis b
18	29	17.9	31	16	050992	050992 borrelia bu
19	28.5	17.6	23	4	086G12	086G12 homo sapien
20	28.5	17.6	30	4	09UD13	09UD13 homo sapien
21	28	17.3	16	2	045663	045663 bacillus su
22	28	17.3	27	12	037183	037183 hepatitis C
23	28	17.3	27	12	037184	037184 hepatitis C
24	28	17.3	27	12	09OHL3	09OHL3 hepatitis C
25	28	17.3	28	7	09EX03	09EX03 campylobact
26	28	17.3	28	7	09GJPA	09GJPA gasterosten
27	28	17.3	28	7	09GJPA	09GJPA gasterosten
28	27	16.7	14	6	09TR07	09TR07 bos taurus
29	27	16.7	22	10	09TR04	09TR04 mustela put
30	27	16.7	22	10	09SBE1	09SBE1 capsicum an
31	27	16.7	27	12	09PXB2	09PXB2 duck hepati
32	27	16.7	28	2	049313	049313 mycoplasma
33	27	16.7	30	2	044171	044171 anabaena sp
34	27	16.7	30	2	0931T8	0931T8 salmonella
35	27	16.7	30	4	015954	015954 homo sapien
36	27	16.7	31	2	09KCT5	09KCT5 streptococ
37	26.5	16.4	29	8	035496	035496 paracentrot
38	26	16.0	9	4	09KRF6	09KRF6 homo sapien
39	26	16.0	12	2	09K3B4	09K3B4 enterococcu
40	26	16.0	12	2	09L8H6	09L8H6 enterococcu
41	26	16.0	12	2	09L8H8	09L8H8 enterococcu
42	26	16.0	17	4	09GZT7	09GZT7 homo sapien
43	26	16.0	19	3	09P7P3	09P7P3 schistosach
44	26	16.0	21	2	007840	007840 rhododactyl
45	26	16.0	21	8	09TD53	09TD53 cynolebias

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	27 AA.
037279	ID	037279		
AC	037279:			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)] (FRAGMENT).			
DE	E2.			
GN	Hepatitis C virus.			
OS	Hepatitis C virus.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;			
OC	Hepacivirus.			
OX	NCBI_TaxID=11103:			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=10:			
RX	MEDLINE=98105815; PubMed=9445070:			
RA	Navas S., Martin J., Quiroga J.A., Castillo I., Carreno V.;			
RT	"Genetic diversity and tissue compartmentalization of the hepatitis C			
RT	virus genome in blood mononuclear cells, liver, and serum from chronic			
RT	hepatitis C patients.";			
RL	J. Virol. 72:1640-1646(1998).			
EMBL	AF018388; AAC03675.1;			
DR	InterPro: IPR002531; HCV_NSI.			
DR	PIfam: PF01560; HCV_NSI; 1.			
KW	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;			
FT	Polyprotein; Transmembrane.			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE	27 AA; 2887 MW; 5C4512B3F39B6EA2 CRC64;		

Query Match 21.6%; Score 35; DB 12; Length 27;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 12 PTHRLVSFQFS 22

RESULT 2
ID 09GUP4 PRELIMINARY; PRT: 28 AA.
AC 09GUP4;
DT 01-MAR-2001 (TREMBLREL. 16, Created)
DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
CN CAAC-D.
OS Gasterosteus aculeatus (three spined stickleback).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Gasterosteidae; Gasterosteus.
OX NCBI_TaxID=69293;
RN [1]
RP SEQUENCE FROM N.A.
RA Birt P.;
RT *SSCP analysis of MHC genes in the stickleback.*;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249305; AAF98328.1; -.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3131 MW; DF7A5AC51F1E6798 CRC64;

Query Match 21.0%; Score 34; DB 7; Length 28;
Best Local Similarity 62.5%; Pred. No. 4e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 2;

OY 10 FIGITFEG 17
Db 1 FVGTFEYG 8

RESULT 3
ID P70861 PRELIMINARY; PRT: 21 AA.
AC P70861;
DT 01-FEB-1997 (TREMBLREL. 02, Created)
DT 01-FEB-1997 (TREMBLREL. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLREL. 08, Last annotation update)
DE THDP (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=212;
RA MEDLINE=97312006; PubMed=9168617;
RA Ge Y., Old I.G., Ghiron I.S., Charon N.W.;
RT *The flag motility operon of Borrelia burgdorferi is initiated by a
RL sigma 70-like promoter.*;
RL Microbiology 143:1681-1690(1997).
DR EMBL; U62901; AAB62742.1; -.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5833 CRC64;

Query Match 19.8%; Score 32; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 5.7e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;

OY 15 EFGPEPHL 23
Db 8 EFDPEGIL 16

RESULT 4
O9R495

ID O9R495 PRELIMINARY; PRT: 23 AA.
AC O9R495;
DT 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE 40 KDA STREPTOCOCCAL GROUP A SURFACE GLYCERALDEHYDE-3-PHOSPHATE
DE DEHYDROGENASE HOMOLOG (FRAGMENT).
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus;
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE.
RA MEDLINE=96355859; PubMed=8751897;
RA Kolberg J., Sletten K.;

RT *Monoclonal antibodies that recognize a common pneumococcal protein
RT with similarities to streptococcal group A surface glyceraldehyde-3-
RT phosphate dehydrogenase.*;
RL Infect. Immun. 64:3544-3547(1996).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
CC + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
CC -1- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DE DEHYDROGENASE FAMILY.
DR InterPro: IPR000173; GAP_DH.
DK Pfam: PF00044; gpdh; 1.
DR Glycolysis; NAD; Oxidoreductase.
SQ SEQUENCE 23 AA; 2391 MW; 5F023652B2A0A8D4 CRC64;

Query Match 19.8%; Score 32; DB 2; Length 23;
Best Local Similarity 35.0%; Pred. No. 6.3e+02; Mismatches 9; Indels 0; Gaps 0;
Matches 7; Conservative 4;

OY 11 IGITFEGPEPHLVPFLOSL 30
Db 4 VGINGFGXIGXIAFDXIONV 23

RESULT 5
ID O9ZG27 PRELIMINARY; PRT: 30 AA.
AC O9ZG27;
DT 01-MAY-1999 (TREMBLREL. 10, Created)
DT 01-MAY-1999 (TREMBLREL. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLREL. 10, Last annotation update)
DE UDP-N-ACETYLGLUCAMATE ALANINE LIGASE (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12 434B;
RA Wang L., Steenburgh S.D., Zheng Y., Larsen S.H.;
RT *Gene identification of Chlamydia trachomatis by random DNA
RL sequencing.*;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087346; AAD04119.1; -.
KW ligase.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3352 MW; D01C685DE67A1A55 CRC64;

Query Match 19.8%; Score 32; DB 2; Length 30;
Best Local Similarity 36.4%; Pred. No. 8.5e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 8; Conservative 4;

OY 10 FIGITFEGPEPHLVDFLOSL 31
Db 2 FLGNOEHIPGAVVYSSSIS 23

RESULT 6
ID Q9TRR6 PRELIMINARY; PRT; 19 AA.
AC Q9TRR6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALYCULIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-3-BINDING PROTEIN
DE L-14 FRAGMENT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=92250478; PubMed=1533622;
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hiyaka H.;
RT "A calyculin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924(1992).
SQ SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;

Query Match 19.1%; Score 31; DB 6; Length 19;
Best Local Similarity 43.8%; Pred. No. 7.2e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 16 FGPEHLVDFLOSL 31
DB 2 FGDEQAIIDKLSRS 17

RESULT 7
ID Q25161 PRELIMINARY; PRT; 23 AA.
AC Q25161;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE SPOX1 PROTEIN (FRAGMENT).
GN SPOX H1.
OS Haliclona sp.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haplosclerida; Chalinidae; Haliclona.
OX NCBI_TaxID=34490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95237605; PubMed=7721087;
RA Degnan B.M., Degnan S.M., Giusti A., Morse D.E.;
RT "A box/hom homedox gene in sponges.";
RL Gene 155:175-178(1995).
DR EMBL; X79263; CAA55850.1; -.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2681 MW; F39ADEDC85BEB60 CRC64;

Query Match 19.1%; Score 31; DB 5; Length 23;
Best Local Similarity 35.3%; Pred. No. 8.9e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 7 NSKFIGTEFGFPHL 23
DB 1 SKKYLSTERSHIAL 17

RESULT 8
ID Q9GJP6 PRELIMINARY; PRT; 28 AA.
AC Q9GJP6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
GN GAAC-D.
OS Gasterosteus aculeatus (three spined stickleback).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Gasterosteidae; Gasterosteus.
ON NCBI_TaxID=69293;
RN [1]
RP SEQUENCE FROM N.A.
RA Binz T.;
RT "SSCP analysis of MHC genes in the stickleback.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249303; AAF98326.1; -.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3214 MW; 5BAA4726B62179F4 CRC64;

Query Match 19.1%; Score 31; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 10 FIGTENG 17
DB 1 YVGFTENG 8

RESULT 9
ID 002800 PRELIMINARY; PRT; 30 AA.
AC 002800;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHETICAL PROTEIN IN PTH4 PROMOTER (FRAGMENT).
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
ON NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE=93163057; PubMed=7679386;
RA Tan H., Chater K.F.;
RT "Two developmentally controlled promoters of Streptomyces coelicolor
RT A3(2) that resemble the major class of motility-related promoters in
RT other bacteria.";
RL J. Bacteriol. 175:933-940(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Bruton C.J.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; X68791; CAA48685.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 30
SQ SEQUENCE 30 AA; 3217 MW; C754FFD68BFB12A9 CRC64;

Query Match 19.1%; Score 31; DB 2; Length 30;
Best Local Similarity 70.0%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 22 LLYDFLOSL 31
DB 8 LLYDFLOSLA 17

RESULT 10
O9R416

ID	Q9DTV7	PRELIMINARY;	PRT;	28	AA
----	--------	--------------	------	----	----

AC Q9DTV7;

DT 01-MAR-2001 (TRENBLREL. 15, Created)
 DT 01-MAR-2001 (TRENBLREL. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE TAX (FRAGMENT).
 GN FX.
 OS Human T-cell lymphotropic virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Deltaretrovirus.
 OX NCBI_TaxID=11908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATL258.
 RA Furukawa Y., Kubota R., Tara M., Izumo S., Osame M.:
 RT "Existence of escape mutation in HTLV-I tax the development of adult
 T-cell leukemia.";
 RL Immunology 97:987-993(2001).
 DR EMBL; AB045431; BAB20130.1; -.
 FT NON_TER
 SO SEQUENCE 28 AA; 3196 MW; 875436AB89BD5A4E CRC64;

Query Match 18.5%; Score 30; DB 15; Length 28;
 Best Local Similarity 38.5%; Pred. NO. 1.6e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 16 FGFPEHLVDFLQ 28
 |||::|:
 DB 11 FGYPVYVFGDCVQ 23

RESULT 15
 ID Q9R415 PRELIMINARY; PRT; 30 AA.
 AC Q9R415;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
 DE ARGININE DEIMINASE (EC 3.5.3.6) (FRAGMENT).
 OS Mycoplasma hominis.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2098;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=96042668; PubMed=7591961;
 RA Takaku H., Matsumoto M., Misawa S., Miyazaki K.:
 RT "Anti-tumor activity of arginine deiminase from Mycoplasma argini and
 its growth-inhibitory mechanism.";
 RL Jpn. J. Cancer Res. 86:840-846(1995).
 SO SEQUENCE 30 AA; 3389 MW; 93DC43752F6D6022 CRC64;

Query Match 18.2%; Score 29.5; DB 2; Length 30;
 Best Local Similarity 47.6%; Pred. NO. 2e+03;
 Matches 10; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 7 NSKFIGI---TEFGPEHLV 24
 :|||::|:
 DB 4 DSKENGIIHYSEIGELFTVLV 24

Search completed: June 18, 2002, 08:21:18
 Job time: 196 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 18, 2002, 08:15:42 ; Search time 29.28 Seconds

(without alignments)
117.599 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYIKANSKFIGITEFGFPHLLVDFGLSL 31

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 281105

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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1: A.Geneseq_032802.*
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3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT.*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT.*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT.*
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT.*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT.*
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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	31	17	AAW06129
2	162	100.0	31	20	AAV02470
3	85	52.5	22	20	AAV13815
4	85	52.5	22	20	AAV13821
5	85	52.5	26	17	AAW06128
6	85	52.5	26	20	AAV13801
7	85	52.5	26	21	AAV91228
8	83	51.2	16	21	AAV91229
9	81	50.0	22	20	AAV13809
10	81	50.0	26	20	AAV13802
11	81	50.0	26	21	AAV91231

12	79	48.8	15	21	AAV91230
13	76	46.9	29	16	AAW83561
14	76	46.9	31	21	AAV82632
15	73	45.1	28	20	AAV53552
16	73	45.1	29	20	AAV53551
17	71.5	44.1	27	15	AAW62701
18	70	43.2	14	11	AAW06309
19	70	43.2	14	14	AAW33497
20	70	43.2	14	14	AAW46509
21	70	43.2	14	16	AAW78918
22	70	43.2	14	16	AAW75943
23	70	43.2	14	16	AAW70910
24	70	43.2	14	16	AAW74160
25	70	43.2	14	17	AAW03003
26	70	43.2	14	18	AAW35437
27	70	43.2	14	19	AAW50108
28	70	43.2	14	20	AAV26601
29	70	43.2	14	20	AAV23251
30	70	43.2	14	21	AAV99035
31	70	43.2	14	21	AAV99127
32	70	43.2	14	21	AAV99277
33	70	43.2	14	21	AAV99261
34	70	43.2	14	22	AAW99514
35	70	43.2	14	22	AAU06292
36	70	43.2	14	22	AAW99705
37	70	43.2	14	22	AAW62427
38	70	43.2	14	22	AAW84516
39	70	43.2	14	22	AAW84532
40	70	43.2	14	22	AAW88268
41	70	43.2	14	22	AAW88284
42	70	43.2	14	22	AAW89365
43	70	43.2	14	22	AAW89380
44	70	43.2	14	22	AAW84432
45	70	43.2	14	22	AAW98456

ALIGNMENTS

RESULT 1	AAW06129	standard; Peptide; 31 AA.
ID	AAW06129	
XX	AAW06129:	
AC		
XX		
DT	07-FEB-1997	(first entry)
XX		
DE	Anti-cholesterol ester transfer peptide vaccine.	
XX		
KW	Cholesterol ester transfer protein; CETP; antigen; vaccine; cardiovascular disease; atherosclerosis.	
XX		
OS	Synthetic.	
XX		
FX	Key	Location/Qualifiers
FT	Misc-difference 1	/note="C-terminal Cys residue is present for use in linking the peptide to itself or other molecules"
FT		
FT		
FT		
FT	Region	2..15 /label="T-cell epitope /note="T-cell epitope comprises amino acids 830-843 of tetanus toxoid protein"
FT		
FT	Region	16..31 /label="B-cell epitope /note="B-cell epitope comprises the C-terminal 16 amino acids of human CETP (Claim 5)"
FT		
PN	W09634888-A1.	
XX		
PD	07-NOV-1996.	
XX		
XX	01-MAY-1996:	96WO-US06147.

XX 01-MAY-1995; 95US-0432483.
 XX (TCEL-) T CELL SCI INC.
 XX
 XX Rittershaus CW, Thomas LJ;
 XX WPI; 1996-506103/50.
 XX
 PT Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CETP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX
 PS Claim 8; Page 41-42; 72pp; English.
 XX
 CC A synthetic peptide vaccine comprises an immunogenic helper T-cell
 CC epitope of tetanus toxoid protein covalently linked to the
 CC C-terminal B-cell epitope of human cholesteryl ester transfer
 CC protein (CETP) (see also AAM06127) that is involved in a neutral
 CC lipid binding or a transfer activity of CETP. The vaccine elicits
 CC an immune response against endogenous CETP activity, and is used to
 CC treat or prevent a cardiovascular disease, such as atherosclerosis.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 162; DB 17; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFTGTEFGPPEHLVDLQSLIS 31
 |||||
 DB 1 cqiYkanskftgitefgfpehllvdlqsls 31

RESULT 2

AA02470
 ID AAY02470 standard; protein; 31 AA.

XX AAY02470;

XX 14-JUL-1999 (first entry)

XX Fusion of a tetanus toxoid fragment and C-terminal of human CETP.

XX Vaccine: antibody; endogenous; cholesteryl ester transfer protein; CETP;
 XX high-density lipoprotein associated cholesterol; metabolism;
 XX low-density lipoprotein associated cholesterol; atherosclerotic lesion;
 XX cholesterol; atherosclerosis; heart disease.
 XX
 OS Synthetic.
 XX
 PN WO9920302-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22145.
 XX
 PR 20-OCT-1997; 97US-0954643.
 XX
 PA (AVANT-) AVANT IMMUNOTHERAPEUTICS INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI; 1999-302645/25.
 XX
 XX Vaccine against cholesteryl ester transfer protein
 XX disclosure; Page 55; 61pp; English.
 XX
 CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein

CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC was used in the course of the invention.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 162; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFTGTEFGPPEHLVDLQSLIS 31
 |||||
 DB 1 cqiYkanskftgitefgfpehllvdlqsls 31

RESULT 3

AA13815
 ID AAY13815 standard; peptide; 22 AA.

XX AAY13815;

XX 08-JUL-1999 (first entry)

XX Rabbit CETP immunogenic fragment.

XX CETP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 XX antibody production; cholesteryl ester transfer; therapy;
 XX high density lipoprotein; HDL cholesterol concentration;
 XX pro-atherogenic dyslipoproteinemia.
 XX
 OS Oryctolagus sp.
 XX
 PN WO9915655-A1.
 XX
 PD 01-APR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI; 1999-276984/23.
 XX
 XX New recombinant DNA vaccines
 XX
 PS Disclosure; Page 75; 99pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CETP).
 CC The invention relates to recombinant DNA vaccines that contain the
 CC encoding CETP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CETP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinemia characterized by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 XX
 SQ Sequence 22 AA;

Query Match 52.5%; Score 85; DB 20; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDLFQSLIS 31
 :|||||
 DB 6 dfgfpehlvdflqslis 22

RESULT 4
 AAY13821
 ID AAY13821 standard; peptide: 22 AA.

XX AC AAY13821.

XX DT 08-JUL-1999 (first entry)

XX DE Human CERP immunogenic fragment.

XX KW CERP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;

XX KW antibody production; cholesteryl ester transfer; therapy;

XX KW high density lipoprotein; HDL cholesterol concentration;

XX KW pro-atherogenic dyslipoproteinaemia.

XX OS Homo sapiens.

XX XX W09J915655-A1.

XX PN 01-APR-1999.

XX PD 17-SEP-1998; 98WO-US19366.

XX PF 19-SEP-1997; 97US-0934367.

XX PR (MONS) MONSANTO CO.

XX PA Glenn K, Needleman P;

XX PI WPI; 1999-276984/23.

XX DR New recombinant DNA vaccines

XX PT Disclosure; Page 88; 99pp; English.

XX PS This sequence represents an immunogenic fragment of the human

XX CC cholesteryl ester transferase protein (CERP).

XX CC The invention relates to recombinant DNA vaccines that contain DNA

XX CC encoding CERP, which can be used for producing antibodies to lessen the

XX CC transfer of cholesteryl esters from high density lipoprotein (HDL). The

XX CC method can provide an autogenic immunological process for lessening the

XX CC transfer of cholesteryl esters from HDL particles and for increasing the

XX CC HDL cholesterol concentration of a mammal whose blood also contains

XX CC CERP. The method may be useful in treating human pro-atherogenic

XX CC dyslipoproteinaemias characterised by low HDL/HDL cholesterol ratios. The

XX CC method can have an effect that lasts for months as compared to the

XX CC short-term effects of the small molecule drugs now available.

XX CC Sequence 22 AA:

XX SQ

AC AAW06128;
 XX 07-FEB-1997 (first entry)

DE Human cholesteryl ester transfer protein C-terminal B-cell epitope.

XX KW Cholesteryl ester transfer protein; CERP; antigen; vaccine;

XX KW cardiovascular disease; atherosclerosis; B-cell epitope.

XX OS Homo sapiens.

XX PN W09634888-A1.

XX PD 07-NOV-1996.

XX PF 01-MAY-1996; 96WO-US06147.

XX PR 01-MAY-1995; 95US-0432483.

XX PA (TCEL-) T CELLS SCI INC.

XX PI Rittershaus CW, Thomas LJ;

XX DR WPI; 1996-506103/50.

XX PT Cholesteryl ester transfer protein B cell epitope linked to T cell

XX PT epitope - used to generate vaccine to regulate CERP activity for

XX PT decreasing the risk of developing a cardiovascular disease e.g.

XX PT atherosclerosis

XX PS Claim 5; Page 41; 72pp; English.

XX CC A B-cell epitope (AAW06128) comprising the C-terminal 26 amino acids

XX CC of human liver mature cholesteryl ester transfer protein (CERP)

XX CC (see also AAW06127) is involved in a neutral lipid binding or a

XX CC transfer activity of CERP. It can be linked to a universal or

XX CC broad range immunogenic T-cell epitope, such as that found at amino

XX CC acids 830-843 of tetanus toxoid protein, to produce a synthetic

XX CC vaccine (see also AAW06129) that elicits an immune response against

XX CC endogenous CERP activity, thereby treating or preventing

XX CC cardiovascular disease, such as atherosclerosis. It may also be

XX CC incorporated into a multivalent vaccine (see also AAW06131)

XX CC including another CERP B-cell epitope.

XX SQ Sequence 26 AA:

XX ID AAY13801 standard; peptide: 26 AA.

XX AC AAY13801;

XX DT 08-JUL-1999 (first entry)

XX DE Rabbit CERP immunogenic fragment.

XX KW CERP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;

XX KW antibody production; cholesteryl ester transfer; therapy;

XX KW high density lipoprotein; HDL cholesterol concentration;

XX KW pro-atherogenic dyslipoproteinaemia.

XX OS Oryctolagus sp.

XX XX

PN WO915655-A1.
 XX 01-APR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19366.
 XX
 XX 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI; 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 XX
 XX Claim 15; Page 85; 99pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERT).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERT, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERT. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 XX Sequence 26 AA:
 SO
 Query Match 52.5%; Score 85; DB 20; Length 26;
 Best Local Similarity 94.1%; Pred. No. 3.4e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 15 EFGEPEHLVDFLOSLUS 31
 :|||||
 Db 10 dfgfpehlvdfllqsls 26
 RESULT 7
 AAY91228 standard; peptide; 26 AA.
 XX
 AC AAY91228;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Human cholesteryl transport protein (CERT) peptide, SEQ ID NO:106.
 XX
 KW Promiscuous T-cell epitope; measles virus F protein; MVR;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin-6; growth promoting hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumporozoite; antimalarial; CERT;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 XX 20-JUN-1998; 98US-0100412.
 PR
 XX (UNBIC-) UNITED BIOMEDICAL INC.
 PA

PI Wang CY;
 XX
 DR WPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 XX Claim 10; Page 49; 129pp; English.
 PS
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CERT) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinizing hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVR Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVR Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERT-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERT peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVR Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the invention.
 CC Note: Sequence AAY91227 is also designated SEQ ID NO:106 in the
 CC specification.
 XX
 SO Sequence 26 AA:
 XX
 Oy 15 EFGEPEHLVDFLOSLUS 31
 :|||||
 Db 10 dfgfpehlvdfllqsls 26
 Query Match 52.5%; Score 85; DB 21; Length 26;
 Best Local Similarity 94.1%; Pred. No. 3.4e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 AAY91229 standard; peptide: 16 AA.
 AAY91229;
 22-MAY-2000 (first entry)
 Human cholesterol transport protein (CETP) peptide, SEQ ID NO:107.
 Promiscuous T-cell epitope; measles virus F protein; MVF.
 hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 cholesterol ester transport protein; anti-arteriosclerotic.
 Homo sapiens.
 MO996957-A2.
 29-DEC-1999.
 21-JUN-1999; 99MO-US13975.
 20-JUN-1998; 98US-0100412.
 (UNBI-) UNITED BIOMEDICAL INC.
 Wang CY;
 WPI; 2000-160564/14.
 New artificial T helper cell epitope and derived immunogens with target
 antigenic site, for immunization against e.g. malaria, arteriosclerosis
 or human immune deficiency virus -
 Claim 10; Page 50; 129pp; English.
 The invention relates to novel promiscuous T helper cell epitopes (Th),
 and immunogenic peptides comprising the Th epitopes of the invention
 along with B cell epitopes. The Th epitopes and peptide immunogens
 containing them, are used to induce a T helper cell response,
 specifically against Plasmodium falciparum, cholesterol ester transport
 protein (CETP) or HIV epitopes, but more generally against any pathogen,
 immunoreactive self-antigen or tumour antigen. The Th epitopes and
 peptide immunogens may be used for prevention and/or treatment of
 infections (HIV, foot-and-mouth disease or malaria); for cancer
 immunotherapy; for inhibition of the action of interleukin hormone
 releasing hormone (LHRH) for contraception, treatment of hormone-
 dependent cancer, prevention of boar taint in meat, and
 immunocastration); for promoting the growth of animals; or for
 treating allergies or arteriosclerosis. Incorporation of a promiscuous
 Th (functional in genetically diverse subjects) into an immunogen
 improves capacity to induce a strong T helper cell-mediated immune
 response, resulting in production of antibodies against a target
 antigen. Th can replace carrier proteins and pathogen-derived T helper
 epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 AAY91226 and AAY91243-Y91246 represent synthetic Th epitopes based on the
 MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 from hepatitis B virus (HBV) surface antigen, and sequences
 AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 is the LHRH target antigenic peptide used in these LHRH antigenic
 peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 peptides comprising somatostatin and a Th epitope. Somatostatin is a
 human CD4 CD82-like domain antigenic site, and AAY91209-Y90211 are MWN Th
 epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV

infection of T cells. AAY90212 is a modified version of a human IGE
 (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 antigenic peptides which may be used in the treatment of allergies.
 AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CETP peptide and a Th epitope which may be used to prevent or treat
 arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MWN Th and HIV-1 B-cell
 epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91158 and AAY91199 are respectively an immunostimulatory invasion
 protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 Sequence 16 AA;
 Query Match 51.2%; Score 83; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 EGPPEHLVDFUSLS 31
 |||||
 Db 1 fgphehlvdfusls 16
 RESULT 9
 AAY13809
 ID AAY13809 standard; peptide: 22 AA.
 AAY13809;
 08-JUL-1999 (first entry)
 Rabbit CETP immunogenic fragment.
 CETP; cholesterol-ester transfer protein; recombinant DNA vaccine; HDL;
 antibody production; cholesterol ester transfer; therapy;
 high density lipoprotein; HDL cholesterol concentration;
 pro-atherogenic dyslipoproteinaemia.
 Oryctolagus sp.
 MO9915655-A1.
 01-APR-1999.
 17-SEP-1998; 98MO-US19366.
 19-SEP-1997; 97US-0934367.
 (MONS) MONSANTO CO.
 Glenn K. Needleman P;
 WPI; 1999-276984/23.
 New recombinant DNA vaccines
 Example 1; Page 73; 99pp; English.
 This sequence represents an immunogenic fragment of the rabbit
 cholesterol ester transferase protein (CETP).
 The invention relates to recombinant DNA vaccines that contain DNA
 encoding CETP, which can be used for producing antibodies to lessen the
 transfer of cholesterol esters from high density lipoprotein (HDL). The
 method can provide an autogenic immunological process for lessening the
 transfer of cholesterol esters from HDL particles and for increasing the

CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX
 SQ Sequence 22 AA;

Query Match 50.0%; Score 81; DB 20; Length 22;
 Best Local Similarity 88.2%; Pred. No. 1.2e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFIQSLG 31
 :||||:|||||
 Db 6 dfgfphkhlvdfiqsls 22

RESULT 10

AA13802 standard; peptide; 26 AA.

XX
 AC AA13802;

XX
 DT 08-JUL-1999 (first entry)

XX
 DE Rabbit CERP immunogenic fragment.

XX
 KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;

KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.

XX
 OS Oryctolagus sp.

XX
 PN W09915655-A1.

XX
 FD 01-APR-1999.

XX
 PF 17-SEP-1998; 98WO-US19366.

XX
 PR 19-SEP-1997; 97US-0934367.

XX
 PA (MONS) MONSANTO CO.

XX
 PI Glenn K. Needleman P;

XX
 DR WPI; 1999-276984/23.

XX
 PR New recombinant DNA vaccines

XX
 PS Claim 15; Page 94; 99pp; English.

XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERP).

CC
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the

CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the

CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains

CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The

CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX
 SQ Sequence 26 AA;

Query Match 50.0%; Score 81; DB 20; Length 26;
 Best Local Similarity 88.2%; Pred. No. 1.4e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFIQSLG 31
 :||||:|||||
 Db 10 dfgfphkhlvdfiqsls 26

RESULT 11

AA13802 standard; peptide; 26 AA.

XX
 AC AA13802;

XX
 DT 22-MAY-2000 (first entry)

XX
 DE Human cholesteryl transport protein (CERP) peptide, SEQ ID NO:109.

XX
 KW Promiscuous T-cell epitope; measles virus F protein; MVE;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;

KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;

KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumporocite; antimalarial; CERP;

KW cholesteryl ester transport protein; anti-arteriosclerotic.

XX
 OS Homo sapiens.

XX
 PN W09966957-A2.

XX
 PD 29-DEC-1999.

XX
 PF 21-JUN-1999; 99WO-US19375.

XX
 PR 20-JUN-1998; 98US-0100412.

XX
 PA (UNBI-) UNITED BIOMEDICAL INC.

XX
 PI Wang CY;

XX
 DR WPI; 2000-160564/14.

XX
 PF New artificial T helper cell epitope and derived immunogens with target
 PF antigenic site, for immunization against e.g. malaria, arteriosclerosis

PT or human immune deficiency virus -

XX
 PS Claim 10; Page 62; 129pp; English.

XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention

CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,

CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,

CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of

CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone

CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and

CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous

CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune

CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper

CC epitopes. Sequence AA13802 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AA13802-Y91142,

CC AA13802 and AA13802-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AA13802 represents a promiscuous Th epitope

CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AA13802-Y91155 are synthetic epitopes derived from this HBV epitope.

CC AA13802-Y91196, AA13802 and AA13802-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA13802

CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AA13802 is somatostatin, and AA13802-Y91207 are antigenic

CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4-CDR2-like domain antigenic site, and AAY91209-190211 are MVA Th
 CC epitope/CD4-CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-190219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-191222 comprise this peptide and a Th
 CC epitope. AAY91223 is a plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-191225 comprise the CS antigen and an MVA Th
 CC epitope and may be used in a malaria vaccine. AAY91226-191231 represent
 CC CEMP-derived peptides and AAY91232-191241 are immunogens comprising a
 CC CEMP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-191257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-191251 and
 CC AAY91258-191273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 26 AA:

Query Match 50.0%; Score 81; DB 21; Length 26;
 Best Local Similarity 88.2%; Pred. No. 1.4e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 15 EGFPEHLVDFLOSLS 31
 Db 10 dfgfphlvdltgls 26

RESULT 12

AA91230 ID AAY91230 standard; peptide; 16 AA.

XX AAY91230:

DT 22-MAY-2000 (first entry)

DE Human cholesterol transport protein (CEMP) peptide, SEQ ID NO:108.

XX Promiscuous T-cell epitope; measles virus F protein; MVA.
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KW plasmodium falciparum; circumsporozoite; anti-malarial; CEMP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Homo sapiens.

PN WO966957-A2.

PD 29-DEC-1999.

PF 21-JUN-1999; 99MO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI: 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus

PS Claim 10; Page 62; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them are used to induce a T helper cell response,
 CC specifically against plasmodium falciparum, cholesterol ester transport
 CC protein (CEMP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of bear taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-191142,
 CC AAY91226 and AAY91245-191246 represent synthetic Th epitopes based on the
 CC MVA Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-191155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-191196, AAY91227 and AAY91247-191248 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-191207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4-CDR2-like domain antigenic site, and AAY91209-190211 are MVA Th
 CC epitope/CD4-CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-190219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-191222 comprise this peptide and a Th
 CC epitope. AAY91223 is a plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-191225 comprise the CS antigen and an MVA Th
 CC epitope and may be used in a malaria vaccine. AAY91228-191231 represent
 CC CEMP-derived peptides and AAY91232-191241 are immunogens comprising a
 CC CEMP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-191257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-191251 and
 CC AAY91258-191273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 16 AA:

Query Match 48.8%; Score 79; DB 21; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.7e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 EGFPEHLVDFLOSLS 31
 Db 1 fgrfphlvdltgls 16

RESULT 13

AA83561 ID AAR83561 standard; peptide; 29 AA.

XX AAR83561:

DT 13-JUN-1996 (first entry)

XX	10-FEB-2000.
ED	
XX	
PF	20-JUL-1999; 99WO-BE00092.
XX	
PR	30-JUL-1998; 98EP-0870167.
XX	
PA	(UNIO) UCB SA.
PI	
PI	Saint-Remy J, Jacquemlin M;
DR	WPI: 2000-422470/36.
XX	
PT	New compound for prevention and treatment of allergies comprises at
PT	least one allergen antigenic determinant recognized by a B cell and at
PT	least one antigenic determinant which does not trigger T cell
PT	activation -
XX	
PS	Claim 8; Page 35; 50pp; English.
XX	
CC	The present invention describes a compound (I) for the prevention and/or
CC	treatment of allergy. The compound comprises at least one allergen
CC	antigenic determinant (I) recognised by a B cell or an antibody secreted
CC	by a B cell of a non-atopic individual and at least one antigenic
CC	determinant (II) different from the allergen that triggers T cell
CC	activation. (I) has anti-allergic, antiasthmatic, anti-inflammatory,
CC	dermatological and immunosuppressive activities, and can be used in a
CC	vaccine. (II) may be used in a pharmaceutical or cosmetic medicament to
CC	treat and/or prevent allergies or a disease of allergic origin,
CC	especially hypersensitivities. These include rhinitis, sinusitis,
CC	bronchial asthma, atopic dermatitis, some forms of acute and chronic
CC	urticaria, gastro-intestinal syndromes associated with the ingestion of
CC	food allergens, oro-pharyngeal syndrome, anaphylactic reactions
CC	associated with drug hypersensitivities and/or a mixture of these. The
CC	use of (I) in the treatment of allergic conditions avoids the need for
CC	drug treatment, which often causes undesirable side-effects. Also, prior
CC	art drug therapies alleviate symptoms, but do not influence their
CC	causes, however (I) actually combats the cause of an allergic reaction.
CC	The present sequence represents a specifically claimed compound peptide
CC	sequence from the present invention.
XX	
CC	
XX	
SQ	Sequence 31 AA;
XX	
Query Match	46.9%; Score 76; DB 21; Length 31;
Best Local Similarity	93.8%; Pred. No. 0.0001;
Matches 15; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	2 QYIKANSKFGITBERG 17
DB	1 QYIKANSKFGITBERG 16
XX	
RESULT 15	
ID	AAV53552
XX	AAV53552 standard; Protein; 28 AA.
AC	
XX	AAV53552;
DT	
XX	18-JAN-2000 (first entry)
DE	
XX	Lipopeptide #3.
XX	
KM	Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
KW	electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
KW	human immunodeficiency virus; hepatitis B virus; papilloma virus;
XX	melanoma; malaria; parasite.
OS	
OS	Synthetic.
XX	
XX	Homo sapiens.
Key	Location/Qualifiers
Modified-site	1

/note- "contains palmitoyl residue attached at the
N-terminus and on the epsilon carbon of the
side chain"

FR2776926-A1.

08-OCT-1999.

07-APR-1998; 98FR-0004323.

07-APR-1998; 98FR-0004323.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

(CNRS) CNRS CENT NAT RECH SCI.

(INSP) INST PASTEUR LILLE.

Le Gal FA, Guillet JC, Gahery SH, Gras MH, Melnyk O, Tartar A;

WPT, 1999-583113/50.

New lipopeptide containing lipid regions and two epitopes, all
separated by peptide spacers that impart hydrophilicity, useful in
vaccines

Example 1; Page 9; 35pp; French.

The invention relates to the generation of a lipopeptide comprising at
least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
epitope and at least one lipid residue with (i) the epitopes and lipid
portion and (ii) the epitopes, being separated independently by peptide
spacers. These spacers comprise sequences of amino acids which carry an
overall electrical charge in neutral media to ensure that the
lipopeptide is hydrophilic. This peptide represents an example of them
lipopeptide of the invention. It contains 2 lipid residues attached at
the N-terminal end of the molecule and 2 epitopes separated by the spacer
residues Ser-Ser and Ala-Ala-Ala. Peptides AAV53501-Y53549 represent
CC peptide epitopes used in the generation of the lipopeptides. These are
used in therapeutic or prophylactic compositions and vaccines to induce
CC specific immune responses against human immunodeficiency, hepatitis B or
papilloma viruses; p53 of melanoma or the malaria parasite.

Sequence 28 AA:

Query Match

45.1%; Score 73; DB 20; Length 28;

Best local similarity 93.8%; Pred. No. 0.00027;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYIKANSKFGITEFG 17

DB 3 gyikanskfigitery 18

Search completed: June 18, 2002, 08:17:57
Job time: 135 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: June 18, 2002, 08:16:47 ; Search time 107.33 seconds
(without alignments)
106,008 Million cell updates/sec

Title: US-09-943-334-2
Perfect score: 162
Sequence: 1 COYIKANSKFIGITREFGPEHLVDFLOSTLS 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 2213444

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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11: /cgn2_6/ptodata/2/paa/US087.COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088.COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089.COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090.COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091.COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092.COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093.COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US094.COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US095.COMB.pep:*
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21: /cgn2_6/ptodata/2/paa/US097.COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US098.COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US099.COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US100.COMB.pep:*
25: /cgn2_6/ptodata/2/paa/US101.COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	31	8 US-08-432-483-2	Sequence 2, App11
2	162	100.0	31	8 US-08-432-483A-2	Sequence 2, App11
3	162	100.0	31	13 US-08-945-289-2	Sequence 2, App11
4	162	100.0	31	13 US-08-945-289-7	Sequence 7, App11
5	162	100.0	31	19 US-09-529-762-7	Sequence 2, App11
6	162	100.0	31	23 US-09-943-334-2	Sequence 2, App11
7	162	100.0	31	23 US-09-943-548-2	Sequence 2, App11

8	85	52.5	22	11 US-08-785-997-10	Sequence 10, App1
9	85	52.5	22	11 US-08-785-997-34	Sequence 34, App1
10	85	52.5	22	11 US-08-788-882-10	Sequence 10, App1
11	85	52.5	22	11 US-08-788-882-34	Sequence 34, App1
12	85	52.5	22	13 US-08-934-367-10	Sequence 10, App1
13	85	52.5	22	13 US-08-934-367-34	Sequence 34, App1
14	85	52.5	22	17 US-09-386-591-10	Sequence 10, App1
15	85	52.5	22	17 US-09-386-591-34	Sequence 34, App1
16	85	52.5	22	17 US-09-387-340-10	Sequence 10, App1
17	85	52.5	22	17 US-09-387-340-34	Sequence 34, App1
18	85	52.5	26	1 PCT-US99-139758-106	Sequence 106, App
19	85	52.5	26	8 US-08-432-483-1	Sequence 1, App11
20	85	52.5	26	8 US-08-432-483A-1	Sequence 29, App1
21	85	52.5	26	11 US-08-785-997-29	Sequence 29, App1
22	85	52.5	26	11 US-08-788-882-29	Sequence 29, App1
23	85	52.5	26	13 US-08-934-367-29	Sequence 29, App1
24	85	52.5	26	13 US-08-945-289-1	Sequence 1, App11
25	85	52.5	26	17 US-09-386-591-29	Sequence 29, App1
26	85	52.5	26	17 US-09-387-340-29	Sequence 29, App1
27	85	52.5	26	21 US-09-701-588-106	Sequence 106, App
28	85	52.5	26	23 US-09-943-334-1	Sequence 1, App11
29	85	52.5	26	23 US-09-943-548-1	Sequence 107, App
30	83	51.2	16	1 PCT-US99-139758-107	Sequence 107, App
31	83	51.2	16	21 US-09-701-588-107	Sequence 4, App11
32	81	50.0	22	11 US-08-785-997-4	Sequence 4, App11
33	81	50.0	22	11 US-08-788-882-4	Sequence 4, App11
34	81	50.0	22	13 US-08-934-367-4	Sequence 4, App11
35	81	50.0	22	17 US-09-386-591-4	Sequence 4, App11
36	81	50.0	22	17 US-09-387-340-4	Sequence 109, App
37	81	50.0	26	11 PCT-US99-139758-109	Sequence 50, App1
38	81	50.0	26	11 US-08-785-997-50	Sequence 50, App1
39	81	50.0	26	11 US-08-788-882-50	Sequence 50, App1
40	81	50.0	26	13 US-08-934-367-50	Sequence 50, App1
41	81	50.0	26	17 US-09-386-591-50	Sequence 50, App1
42	81	50.0	26	17 US-09-387-340-50	Sequence 109, App
43	81	50.0	26	21 US-09-701-588-109	Sequence 109, App
44	79	48.8	16	1 PCT-US99-139758-108	Sequence 1, App11
45	79	48.8	9	9 US-08-577-106-1	Sequence 1, App11

ALIGNMENTS

RESULT 1

US-08-432-483-2

Sequence 2, Application US/08432483

GENERAL INFORMATION:

APPLICANT: Rittershaus, Charles, W.

TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSER: Banner & Allegretti, Ltd.

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-7407

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,483

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Leon R. Yankwich

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)

```

? INFORMATION FOR SEQ ID NO: 2:
?   SEQUENCE CHARACTERISTICS:
?     LENGTH: 31 amino acids
?     TYPE: amino acid
?     TOPOLOGY: linear
?   MOLECULE TYPE: peptide
?   HYPOTHETICAL:
?   ANTI-SENSE:
?   FEATURE:
?   NAME/KEY:
?   LOCATION:
?   US-08-432-483-2

Query Match          100.0%; Score 162; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 COYIKANSKFIGITEFGFPEHLVDPLQSLS 31
DB      1 COYIKANSKFIGITEFGFPEHLVDPLQSLS 31

RESULT 2
? Sequence 2, Application US/08432483A
? GENERAL INFORMATION:
?   APPLICANT: Rittershaus, Charles W.
?   TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
?   TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
?   NUMBER OF SEQUENCES: 5
?   CORRESPONDENCE ADDRESS:
?     ADDRESSEE: Banner & Witcoff, Ltd.
?     STREET: Ten South Wacker Drive
?     CITY: Chicago
?     STATE: Illinois
?     COUNTRY: USA
?     ZIP: 60606-7407
?   COMPUTER READABLE FORM:
?     MEDIUM TYPE: diskette
?     COMPUTER: IBM PC compatible
?     OPERATING SYSTEM: PC-DOS/MS-DOS
?     SOFTWARE: Wordperfect 6.1
?   CURRENT APPLICATION DATA:
?     APPLICATION NUMBER: US/08/432,483A
?     FILING DATE: 1-May-1995
?     CLASSIFICATION: 424
?     PRIOR APPLICATION DATA:
?       APPLICATION NUMBER:
?       FILING DATE:
?   ATTORNEY/AGENT INFORMATION:
?     NAME: Leon R. Yankwich
?     REGISTRATION NUMBER: 30,237
?     REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
?   INFORMATION FOR SEQ ID NO: 2:
?     SEQUENCE CHARACTERISTICS:
?       LENGTH: 31 amino acids
?       TYPE: amino acid
?       TOPOLOGY: linear
?     MOLECULE TYPE: peptide
?     HYPOTHETICAL:
?     ANTI-SENSE:
?     FEATURE:
?     NAME/KEY:
?     LOCATION:
?     US-08-432-483A-2

Query Match          100.0%; Score 162; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 COYIKANSKFIGITEFGFPEHLVDPLQSLS 31
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```

DB      1 COYIKANSKFIGITEFGFPEHLVDPLQSLS 31

RESULT 3
? Sequence 2, Application US/08945289
? GENERAL INFORMATION:
?   APPLICANT: Rittershaus, Charles W.
?   TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
?   TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
?   NUMBER OF SEQUENCES: 9
?   CORRESPONDENCE ADDRESS:
?     ADDRESSEE: Yankwich & Associates
?     STREET: 130 Bishop Allen Drive
?     CITY: Cambridge
?     STATE: Massachusetts
?     COUNTRY: USA
?     ZIP: 02139
?   COMPUTER READABLE FORM:
?     MEDIUM TYPE: floppy disk
?     COMPUTER: IBM PC compatible
?     OPERATING SYSTEM: Windows 95
?     SOFTWARE: Word 97
?   CURRENT APPLICATION DATA:
?     APPLICATION NUMBER: US/08/945,289
?     FILING DATE: October 17, 1997
?     CLASSIFICATION: 514
?     PRIOR APPLICATION DATA:
?       APPLICATION NUMBER: 08/432,483
?       FILING DATE: May 1, 1995
?     ATTORNEY/AGENT INFORMATION:
?       NAME: Leon R. Yankwich
?       REGISTRATION NUMBER: 30,237
?       REFERENCE/DOCKET NUMBER: TCS-411.1P US
?   INFORMATION FOR SEQ ID NO: 2:
?     SEQUENCE CHARACTERISTICS:
?       LENGTH: 31 amino acids
?       TYPE: amino acid
?       TOPOLOGY: linear
?     MOLECULE TYPE: peptide
?     HYPOTHETICAL:
?     ANTI-SENSE:
?     FEATURE:
?     NAME/KEY:
?     LOCATION:
?     US-08-945-289-2

Query Match          100.0%; Score 162; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 COYIKANSKFIGITEFGFPEHLVDPLQSLS 31
DB      1 COYIKANSKFIGITEFGFPEHLVDPLQSLS 31

RESULT 4
? Sequence 7, Application US/08954643
? GENERAL INFORMATION:
?   APPLICANT: Rittershaus, Charles W.
?   TITLE OF INVENTION: XENOGENEIC CHOLESTERYL ESTER
?   TITLE OF INVENTION: TRANSFER PROTEIN (CETP) FOR MODULATION OF CETP ACTIVITY
?   NUMBER OF SEQUENCES: 7
?   CORRESPONDENCE ADDRESS:
?     ADDRESSEE: Yankwich & Associates
?     STREET: 130 Bishop Allen Drive
?     CITY: Cambridge
?     STATE: MA
```

COUNTRY: U.S.A.
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,643
FILING DATE: concurrently herewith
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-420.0 US
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-954-643-7

Query Match 100.0%; Score 162; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31

RESULT 5
US-09-529-762-7
Sequence 7, Application US/09529762
GENERAL INFORMATION:
APPLICANT: AVANT Immunotherapeutics, Inc.
APPLICANT: Rittershaus, Charles
TITLE OF INVENTION: Xenogeneic Cholesteryl Ester Transfer Protein (CETP) for
FILE REFERENCE: sequence listing for TCS-420.1 PCT
CURRENT APPLICATION NUMBER: US/09/529,762
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: USSN 08/954,643
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 7
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: fusion protein containing tetanus toxoid segment
OTHER INFORMATION: linked to human CETP C-terminus
US-09-529-762-7

Query Match 100.0%; Score 162; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31

RESULT 6

US-09-943-334-2
Sequence 2, Application US/09943334
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,334
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: vaccine peptide of the invention
US-09-943-334-2

Query Match 100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31

RESULT 7
US-09-943-548-2
Sequence 2, Application US/09943548
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,548
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-2

Query Match 100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31
DB 1 COYIKANSKFIGITEFGFPEHLLVDFLOSL 31

RESULT 8
US-08-785-997-10

```
Sequence 10, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
TITLE OF INVENTION: An Immunological Process for Increasing
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gansson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-997-10

Query Match          52.5%; Score 85; DB 11; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPHLLVDFIQSLIS 31
Db 6 DFGFPHLLVDFIQSLIS 22

RESULT 9
US-08-785-997-34
Sequence 34, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
TITLE OF INVENTION: An Immunological Process for Increasing
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gansson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-997-34

Query Match          52.5%; Score 85; DB 11; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPHLLVDFIQSLIS 31
Db 6 DFGFPHLLVDFIQSLIS 22

RESULT 10
US-08-788-882-10
Sequence 10, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
TITLE OF INVENTION: An Immunological Process and Constructs
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gansson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-882-10

Query Match          52.5%; Score 85; DB 11; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
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Matches 16: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSL 31
:|||||
DB 6 DFGPEHLVDFLOSL 22

RESULT 11

US-08-788-882-34

Sequence 34, Application US/08788882

GENERAL INFORMATION:

APPLICANT: Needleman, Phillip

APPLICANT: Glenn, Kevin

APPLICANT: Krul, Elaine

TITLE OF INVENTION: An Immunological Process and Constructs

TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESS: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/788,882

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)655-1501

TELEFAX: (312)655-1501

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-788-882-34

Query Match 52.5%; Score 85; DB 11; Length 22;

Best Local Similarity 94.1%; Pred. No. 1.9e-05;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSL 31
:|||||

DB 6 DFGPEHLVDFLOSL 22

RESULT 12

US-08-934-367-10

Sequence 10, Application US/08934367

GENERAL INFORMATION:

APPLICANT: Needleman, Phillip

APPLICANT: Glenn, Kevin

TITLE OF INVENTION: An Immunological Process and Constructs

TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESS: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,367

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gamson Ph.D., Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)655-1501

TELEFAX: (312)655-1501

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-367-10

Query Match 52.5%; Score 85; DB 13; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;OY 15 EFGPEHLVDFLOSL 31
:|||||

DB 6 DFGPEHLVDFLOSL 22

RESULT 13

US-08-934-367-34

Sequence 34, Application US/08934367

GENERAL INFORMATION:

APPLICANT: Needleman, Phillip

APPLICANT: Glenn, Kevin

TITLE OF INVENTION: An Immunological Process and Constructs

TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESS: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,367

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gamson Ph.D., Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)655-1501

TELEFAX: (312)655-1501

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-386-591-10

Query Match 52.5%; Score 85; DB 13; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFIQSLT 31
:|||||
DB 6 DFGPEHLVDFIQSLT 22

RESULT 14
US-09-386-591-10
; Sequence 10, Application US/09386591
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/386,591
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-386-591-10

Query Match 52.5%; Score 85; DB 17; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFIQSLT 31
:|||||
DB 6 DFGPEHLVDFIQSLT 22

RESULT 15
US-09-386-591-34
; Sequence 34, Application US/09386591

GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/386,591
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-386-591-34

Query Match 52.5%; Score 85; DB 17; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFIQSLT 31
:|||||
DB 6 DFGPEHLVDFIQSLT 22

Search completed: June 18, 2002, 08:20:26
Job time: 219 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:17:22 ; Search time 13.61 Seconds
(Without alignments)
192.857 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
1 COYIKANSKPIGTETGEPGPHLLVDFLOSL 31

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 257105 segs, 84670655 residues

Total number of hits satisfying chosen parameters: 46494

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78.5	48.5	24	6	US-10-128-711-110 Sequence 110, App
2	71.5	44.1	27	6	US-10-076-674-7 Sequence 7, Appl
3	71.5	44.1	27	6	US-10-076-674-7 Sequence 7, Appl
4	70	43.2	14	5	US-09-707-738-5 Sequence 5, Appl
5	70	43.2	14	5	US-09-543-608A-38 Sequence 38, Appl
6	70	43.2	14	5	US-09-709-774-5 Sequence 5, Appl
7	70	43.2	14	5	US-09-462-052-710 Sequence 710, Appl
8	70	43.2	14	5	US-09-260-714B-1 Sequence 1, Appl
9	70	43.2	14	6	US-10-128-711-95 Sequence 95, Appl
10	70	43.2	14	6	US-10-001-469-1403 Sequence 1403, Ap
11	70	43.2	17	1	PCR-US02-10293-3 Sequence 3, Appl
12	70	43.2	25	5	US-09-413-186A-14 Sequence 14, Appl
13	70	43.2	25	5	US-09-413-186A-14 Sequence 13, Appl
14	70	43.2	25	5	US-09-413-186A-14 Sequence 13, Appl
15	70	43.2	25	5	US-09-413-186A-14 Sequence 13, Appl
16	70	43.2	27	6	US-10-128-711-111 Sequence 111, App
17	70	43.2	27	6	US-10-128-711-111 Sequence 112, App
18	53	32.7	11	5	US-09-523-033A-3 Sequence 3, Appl
19	34	21.0	21	1	PCR-US02-09257-427 Sequence 427, App
20	34	21.0	21	6	PCR-US02-09370-671 Sequence 671, App
21	34	21.0	21	6	US-10-105-299-5439 Sequence 5439, Ap
22	32	19.8	22	5	US-09-453-834-133 Sequence 133, App
23	32	19.8	22	5	US-09-453-834-133 Sequence 133, App
24	32	19.8	22	6	US-10-099-574A-133 Sequence 133, App
25	32	19.8	22	6	US-10-147-849-133 Sequence 133, App
26	32	19.8	22	6	US-10-147-993-133 Sequence 133, App

27	31	19.1	21	5	US-09-924-841-15	Sequence 15, Appl
28	31	19.1	31	5	US-09-956-206A-32	Sequence 32, Appl
29	30	18.5	9	6	US-10-014-340-19	Sequence 19, Appl
30	30	18.5	12	5	US-09-862-179A-20	Sequence 20, Appl
31	30	18.5	12	5	US-09-652-169-13	Sequence 13, Appl
32	30	18.5	12	5	US-09-945-166A-3	Sequence 3, Appl
33	30	18.5	12	5	US-09-575-580B-32	Sequence 32, Appl
34	30	18.5	12	5	US-09-936-035-14	Sequence 14, Appl
35	30	18.5	12	6	US-10-145-415-68	Sequence 68, Appl
36	30	18.5	16	5	US-09-050-359B-136	Sequence 136, App
37	30	18.5	16	5	US-09-059-827A-136	Sequence 136, App
38	30	18.5	20	6	US-10-043-887-403	Sequence 403, App
39	30	18.5	27	6	US-10-105-299-4415	Sequence 4415, App
40	29.5	18.2	20	5	US-09-656-417-2	Sequence 2, Appl
41	29.5	18.2	28	5	US-09-636-596C-27	Sequence 27, Appl
42	29.5	18.2	31	6	US-10-004-860-1163	Sequence 1163, App
43	29	17.9	11	6	US-10-105-232-72	Sequence 72, Appl
44	29	17.9	21	6	US-10-105-299-4564	Sequence 4564, App
45	29	17.9	23	5	US-09-242-772-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-128-711-110
Sequence 110, Application US/10128711
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
CHESTNUT, Robert W.
SETTE, Alessandro D.
CELIS, Bateban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128, 711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids

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?      TYPE: amino acid
?      STRANDEDNESS: unknown
?      TOPOLOGY: unknown
?      MOLECULE TYPE: peptide
?      SEQUENCE DESCRIPTION: SEQ ID NO: 110
US-10-128-711-110

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Query Match	48.5%;	Score 78.5;	DB 6;	Length 24;
Best Local Similarity	65.5%;	Pred. No. 1.8e-05;		
Matches 19;	Conservative 1;	Mismatches 4;	Indels 5;	Gaps 1.

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QY      2 QYKANSKFIGITEFEGPEHLVDLQSL 30
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          |   |
          :
Db       1 QYKANSKFIGITEF-----LPSEDFPSV 24
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RESULT 2
US-10-076-674-7
; Sequence 7, Application US/10076674

Query Match	44.18;	Score 71.5;	DB 6;	Length 27;
Best Local Similarity	80.08;	Pred. No. 0.00024;		
Matches 16;	Conservative 0;	Mismatches 1;	Indels 3;	Gaps 1;

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QY      2 QYIKANSKFIGITEFGFPEH 21
        |||||
Db      3 QYIKANSKFIGITEL---EH 19
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RESULT      3
US-10-076-674A-7
: Sequence 7, Application US/10076674A
:
: GENERAL INFORMATION:
:
: APPLICANT: SOKOLL, Kenneth K.
:
: TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
:
: FILE REFERENCE: Immunogen Delivery System
:
: CURRENT APPLICATION NUMBER: US/10/076,674A
:
: CURRENT FILING DATE: 2002-04-23
:
: NUMBER OF SEQ. ID NOS: 11
:
: SOFTWARE: PatentIn version 3.1
:
: SEQ. ID NO. 7
:
: LENGTH: 27
:
: TYPE: PRT
:
: ORGANISM: Human
:
: US-10-076-674A-7

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Query Match	44.18;	Score 71.5;	DB 6;	Length 27;
Best Local Similarity	80.08;	Pred. No. 0.00024;		
Matches 16; Conservative	0;	Mismatches 1;	Indels 3;	Gaps 1;

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QY 2 QYIKANSKFIGITEFGPPEH 21
    |||||
Db 3 QYIKANSKFIGITEL--EH 19
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RESULT 4
US-09-707-738-5

Sequence 5, Application US/09707736
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Caletto, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffery L.
APPLICANT: Epimmune Inc.

```

Query Match      43.28;  Score 70;  DB 5;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 0.00019;
Matches 14;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

Qy	2 QYIKANSKFIGITE 15
Db	1 QYIKANSKFIGITE 14

```

RESULT      5
US-09-543-608A-38
: Sequence 38, Application US/09543608A
: GENERAL INFORMATION:
: APPLICANT: Fikes, John D.
: APPLICANT: Settle, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Celis, Esteban
: APPLICANT: Keogh, Elissa A.
: APPLICANT: Chesnut, Robert
: APPLICANT: Epimmune Inc.
: TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
: TITLE OF INVENTION: Peptides and Vaccine Compositions
: FILE REFERENCE: 018623-015710HS
: CURRENT APPLICATION NUMBER: US/09/543,608A
: CURRENT FILING DATE: 2002-04-05
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 38
: LENGTH: 14
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: tetanus toxoid positions 830-843, Standard Peptide
: US-09-543-608A-38

```

1

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
|||||
DB 1 QYKANSKFIGITE 14

RESULT 6
US-09-709-774-5
; Sequence 5, Application US/09709774
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffery L.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan DR-Binding
; FILE REFERENCE: 018623-006240US
; CURRENT APPLICATION NUMBER: US/09/709,774
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 08/121,101
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: US 08/305,871
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: US 60/010,510
; PRIOR FILING DATE: 1996-01-24
; PRIOR APPLICATION NUMBER: US 08/788,822
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tet Tox 830-843
US-09-709-774-5

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
|||||
DB 1 QYKANSKFIGITE 14

RESULT 7
US-09-942-052-710
; Sequence 710, Application US/09942052
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afari, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Chailita Eid, Pla M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/328,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 710
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tetanus toxoid
US-09-942-052-710

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
|||||
DB 1 QYKANSKFIGITE 14

RESULT 8
US-09-260-714B-1
; Sequence 1, Application US/09260714B
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chesnut, Robert
; APPLICANT: Sidney, John
; TITLE OF INVENTION: PEPTIDES WITH INCREASED BINDING AFFINITY
; FILE REFERENCE: 39963-20028.00
; CURRENT APPLICATION NUMBER: US/09/260,714B
; CURRENT FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Tetanus toxoid
US-09-260-714B-1

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
|||||
DB 1 QYKANSKFIGITE 14

RESULT 9
US-10-128-711-95
; Sequence 95, Application US/10128711
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CORRESPONDENCE ADDRESSES: 153
; NUMBER OF SEQUENCES: 153
; ADDRESSER: Townsend and Townsend Hourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Patmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
;
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /note="Tetanus toxoid 830-843"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-128-711-95

Query Match          43.2%; Score 70; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYIKANSKFIGITE 15
Db      1 QYIKANSKFIGITE 14

RESULT 10
US-10-001-469-1403
; Sequence 1403, Application US/10001469
; GENERAL INFORMATION:
; APPLICANT: JAKOBOWITS, AYA
; APPLICANT: RATTANO, ARTHUR
; APPLICANT: ARAR, DANIEL
; APPLICANT: SAFERAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: FARIS, MARY
; APPLICANT: CHALILITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20024,20
; CURRENT APPLICATION NUMBER: US/10/001,469
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1403
; LENGTH: 14
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; TYPE: PRT
; ORGANISM: Clostridium sp.
; US-10-001-469-1403

Query Match          43.2%; Score 70; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYIKANSKFIGITE 15
Db      1 QYIKANSKFIGITE 14

RESULT 11
US-09-413-186A-11
; Sequence 11, Application US/09413186A
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Haaning, Jesper
; APPLICANT: Dalum, Ibren
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 3631-0115P
; CURRENT APPLICATION NUMBER: US/09/413,186A
; CURRENT FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-413-186A-11

Query Match          43.2%; Score 70; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYIKANSKFIGITE 15
Db      1 QYIKANSKFIGITE 14

RESULT 12
PCT-US02-10293-3
; Sequence 3, Application PC/TUS0210293
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: PCT/US02/10293
; CURRENT FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Clostridium tetani
PCT-US02-10293-3

Query Match          43.2%; Score 70; DB 1; Length 17;
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Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 OYKANSKFIGITE 15
DB 3 OYKANSKFIGITE 16

RESULT 13
US-09-413-186A-14
; Sequence 14, Application US/09413186A
; GENERAL INFORMATION:
; APPLICANT: Steinnae, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Haanling, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 3631-0115P
; CURRENT APPLICATION NUMBER: US/09/413,186A
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
US-09-413-186A-14

Query Match 43.2%; Score 70; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 OYKANSKFIGITE 15
DB 6 OYKANSKFIGITE 19

RESULT 14
US-09-413-186A-15
; Sequence 15, Application US/09413186A
; GENERAL INFORMATION:
; APPLICANT: Steinnae, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Haanling, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 3631-0115P
; CURRENT APPLICATION NUMBER: US/09/413,186A
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15

LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
US-09-413-186A-15

Query Match 43.2%; Score 70; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 OYKANSKFIGITE 15
DB 6 OYKANSKFIGITE 19

RESULT 15
US-09-413-186A-16
; Sequence 16, Application US/09413186A
; GENERAL INFORMATION:
; APPLICANT: Steinnae, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Haanling, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 3631-0115P
; CURRENT APPLICATION NUMBER: US/09/413,186A
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
US-09-413-186A-16

Query Match 43.2%; Score 70; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 OYKANSKFIGITE 15
DB 6 OYKANSKFIGITE 19

Search completed: June 18, 2002, 08:20:46
Job time: 204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:16:02 ; Search time 12.95 Seconds
(without alignments)
58,471 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYIKANSKFTGITEFGFPHLTVDFIQLSL 31

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 145535

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78.5	48.5	24	5	PCT-US92-07218-25
2	78.5	48.5	24	5	PCT-US95-02121-110
3	78.5	48.5	27	5	PCT-US92-07218-32
4	71.5	44.1	27	1	US-08-446-692-13
5	71.5	44.1	27	2	US-08-488-351A-13
6	70	43.2	14	1	US-08-186-266-5
7	70	43.2	14	1	US-08-305-871A-5
8	70	43.2	14	1	US-08-465-167A-18
9	70	43.2	14	2	US-08-817-933A-9
10	70	43.2	14	5	PCT-US92-07218-15
11	70	43.2	14	5	PCT-US92-07218-30
12	70	43.2	14	5	PCT-US95-02121-95
13	70	43.2	15	2	US-08-319-704-10
14	70	43.2	15	2	US-08-661-052-6
15	70	43.2	15	2	US-08-460-502-7
16	70	43.2	15	4	US-09-046-373-2
17	70	43.2	15	4	US-09-188-082-6
18	70	43.2	15	5	PCT-US93-11703-69
19	70	43.2	16	4	US-09-248-588-55
20	70	43.2	17	4	US-08-446-692-4
21	70	43.2	17	3	US-08-488-351A-4
22	70	43.2	17	3	US-09-100-409A-40
23	70	43.2	17	5	PCT-US95-08596-23
24	70	43.2	17	5	PCT-US95-13841-7
25	70	43.2	24	5	PCT-US92-07218-31
26	70	43.2	27	5	PCT-US92-07218-26
27	70	43.2	27	5	PCT-US92-07218-27

28	70	43.2	27	5	PCT-US92-07218-28	Sequence 28, Appl
29	70	43.2	27	5	PCT-US95-02121-111	Sequence 111, App
30	70	43.2	27	5	PCT-US95-02121-112	Sequence 112, App
31	70	43.2	29	3	US-09-075-257A-13	Sequence 13, Appl
32	70	43.2	29	3	US-09-075-257A-14	Sequence 14, Appl
33	70	43.2	29	4	US-09-534-639-13	Sequence 13, Appl
34	70	43.2	29	4	US-09-534-639-14	Sequence 14, Appl
35	70	43.2	30	5	PCT-US92-07218-29	Sequence 29, Appl
36	70	43.2	31	5	PCT-US93-11703-63	Sequence 63, Appl
37	66	40.7	14	4	US-09-082-279B-510	Sequence 510, App
38	66	40.7	14	4	US-09-315-304B-510	Sequence 510, App
39	65	40.1	13	1	US-08-787-547-42	Sequence 42, Appl
40	65	40.1	15	2	US-08-661-052-9	Sequence 9, Appl
41	65	40.1	15	4	US-09-188-082-9	Sequence 9, Appl
42	64	39.5	19	1	US-08-787-547-41	Sequence 41, Appl
43	60	37.0	13	5	PCT-US94-10257A-26	Sequence 26, Appl
44	36	22.2	15	2	US-08-671-094B-7	Sequence 7, Appl
45	36	22.2	17	1	US-08-311-307B-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
PCT-US92-07218-25
Sequence 25, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitello, Maria A.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPITOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-07218-25

Query Match 48.5%; Score 78.5; DB 5; Length 24;
Best Local Similarity 65.5%; Pred. No. 2.2e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY 2 OYKANSKFIGITEFGFPEHLVDFLOSL 30
|||||
DB 1 OYKANSKFIGITEF-----LPSDFPPSV 24

RESULT 2
PCT-US95-02121-110
; Sequence 110, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-110

Query Match 48.5%; Score 78.5; DB 5; Length 24;
Best Local Similarity 65.5%; Pred. No. 2.2e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY 2 OYKANSKFIGITEFGFPEHLVDFLOSL 30
|||||
DB 1 OYKANSKFIGITEF-----LPSDFPPSV 24

RESULT 3
PCT-US92-07218-32
; Sequence 32, Application PC/TUS9207218
; GENERAL INFORMATION:
; APPLICANT: Vitello, Maria A.

APPLICANT: Chesnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPITOPES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07218
; FILING DATE: 19920826
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-26-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-07218-32

Query Match 48.5%; Score 78.5; DB 5; Length 27;
Best Local Similarity 65.5%; Pred. No. 2.6e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY 2 OYKANSKFIGITEFGFPEHLVDFLOSL 30
|||||
DB 4 OYKANSKFIGITEF-----LPSDFPPSV 27

RESULT 4
US-08-446-692-13
; Sequence 13, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and sythetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-692-13

Query Match 44.1%; Score 71.5; DB 1; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 QYKANSKFIGITEFGFPEH 21
Db 3 QYKANSKFIGITEL---EH 19

RESULT 5
US-08-488-351A-13
Sequence 13, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang YI
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulants for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-13

Query Match 44.1%; Score 71.5; DB 2; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 QYKANSKFIGITEFGFPEH 21
Db 3 QYKANSKFIGITEL---EH 19

RESULT 6
US-08-186-266-5
Sequence 5, Application US/08186266
Patent No. 5662907
GENERAL INFORMATION:
APPLICANT: KUBO, Ralph T.
APPLICANT: GREY, Howard M.
APPLICANT: SETTE, Alessandro
APPLICANT: CELIS, Esteban
TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,266
FILING DATE: 25-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/159,339
FILING DATE: 29-NOV-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-50-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION:
; OTHER INFORMATION: 830-843."
US-08-186-266-5

Query Match      43.2%, Score 70; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYKANSKFIGITE 15
Db      1 QYKANSKFIGITE 14

RESULT 7
US-08-305-871A-5
; Sequence 5, Application US/08305871A
; Patent No. 5736142
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffrey L.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan
; TITLE OF INVENTION: DR-Binding Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,871A
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,101
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-0062-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acid
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-305-871A-5

Query Match      43.2%, Score 70; DB 1; Length 14;
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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION:
; OTHER INFORMATION: 830-843."
US-08-186-266-5

Query Match      43.2%, Score 70; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYKANSKFIGITE 15
Db      1 QYKANSKFIGITE 14

RESULT 8
US-08-465-167A-18
; Sequence 18, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,167A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,623
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-60-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-167A-18

Query Match      43.2%, Score 70; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYKANSKFIGITE 15
Db      1 QYKANSKFIGITE 14

RESULT 9
US-08-817-933A-9
; Sequence 9, Application US/08817933A
; Patent No. 5945104
; GENERAL INFORMATION:
; APPLICANT: STANMORTH, DENIS R.
; APPLICANT: LEWIN, IAN V.
; TITLE OF INVENTION: PEPTIDES FOR ANTI-ALLERGY TREATMENT
```

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhwe
STREET: 1100 No. 5945104th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,933A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422294.0
FILING DATE: 04-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mitchell, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 179-23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4005
TELEFAX: (703) 816-4100
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-933A-9

Query Match 43.2%; Score 70; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2,9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
DB 1 OYKANSKFIGITE 14

RESULT 10
PCT-US92-07218-15
Sequence 15, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitello, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPTOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-343-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-07218-15

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2,9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
DB 1 OYKANSKFIGITE 14

RESULT 11
PCT-US92-07218-30
Sequence 30, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitello, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPTOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-07218-30

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
|||||
Db 1 OYKANSKFIGITE 14

RESULT 12

PCT-US95-02121-95
Sequence 95, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Patmelee, Steven W.
REGISTRATION/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 1437-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..14
OTHER INFORMATION: /note- "Tetanus toxoid 830-843"
PCT-US95-02121-95

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
|||||
Db 1 OYKANSKFIGITE 14

RESULT 13

US-08-319-704-10
Sequence 10, Application US/08319704
Patent No. 5814617
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard C.
APPLICANT: Doonan, Denise L.
TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and
Erythrocytic Stage Immunogen and Gene
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medical R & D Command
STREET: Bldg 1, T-12, 8901 Wisconsin Avenue
CITY: Bethesda
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,704
FILING DATE: 07-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: A. David Spevack
REGISTRATION/DOCKET NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75,206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-1022
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-319-704-10

Query Match 43.2%; Score 70; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
|||||
Db 1 OYKANSKFIGITE 14

RESULT 14

US-08-661-052-6
Sequence 6, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezia Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRSED

```

? TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES
? NUMBER OF SEQUENCES: 16
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD
? STREET: 60 State Street, Suite 510
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109-1875
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/661,052
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/484,172
? FILING DATE: 07-JUNE-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Arnold, Beth E.
? REGISTRATION NUMBER: 35,430
? REFERENCE/DOCKET NUMBER: MXI-043CP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)227-5941
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FRAGMENT TYPE: internal
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US-08-661-052-6

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Query Match 43.2%; Score 70; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 OYKANSKFICITE 15
Db 1 OYKANSKFICITE 14

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RESULT 15
US-08-460-502-7
? Sequence 7, Application US/08460502
? Patent No. 5843464
? GENERAL INFORMATION:
? APPLICANT: Bakaletz, Lauren O.
? APPLICANT: Kaumaya, Parvin T.
? TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Calfee, Halter and Griswold
? STREET: 800 Superior Avenue
? CITY: Cleveland
? STATE: Ohio
? COUNTRY: U.S.A.
? ZIP: 44114-2688
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/460,502
? FILING DATE:
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Goltick, Mary E.

```

```

? REGISTRATION NUMBER: 34,829
? REFERENCE/DOCKET NUMBER: 22727/00120
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (216) 622-8458
? TELEFAX: (216) 241-0816
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
?
US-08-460-502-7

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Query Match 43.2%; Score 70; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 OYKANSKFICITE 15
Db 1 OYKANSKFICITE 14

```

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Search completed: June 18, 2002, 08:18:16
Job time: 134 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:06:16 ; Search time 14.7 Seconds

(without alignments)
169,954 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26
Sequence: 1 RDGFLLQMDGFEPHLLVDFLOSL 26

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 segs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

1: PIR.71:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	493	A53176	cholestereryl ester
2	26	100.0	493	A26941	cholestereryl ester
3	25	96.2	289	A38700	cholestereryl ester
4	11	42.3	497	I46692	cholestereryl ester
5	7	26.9	263	F86278	hypothetical prote
6	7	26.9	280	D84015	maltose/maltodextr
7	7	26.9	378	AH3635	c-di-GMP phosphodi
8	7	26.9	405	F86314	protein F8H5.16 f
9	7	26.9	547	E82422	anaerobic glycerol
10	7	26.9	825	T00818	hypothetical prote
11	7	26.9	903	T26743	hypothetical prote
12	7	26.9	961	PXRRAU	outer capsid prote
13	7	26.9	961	PXRRAU	outer capsid prote
14	7	26.9	961	A60017	outer capsid prote
15	7	26.9	1300	T00317	probable serine pr
16	6	23.1	96	F80932	hypothetical prote
17	6	23.1	96	D84931	hypothetical prote
18	6	23.1	115	T44558	hypothetical prote
19	6	23.1	130	H70454	conserved hypotnet
20	6	23.1	144	E71298	hypothetical prote
21	6	23.1	156	E84861	hypothetical prote
22	6	23.1	163	G90437	hypothetical prote
23	6	23.1	167	A95366	NADH dehydrogenase
24	6	23.1	189	1	interferon alpha-I
25	6	23.1	189	2	interferon alpha-M
26	6	23.1	204	1	hypothetical prote
27	6	23.1	210	1	transcriptional regu
28	6	23.1	214	2	adenylate kinase (
29	6	23.1	214	2	adenylate kinase (

o ligo

30	6	23.1	234	1	D69093	DNA repair protein
31	6	23.1	235	2	AC1368	amino acid ABC tra
32	6	23.1	241	2	T35437	hypothetical prote
33	6	23.1	260	2	C84005	enoyl-l-acyl-carrie
34	6	23.1	268	2	T46631	phospholipid biosy
35	6	23.1	269	2	G69845	enoyl-l-acyl-carrie
36	6	23.1	275	2	D89902	conserved hypotnet
37	6	23.1	279	2	T35791	probable transmemb
38	6	23.1	283	2	F70038	maltodextrin trans
39	6	23.1	283	2	E83902	maltose/maltodextr
40	6	23.1	283	2	AB0105	probable maltodext
41	6	23.1	285	2	T10069	membrane associate
42	6	23.1	286	2	G83211	conserved hypotnet
43	6	23.1	298	2	B83823	endonuclease IV BH
44	6	23.1	303	2	H89881	hypothetical prote
45	6	23.1	313	2	F90026	hypothetical prote
46	6	23.1	393	2	H69679	involved in fatty
47	6	23.1	393	2	H90440	muconate cyclisom
48	6	23.1	394	2	G90114	PIIB related fact
49	6	23.1	397	2	G64703	type IIS restrict
50	6	23.1	406	2	G71816	probable type II r
51	6	23.1	414	2	T19912	hypothetical prote
52	6	23.1	416	2	T37023	probable oxidoredu
53	6	23.1	419	2	T08683	hypothetical prote
54	6	23.1	422	2	A49837	clathrin-associate
55	6	23.1	425	2	T23603	hypothetical prote
56	6	23.1	472	2	AD2284	hypothetical prote
57	6	23.1	489	2	T10334	late expression fa
58	6	23.1	490	2	T41806	late expression fa
59	6	23.1	491	1	ITRHUA2	alpha-2-antiplasmi
60	6	23.1	496	2	T30412	late expression fa
		23.1	500	1	JC4157	cytochrome P450 2D
		23.1	516	2	G72857	late expression fa
		23.1	532	2	T07903	tubulin delta chaf
		23.1	538	2	B81376	probable membrane
		23.1	626	2	C87672	peptide transport
		23.1	637	2	F83939	myo-inositol catib
		23.1	677	2	S40992	hypothetical prote
		23.1	778	2	H84845	hypothetical prote
		23.1	771	2	T43423	probable replicati
		23.1	868	2	T50339	mis protein limpo
		23.1	892	2	F71426	hypothetical prote
		23.1	900	2	JC6016	chitin synthase (E
		23.1	911	2	T30580	P-type ATPase - s1
		23.1	1058	2	AB9135	protein F2566.2 f1
		23.1	1183	2	S50434	hypothetical prote
		23.1	1188	2		

ALIGNMENTS

RESULT 1
A53176
cholestereryl ester transfer protein - crab-eating macaque
C:Species: Macaca fascicularis (Crab-eating macaque)
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A53176
R:Page, M.E.; Rehberg, E.F.; Marotti, K.R.; Melchior, G.W.
Arterioscler. Thromb. 11, 1759-1771, 1991
A:Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl
asma high density lipoprotein levels.
A:Reference number: A53176; MUID:92031355
A:Accession: A53176
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <PAP>
A:Cross-references: GB:M66343

Query Match 100.0% Score 26; DB 2; Length 493;
Best Local Similarity 100.0% Pred. No. 5.5e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILQMDGFPPEHLVDFLOSL 26
 DB 468 RDGFLILQMDGFPPEHLVDFLOSL 493

RESULT 2

A26941
 cholesteryl ester transfer protein precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jul-2000
 C:Accession: A26941
 R:Dryden, D.; Jarnagin, A.S.; McLean, J.; Henzel, W.; Kohr, W.; Fielding, C.; Lawn, R.
 Nature 337, 632-634, 1987
 A:Title: Cloning and sequencing of human cholesteryl ester transfer protein cDNA.
 A:Reference number: A26941; MUID:87258172
 A:Accession: A26941
 A:Molecule type: mRNA
 A:Residues: 1-493 <DEA>
 A:Cross-references: EMBL:M30185; NID:g180259; PIDN:AAA51977.1; PID:g180260
 C:Genetics:
 A:Gene: GDB:CEMP
 A:Cross-references: GDB:119773; OMIM:118470
 A:Map position: 16q13-16q13
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-493/Product: cholesteryl ester transfer protein #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 5, 5e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILQMDGFPPEHLVDFLOSL 26
 DB 468 RDGFLILQMDGFPPEHLVDFLOSL 493

RESULT 3

A38700
 cholesteryl ester transfer protein - golden hamster (fragment)
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 05-Nov-1999
 C:Accession: A38700
 R:Jiang, X.C.; Koulfin, P.; Quinet, E.; Goldberg, I.J.; Yacoub, L.K.; Agellon, L.B.; Comp
 J. Biol. Chem. 266, 4631-4639, 1991
 A:Title: Mammalian adipose tissue and muscle are major sources of lipid transfer protein
 A:Reference number: A38700; MUID:91154277
 A:Accession: A38700
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-289 <TIA>
 A:Cross-references: GB:M63992; NID:g191342; PIDN:AAA37066.1; PID:g191343
 A:Note: the authors translated the codon CTG for residue 68 as Gly, GGG for residue 69 a
 as Ser, and TTC for residue 267 as Ser

Query Match 96.2%; Score 25; DB 2; Length 289;
 Best Local Similarity 100.0%; Pred. No. 3, 6e-18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILQMDGFPPEHLVDFLOSL 25
 DB 264 RDGFLILQMDGFPPEHLVDFLOSL 288

RESULT 4

I46692
 cholesteryl ester transfer protein - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 C:Accession: I46692
 R:Nagashima, M.; McLean, J.W.; Lawn, R.M.
 J. Lipid Res. 29, 1643-1649, 1988
 A:Title: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protei

A:Reference number: I46692; MUID:89215620
 A:Accession: I46692
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-497 <NAG>
 A:Cross-references: GB:M27486; NID:g530906; PIDN:AAA31199.1; PID:g530907
 C:Genetics:
 A:Gene: CESTP

Query Match 42.3%; Score 11; DB 2; Length 497;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLIVDFLOSL 26
 DB 487 HLIVDFLOSL 497

RESULT 5

F86278
 hypothetical protein F1417.18 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C:Accession: F86278
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 ansen, N.E.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Matli, R.; Marzla
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ventner, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: AB6141; MUID:21016719
 A:Accession: F86278
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-263 <STO>
 A:Cross-references: GB:AB005172; NID:g7262603; PIDN:AAF3941.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 26.9%; Score 7; DB 2; Length 263;
 Best Local Similarity 100.0%; Pred. No. 7, 8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLQ 8
 DB 116 DGFLLQ 122

RESULT 6

BD4015
 maltose/maltooligosaccharin transport system (permease) BH2924 [imported] - Bacillus halodurans
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: BD4015
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: AB3650; MUID:20512582; PMID:11058132
 A:Accession: BD4015
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-280 <STO>
 A:Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA06643.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH2924
 C:Superfamily: maltose transport protein malt

Query Match 26.9%; Score 7; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIOW 9
|||||||
Db 112 GFLIOW 118

RESULT 7
AH3635
c-di-GMP phosphodiesterase A [Imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AH3635
R:DelVecchio, V.G.; Kapetrak, V.; Redkar, R.J.; Patra, G.; Wujer, C.; Ios, T.; Ivanova,
; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3635
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1378 <RUB>
A:Cross-references: GB:AE008918; PIDN:RAL54251.1; PID:q17985224; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1009
A:Map position: II

Query Match 26.9%; Score 7; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 7
|||||||
Db 241 RDGFLL 247

RESULT 8
F86314
protein F2H15.16 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86314
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chlu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Crensy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzler, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Kian, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Mailli, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, G.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719
A:Accession: F86314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: GB:AE005172; NID:g9665071; PIDN:AAF97273.1; GSPDB:GN00141
C:Genetics:
A:Gene: F2H15.16
A:Map position: 1

Query Match 26.9%; Score 7; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLOSL 25
|||||||
Db 37 VDFLOSL 43

RESULT 9
E82422
anaerobic glycerol-3-phosphate dehydrogenase, chain A VCA0747 [Imported] - Vibrio cho
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82422
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833
A:Accession: E82422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <HEI>
A:Cross-references: GB:AE004403; GB:AE003853; NID:g9658159; PIDN:AAF96645.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0747
A:Map position: 2
C:Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)

Query Match 26.9%; Score 7; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDFL 22
|||||||
Db 495 HLLVDFL 501

RESULT 10
T00818
hypothetical protein At2g41620 [Imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T3266.14
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00818; AB4844
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T3266 genomic sequence.
A:Reference number: Z14163
A:Accession: T00818
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-825 <ROU>
A:Cross-references: EMBL:AC002510; NID:g2618683; PID:g2618698
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beaulieu, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
eusa, D.; Nielsen, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487
A:Accession: T00818
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-825 <STO>
A:Cross-references: GB:AE002093; NID:g2618698; PIDN:AAF84345.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g41620; T3266.14
A:Map position: 2
A:Introns: 43/3; 74/2; 96/3; 116/3; 146/3; 234/3; 266/3; 311/3; 329/3; 368/3; 669/3;
A:Note: T3266.14
C:Superfamily: Arabidopsis thaliana hypothetical protein At2g41620

Query Match 26.9%; Score 7; DB 2; Length 825;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 20 DFLQSL 26
|||||||
DB 155 DFLQSL 161

RESULT 11

T26743

hypothetical protein Y39A1A.15c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26743

R:Wall, M.

submitted to the EMBL Data Library, September 1998

A:Reference number: 220257

A:Accession: T26743

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-903 <MIL>

A:Cross-references: EMBL:AL031633; PTDN:CMA21032.1; GSPDB:GN00021; CESP:Y39A1A.15c

A:Experimental source: clone Y39A1A

C:Genetics:

A:Gene: CESP:Y39A1A.15c

A:Map position: 3

A:Introns: 33/3; 63/1; 139/3; 185/1; 382/3; 424/2; 798/3; 852/3

Query Match 26.9%; Score 7; DB 2; Length 903;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 17 LTVDFLQ 23
|||||||
DB 7 LTVDFLQ 13

RESULT 12

P2XRNU

outer capsid protein VP2 - bluetongue virus (serotype 1, strain Australia)

C:Species: bluetongue virus

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C:Accession: S03654; JS0322

R:Yamaguchi, S.; Fukusho, A.; Roy, P.

Nucleic Acids Res. 16, 2725, 1988

A:Title: Complete sequence of VP2 gene of the bluetongue virus serotype 1 (BTV-1).

A:Reference number: S03654; M01D:88203217

A:Accession: S03654

A:Molecule type: genomic RNA

A:Residues: 1-961 <YAM>

R:Gould, A.R.

Virus Res. 9, 145-158, 1988

A:Title: Conserved and non-conserved regions of the outer coat protein, VP2, of the Aust

A:Reference number: JS0322; M01D:88180013

A:Accession: JS0322

A:Molecule type: genomic RNA

A:Residues: 1-12, 'V', '14-71', 'V', '73-185', 'LTF', '189-199', 'D', '201-350', 'F', '352-556', 'D', '558-749',

A:Cross-references: GB:M21844; NID:9323187; PTDN:AAA42844.1; PID:9323188

C:Genetics:

A:Map position: segment 2

C:Superfamily: bluetongue virus VP2 protein

C:Keywords: capsid protein

DB 12 GFPEHLL 18
|||||||

RESULT 13

P2XRSA

outer capsid protein VP2 - bluetongue virus (serotype 1, strain South Africa)

C:Species: bluetongue virus

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 07-May-1999

C:Accession: A60014; B60014

R:Wade-Evans, A.M.; Mertens, P.P.C.

Virus Res. 15, 213-230, 1990

A:Title: Expression of the outer capsid protein, VP2, from a full length cDNA clone o

a comparison of the nucleic acid sequence of this segment with those of other seroty

A:Reference number: A60014; M01D:90261331

A:Accession: A60014

A:Molecule type: mRNA

A:Residues: 1-961 <WAL>

A:Accession: B60014

A:Molecule type: protein

A:Residues: 322-346; 492-503 <WAZ>

C:Genetics:

A:Map position: segment 2

C:Superfamily: bluetongue virus VP2 protein

C:Keywords: capsid protein; glycoprotein; transmembrane protein

F:66-682/Domain: transmembrane #status predicted <TMN>

F:303/432/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.9%; Score 7; DB 1; Length 961;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFPEHLL 18
|||||||
DB 12 GFPEHLL 18

RESULT 14

A60017

outer capsid protein VP2 - bluetongue virus (serotype 1, strain South Africa-VACC)

C:Species: bluetongue virus

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C:Accession: A60017

R:Gould, A.R.; Pritchard, L.I.

Virus Res. 17, 31-52, 1990

A:Title: Relationships amongst bluetongue viruses revealed by comparisons of capsid a

A:Reference number: A60017; M01D:91021485

A:Accession: A60017

A:Molecule type: genomic RNA

A:Residues: 1-961 <GOU>

A:Cross-references: GB:X55800; NID:9297132; PTDN:CMA39322.1; PID:9297133

C:Genetics:

A:Map position: segment 2

C:Superfamily: bluetongue virus VP2 protein

C:Keywords: capsid protein; glycoprotein; membrane protein

F:303/432/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.9%; Score 7; DB 1; Length 961;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFPEHLL 18
|||||||
DB 12 GFPEHLL 18

RESULT 15

T00317

probable serine proteinase esp, extracellular - Escherichia coli plasmid p0157

N:Alternate names: putative exoprotein-precursor

C:Species: Escherichia coli

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 08-Dec-2000
 C/Accession: T00317; T42120
 R/Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota, S.; Shinagawa, H.
 DNA Res. 5; 1-9, 1998
 A>Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic E. coli O157:H7
 A/Reference number: 214127; MUID:98290540
 C/Accession: T00317
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1300 <MAX>
 A/Cross-references: EMBL:AB011549; NID:94589740; PIDN:BA31935.1; PID:93337077
 A/Experimental source: strain EHEC O157:H7, substrain RMD 050952
 R/Burland, V.; Shao, T.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
 Nucleic Acids Res. 26; 4196-4204, 1998
 A>Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157:H7
 A/Reference number: 222068; MUID:98391744
 C/Accession: T42120
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1300 <BUR>
 A/Cross-references: EMBL:AF074613; PIDN:AC70088.1
 A/Experimental source: strain EDL933; serotype O157:H7
 C/Genetics:
 A/Gene: espP
 A/Genome: plasmid pO157
 A/Superfamily: IGA-specific metalloendopeptidase
 C/Keywords: serine proteinase

Query Match 26.9%; Score 7; DB 2; Length 1300;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LVDPLQ 23
 DB 933 LVDPLQ 939

RESULT 16
 F90932
 hypothetical protein ECs2430 [imported] - Escherichia coli (strain O157:H7, substrain RMD 050952)
 C/Accession: F90932
 C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8; 11-22, 2001
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands
 A/Reference number: A99629; MUID:21156231; PMID:11258796
 C/Accession: F90932
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-96 <HAY>
 A/Cross-references: GB:BA000007; PIDN:BA35853.1; PID:G1336197; GSPDB:GN00154
 A/Experimental source: strain O157:H7, substrain RMD 050952
 C/Genetics:
 A/Gene: ECs2430

Query Match 23.1%; Score 6; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 DB 32 RDGFLL 37

RESULT 17
 D64531
 hypothetical protein b1724 - Escherichia coli
 C/Species: Escherichia coli

C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
 C/Accession: D64931
 R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277; 1453-1462, 1997
 A>Title: The complete genome sequence of Escherichia coli K-12.
 A/Reference number: A64720; MUID:97426617
 C/Accession: D64931
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-96 <BLAT>
 A/Cross-references: GB:AE000267; GB:U00096; NID:91788011; PIDN:AC74794.1; PID:917880
 A/Experimental source: strain K-12, substrain NG1055

Query Match 23.1%; Score 6; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 DB 32 RDGFLL 37

RESULT 18
 T44558
 hypothetical protein PRF29 [imported] - Pseudomonas aeruginosa
 C/Species: Pseudomonas aeruginosa
 C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Dec-2000
 C/Accession: T44558; C83565
 R/Nakayama, K.; Takashima, K.; Ishihara, H.; Shinomiya, T.; Kageyama, M.; Kanaya, S.; submitted to the EMBL data library, August 1999
 A/Description: Genetic relationship between bacteriophages and bacteriophages.
 A/Reference number: 222790
 C/Accession: T44558
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-115 <NAK>
 A/Cross-references: EMBL:AB030825; PIDN:BAAB3173.1
 A/Experimental source: strain PA01
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.

.. Lory, S.; Olson, M.V.
 Nature 406; 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A/Reference number: AB2850; MUID:20437337
 C/Accession: C83565
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-115 <STO>
 A/Cross-references: GB:AE004499; GB:AE004091; NID:99946508; PIDN:AC04023.1; GSPDB:GN

A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: PA0634
 C/Superfamily: Pseudomonas aeruginosa hypothetical protein PRF29

Query Match 23.1%; Score 6; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLDLQ 8
 DB 96 GFLDLQ 101

RESULT 19
 H70454
 conserved hypothetical protein aq_1797 - Aquifex aeolicus
 C/Species: Aquifex aeolicus
 C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
 C/Accession: H70454
 R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.;

V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A:Reference number: AT0300; MUID:98196666
 A:Accession: H70454
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-130 <AOF>
 A:Cross-references: GB:AE000756; NID:92984076; PIDN:AAC07630.1; PID:92984091; GB:AE00065
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: aq_1797

Query Match 23.1%; Score 6; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LVDPL 22
 |||||
 Db 80 LVDPL 85

RESULT 20
 E71298
 hypothetical protein TP0638 - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1998
 C:Accession: E71298
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uitterback, T.; McDe
 lney, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770
 A:Accession: E71298
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-144 <COL>
 A:Cross-references: GB:AE001239; GB:AE000520; NID:93322937; PIDN:AAC65625.1; PID:9332295
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0638
 C:Superfamily: syphilis spirochete hypothetical protein TP0638

Query Match 23.1%; Score 6; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LVDPL 22
 |||||
 Db 71 LVDPL 76

RESULT 21
 E84861
 hypothetical protein At2g43060 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: E84861
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bonito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vandenbroucke, S.E.; Umayam, L.; Mallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487
 A:Accession: E84861
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-156 <STO>
 A:Cross-references: GB:AE002093; NID:94531440; PIDN:AA022125.1; GSPDB:GN00139
 C:Genetics:

A:Gene: At2g43060
 A:Map position: 2

Query Match 23.1%; Score 6; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSL 26
 |||||
 Db 22 FLOSL 27

RESULT 22
 G90437
 hypothetical protein cutC-2 [imported] - *Sulfolobus solfataricus*
 C:Species: *Sulfolobus solfataricus*
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 C:Accession: G90437
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aveyez, M.J.; Ch
 jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
 arett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
 submitted to Genbank, April 2001
 A:Description: *Sulfolobus solfataricus* complete genome.
 A:Reference number: A99139
 A:Accession: G90437
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-163 <KOR>
 A:Cross-references: GB:AE006641; NID:913815949; PIDN:AAK42758.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: cutC-2
 C:Superfamily: isoguinoline-1-oxidoreductase alpha chain; ferredoxin [2Fe-2S] homolog
 C:Keywords: 2Fe-2S; metalloprotein
 F:48,55,56,66/Binding site: 2Fe-2S cluster (Cys) (covalent) *status predicted

Query Match 23.1%; Score 6; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LVDPL 22
 |||||
 Db 30 LVDPL 35

RESULT 23
 A95366
 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain B NuoB2 - *Sinorhizobium meliloti* (C
 C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: A95366
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meli*
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: A95366
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-167 <UR>
 A:Cross-references: GB:AE006469; PIDN:AAK65491.1; PID:914523963; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Flan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
 pella, D.; Chahin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 C:Genetics:

A:Gene: nuob2
A:Genome: plasmid
C:Superfamily: psbg protein
C:Keywords: oxidoreductase; NAD

Query Match 23.1%; Score 6; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIQ 8
DB 142 GFLIQ 147

RESULT 24
I:VH04B
Interferon alpha-I-4b precursor - human
N:Alternate names: HuIFN-alpha-I-4b; type I Interferon
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C:Accession: E23753
R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Koy
J. Mol. Biol. 185, 227-260, 1995
A:Title: Structural relationship of human Interferon alpha genes and pseudogenes.
A:Reference number: A92916; MUID:86037205
A:Accession: E23753
A:Molecule type: DNA
A:Residues: 1-189 <HEM>
A:Cross-references: GB:X02955; NID:g32656; PIDN:CAA26701.1; PID:g758078
C:Genetics:
A:Gene: GDB:IFN1@
A:Cross-references: GDB:119328; OMIM:147660
A:Map position: 9p22-qp22
C:Superfamily: interferon alpha
C:Keywords: antiviral
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-189/Product: Interferon alpha-I-4b #status predicted <MAT>
F:24-122,57-162/Disulfide bonds: #status predicted

Query Match 23.1%; Score 6; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGPE 15
DB 58 DFGPE 63

RESULT 25
I:52347
Interferon alpha-M1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I52347
R:Linnane, A.W.; Bellinz, M.W.; McMullen, G.L.; Macreadie, C.G.; Murphy, M.; Nisbet, I.
Biochem. Int. 8, 725-732, 1984
A:Title: Nucleotide sequence and expression in E. coli of a human Interferon-alpha gene
A:Reference number: I52347; MUID:64307815
A:Accession: I52347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <HEM>
A:Cross-references: GB:M27318; NID:g184617; PIDN:AAA52726.1; PID:g306909
C:Genetics:
A:Gene: IFNA
C:Superfamily: Interferon alpha

Query Match 23.1%; Score 6; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGPE 15
DB 58 DFGPE 63

RESULT 26
S:76652
Hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.

A:Variety: PCC 6803
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S76652
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asemlzu, E.; Nakamura, Y.; Miyajima,
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S76652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <KAN>

A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PID:g1001758
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Bacillus subtilis conserved hypothetical protein ydg6

Query Match 23.1%; Score 6; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LVVDF 22
DB 23 LVVDF 28

RESULT 27
F87455
transcription regulator, tetr family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: F87455
R:Nierman, W.C.; Denoy, R.T.; Dodson, R.J.; Dutkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: F87455
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <STO>
A:Cross-references: GB:AE005673; NID:g1423072; PIDN:AAK23642.1; GSPDB:GN00148
C:Genetics:
A:Gene: CCL664

Query Match 23.1%; Score 6; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLO 24
DB 182 VDFLO 187

RESULT 28
S70734
adenylate kinase (EC 2.7.4.3) - Yersinia enterocolitica
N:Alternate names: ATP-AMP transphosphorylase
C:Species: Yersinia enterocolitica
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C:Accession: S70734; SS1258
 M.:Skurdat, M.; Venho, R.; Toivanen, P.; Al-Hendy, A.
 A:Title: Microbiol. 117, 575-594, 1995
 A:Reference number: S70734; MIMD:96100456
 A:Accession: S70734
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-214 <SMU>
 A:Cross-references: EMBL:247767; NID:9633689; PIDN:CAA87696.1; PID:g633690
 A:Experimental source: strain 6471/76 serotype O:3
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 C:Genetics:
 A:Gene: adx
 C:Function:
 A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A:Note: magnesium required
 C:Superfamily: adenylate kinase
 C:Keywords: ATP; P-loop; phosphotransferase
 F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
 F:80-85/Region: nucleotide-binding motif B #status atypical
 F:126/Active site: His #status predicted

Query Match 23.1%; Score 6; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFL 6
 |||||
 Db 78 RDGFL 83

RESULT 29
 AC0378
 adenylate kinase (EC 2.7.4.3) [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AC0378
 R:Parkhill, J.; Wen, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MIMD:21470413; PMID:11586360
 A:Accession: AC0378
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-214 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CA092354.1; PID:g15981059; GSPDB:GN00175
 C:Genetics:
 A:Gene: adx
 C:Superfamily: adenylate kinase
 C:Keywords: phosphotransferase

Query Match 23.1%; Score 6; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFL 6
 |||||
 Db 78 RDGFL 83

RESULT 30
 D69093
 DNA repair protein Rad51 homolog - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: D69093
 R:Smith, D.R.; Doucette-Stamm, L.A.; DeJonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qiu, D.; Spadator, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.

kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
 A:Reference number: A69000; MIMD:98037514
 A:Accession: D69093
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-234 <MTH>
 A:Cross-references: GB:AE000927; GB:AE000666; NID:62622822; PIDN:AAB86165.1; PID:g262
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1693
 C:Superfamily: Methanococcus DNA repair protein RAD51

Query Match 23.1%; Score 6; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FILLDM 9
 |||||
 Db 150 FILLDM 155

RESULT 31
 AC1368
 amino acid ABC transporter (permease) homolog Imo2347 [imported] - Listeria monocytogenes
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C:Accession: AC1368
 R:Glaser, P.; Franke, L.; Buchleser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioc
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fahl,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurupkat, G.; Madueno, E.; Maltournam, A.;
 Ok, C.; Schuster, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MIMD:21537279; PMID:11679669
 A:Accession: AC1368
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-235 <GUA>
 A:Cross-references: GB:NC_003210; PIDN:CAD00425.1; PID:g16411835; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: Imo2347
 C:Superfamily: histidine permease protein M

Query Match 23.1%; Score 6; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LUVDF 22
 |||||
 Db 80 LUVDF 85

RESULT 32
 T35437
 hypothetical protein SC6A9.06 SC6A9.06 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
 C:Accession: T35437
 R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL data library, July 1998
 A:Reference number: Z21578
 A:Accession: T35437
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-241 <MUR>
 A:Cross-references: EMBL:AL031035; PIDN:CAA19891.1; GSPDB:GN00070; SCOEDB:SC6A9.06
 A:Experimental source: strain A3(2)

C:Genetics:
A:Gene: SCOE8B:SC6A9.06
C:Superfamily: glycerophosphodiester phosphodiesterase

Query Match 23.1% Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFL 6
|||||
Db 193 RDGFL 198

RESULT 33
C84005
enoyl-[acyl-carrier protein] reductase BH2843 [imported] - *Bacillus halodurans* (strain C
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: C84005
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, F.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C84005
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-260 <STO>
A:Cross-references: GB:AP001516; GB:BA000004; NID:910175192; PIDN:BA06562.1; GSPDB:GN0C
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2843
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol dehydr

Query Match 23.1% Score 6; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RDGFL 6
|||||
Db 113 RDGFL 118

RESULT 34
T46631
phospholipid biosynthesis protein plx [validated] - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 02-Sep-2000
C:Accession: T46631
R:Cronan, J.E.; Moridoni, H.R.; de Mendoza, D.
J. Bacteriol. 178, 4794-4800, 1996
A>Title: *Bacillus subtilis* acyl carrier protein is encoded in a cluster of lipid biosynt
A:Reference number: Z23107; MUID:96326321
A:Accession: T46631
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <CRO>
A:Cross-references: EMBL:U59433; NID:91502418; PIDN:AMC44305.1; PID:91502419
A:Experimental source: strain 168
C:Genetics:
A:Gene: plx
A:Map position: 135-145 degrees
C:Function:
A:Description: plays a poorly understood role in phospholipid biosynthesis
A:Pathway: phospholipid synthesis [validated, MUID:96326321]
C:Superfamily: phospholipid synthesis protein

Query Match 23.1% Score 6; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
|||||
Db 68 DGFLL 73

RESULT 35
G69845
enoyl-[acyl-carrier-protein] reductase (NADH) (EC 1.3.1.9) yjbm - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: G69845
R:Kunst, F.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gal
lechi, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A.; Authors: Lander, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y., M.; Ogawa, K.; Ogilawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portele
Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchlya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamato, K.; Yasunoto, K.; Yata, K.; Yoshida
A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
A:Reference number: A69580; MUID:98044033
A:Accession: G69845
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-269 <KUN>
A:Cross-references: GB:Z59110; GB:AL009126; NID:92633472; PIDN:CAB13029.1; PID:926335
A:Experimental source: strain 168
C:Genetics:
A:Gene: yjbm
C:Function:
A:Description: catalyzes reduction by NADH of enoyl-acyl-carrier-protein to the corre
A:Pathway: fatty acid biosynthesis
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol deh
C:Keywords: fatty acid biosynthesis; inner membrane; NAD; oxidoreductase
F:19-203/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 23.1% Score 6; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RDGFL 6
|||||
Db 123 RDGFL 128

RESULT 36
D89902
conserved hypothetical protein SA1124 [imported] - *Staphylococcus aureus* (strain N315
C:Species: *Staphylococcus aureus*
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89902
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K
C.; Shida, T.; Hattori, M.; Ogatawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89902
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KUN>
A:Cross-references: GB:BA000018; PID:913701081; PIDN:BA42376.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1124

Query Match 23.1%; Score 6; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 17 LLVDFL 22
|||||
DB 114 LLVDFL 119

RESULT 37
T35791
Probable transmembrane sugar transport protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T35791
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, July 1998
A:Reference number: Z21570
A:Accession: T35791
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-279 <SEE>
A:Cross-references: EMBL:AL031013; PTDN:CAA19796.1; GSPDB:GN00070; SCOEDB:SC8A6.24
C:Genetics:
A:Gene: SCOEDB:SC8A6.24
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLQ 8
|||||
DB 261 GFLLQ 266

RESULT 38
E70038
maltoedextrin transport system permease homolog yvfm - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E70038
R:Kunst, F.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteu
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Enlian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Hentut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapius, A.; Lardinois,
A:Authors: Lamber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y. M.; Ogawa, K.; Ogura, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schreier, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Serot
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumschein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:1980444033
A:Accession: E70038
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-283 <KUN>
A:Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PTDN:CAB15419.1; PID:g2635927
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvfm
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 283;

Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 FLLQW 9
|||||
DB 116 FLLQW 121

RESULT 39
E83902
Maltose/maltodextrin transport system (permease) BH2021 [imported] - Bacillus halodur
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: E83902
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83902
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <STO>
A:Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PTDN:BA805740.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2021
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLQW 9
|||||
DB 116 FLLQW 121

RESULT 40
AB0105
Probable maltodextrin permease protein YP00854 [imported] - Yersinia pestis (strain C
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0105
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0105
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <KUN>
A:Cross-references: GB:AL590842; PTDN:CAC89701.1; PID:g15978928; GSPDB:GN00175
C:Genetics:
A:Gene: YP00854
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLQW 9
|||||
DB 116 FLLQW 121

RESULT 41
T10069
membrane associated protein - Methylophilus methylotrophus
C:Species: Methylophilus methylotrophus

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: J110069
R:Christoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.
J. Bacteriol. 176, 4073-4080, 1994
A>Title: Organization of the methylamine utilization (mau) genes in *Methylobacillus methylotrophicus*
A/Reference number: Z16936; MUID:94292427
C/Accession: J110069
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-285 <STO>
A/Cross-references: EMBL:L26407; NID:9561931; PIDN:AB46947.1; PID:9556330
C/Experimental source: strain W3A1
C/Genetics:
A/Gene: mauA

Query Match 23.1%; Score 6; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 268 DGFLL 273

RESULT 42
G83211
conserved hypothetical protein PA3474 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: G83211
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Llm,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
gen
A/Reference number: AB2850; MUID:20437337
C/Accession: G83211
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <STO>
A/Cross-references: GB:AE004768; GB:AE004091; NID:99949611; PIDN:AG06862.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA3474

Query Match 23.1%; Score 6; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 139 GFLLLQ 144

RESULT 43
B83823
endonuclease IV BH1386 [imported] - *Bacillus halodurans* (strain C-125)
C/Species: *Bacillus halodurans*
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: B83823
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A/Reference number: AB3650; MUID:2051582; PMID:11058132
C/Accession: B83823
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-298 <STO>
A/Cross-references: GB:AP001511; GB:BA000004; NID:910173727; PIDN:BA05105.1; GSPDB:GN00
A/Experimental source: strain C-125
C/Genetics:

A/Gene: BH1386
C/Superfamily: deoxyribonuclease IV (phage T4-induced)

Query Match 23.1%; Score 6; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 90 VDFLOS 95

RESULT 44
H89881
hypothetical protein SA0964 [imported] - *Staphylococcus aureus* (strain N315)
C/Species: *Staphylococcus aureus*
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: H89881
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A/Reference number: AB9758; MUID:21311952; PMID:11418146
C/Accession: H89881
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-303 <KUR>
A/Cross-references: GB:BA000018; PID:913700916; PIDN:BA842212.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: SA0964
C/Superfamily: cytochrome caa3 oxidase ctaA

Query Match 23.1%; Score 6; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 100 GFLLLQ 105

RESULT 45
F90026
hypothetical protein SA2078 [imported] - *Staphylococcus aureus* (strain N315)
C/Species: *Staphylococcus aureus*
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: F90026
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A/Reference number: AB9758; MUID:21311952; PMID:11418146
C/Accession: F90026
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-313 <KUR>
A/Cross-references: GB:BA000018; PID:913702083; PIDN:BA843375.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: SA2078

Query Match 23.1%; Score 6; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 4 FFLLOW 9

Db 20 ELLIUM 25

RESULT 46

Involved in fatty acid/phospholipid synthesis plsx - *Bacillus subtilis*C:Species: *Bacillus subtilis*

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: H69679

R:Kunst, F.; Onasawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berlet

C.; Bron, S.; Bouilliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehllich, S.D.; Emerson, P.T.; Ertlan, K.D.; Errington, J.; Fedret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Galazzi, A.; Gall

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koeter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

Y. M.; Ogawa, K.; Ogilawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel

Rieger, M.; Rivoira, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schreier, R.; Scifoone, F.; Sekiguchi, J.; Sekowska, A.; Seron

T.; Whitors, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasamoto, K.; Yata, K.; Yoshida, K

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A:Reference number: A09380; MUID:9804033

A:Accession: H69679

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-333 <NU>

A:Cross-references: GB:Z99112; GB:AL009126; NID:92633902; PIDN:CAB13462.1; PID:92633961

A:Experimental source: strain 168

C:Genetics:

A:Gene: plsx

C:Superfamily: phospholipid synthesis protein

Query Match

Best Local Similarity 23.1%; Score 6; DB 2; Length 333;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGFLL 7

DB 133 DGFLL 138

RESULT 47

H90440 muconate cycloisomerase related protein [imported] - *Sulfolobus solfataricus*C:Species: *Sulfolobus solfataricus*

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: H90440

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan

Jong, I.; Jettles, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F

submitted to GenBank, April 2001

A:Description: *Sulfolobus solfataricus* complete genome.

A:Reference number: A99139

A:Accession: H90440

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-393 <NU>

A:Cross-references: GB:AE006641; NID:g13815980; PIDN:AAK2783.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO2665

Query Match

Best Local Similarity 23.1%; Score 6; DB 2; Length 393;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 LVDFIQ 23

DB 265 LVDFIQ 270

RESULT 48

TFIID related factor hBRF [imported] - *Gaillardia theta* nucleomorphC:Species: nucleomorph *Gaillardia theta*

A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C:Accession: G90114

R:Donagias, S.; Zanner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.

Nature 410, 1091-1096, 2001

A:Title: The highly reduced genome of an enslaved algal nucleus.

A:Reference number: A99082; MUID:11323671

A:Accession: G90114

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <NU>

A:Cross-references: GB:AF010592; NID:g12580771; PIDN:CAC27089.1; GSPDB:GN00151

C:Genetics:

A:Map position: 2

A:Genome: nucleomorph

C:Keywords: nucleomorph

Query Match

Best Local Similarity 23.1%; Score 6; DB 2; Length 394;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLVDVF 21

DB 131 HLVDVF 136

RESULT 49

type IIS restriction enzyme R protein - *Helicobacter pylori* (strain 26695)C:Species: *Helicobacter pylori*

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: G64703

R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodex, A.; McKe

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney,

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,

A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A:Reference number: A64520; MUID:97394467

A:Accession: G64703

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-397 <NU>

A:Cross-references: GB:AE00647; GB:AE000511; NID:g2314645; PIDN:AAD08511.1; PID:g231

C:Genetics:

A:Start codon: GTG

Query Match

Best Local Similarity 23.1%; Score 6; DB 2; Length 397;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLQMDF 11

DB 267 LLQMDF 272

RESULT 50

G71816 probable type II restriction enzyme - *Helicobacter pylori* (strain J99)C:Species: *Helicobacter pylori*

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C:Accession: G71816

R:Alm, R.A.; Lind, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doly, P.C.; Smith, D.

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F

Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557
A:Accession: G71816
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1406 <ARN>
A:Cross-references: GB:AE001559; GB:AE001439; NID:94155974; PIDN:AAD06939.1; PID:9415597
A:Experimental source: strain 399
C:Genetics:
A:Gene: jhp1364

Query Match 23.1%; Score 6; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 LLQMDP 11
DB 276 LLQMDP 281

Search completed: June 19, 2002, 11:08:20
Job time: 124 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:08:01 ; Search time 10.35 Seconds

(without alignments)
97.267 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26

Sequence: 1 RDGFLLQMDFGFPEHLVDFLQSLSS 26

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	26	100.0	493	1 CERP_HUMAN	P11597 homo sapien
2	26	100.0	493	1 CERP_MACFA	P47896 macaca fasc
3	25	96.2	289	1 CERP_MESAU	P25914 mesocricetu
4	11	42.3	497	1 CERP_RABIT	P22687 oryctolagus
5	7	26.9	421	1 SNAK_STRPK	F54591 streptomyce
6	7	26.9	825	1 Y240_ARATH	Q22224 arabidopsis
7	7	26.9	961	1 VP2_BTVIA	F12434 bluetongue
8	7	26.9	961	1 VP2_BTVIA	F32508 bluetongue
9	7	26.9	961	1 VP2_BTVIA	Q06997 bluetongue
10	6	23.1	144	1 YDIZ_ECOLI	P76507 escherichia
11	6	23.1	144	1 Y638_TREPA	Q83445 treponema p
12	6	23.1	153	1 MAUF_MERTL	Q50418 methylcobact
13	6	23.1	167	1 NIB2_RHIME	F56897 rhizobium m
14	6	23.1	189	1 INM4_HUMAN	P05014 homo sapien
15	6	23.1	214	1 KAD_YEREN	P43412 yersinia en
16	6	23.1	234	1 RADB_METH	Q27728 methanobact
17	6	23.1	258	1 FABI_BACSU	F54616 bacillus su
18	6	23.1	269	1 CYST_MESVI	Q99m19 mesostigma
19	6	23.1	285	1 MAUF_MERTL	Q50230 pseudostigma
20	6	23.1	285	1 YV74_PSEAE	Q68826 pseudomonas
21	6	23.1	295	1 TF_RAT	P42333 rattus norv
22	6	23.1	298	1 END4_BACID	Q9K833 bacillus ha
23	6	23.1	333	1 PSUX_BACIU	P71018 bacillus su
24	6	23.1	410	1 AUP1_MOUSE	F70295 mus musculu
25	6	23.1	422	1 AP47_CAEBL	F35602 caenorhabdi
26	6	23.1	423	1 AIM2_HUMAN	Q9Y6G5 h adaptor-r
27	6	23.1	423	1 AIM2_MOUSE	Q9Y6G5 h adaptor-r
28	6	23.1	443	1 MT17_KLULA	Q92441 kluyveromyc
29	6	23.1	489	1 LEF9_NPYOP	Q10319 oryza piseu
30	6	23.1	491	1 A2AP_HUMAN	P08697 homo sapien
31	6	23.1	491	1 CPDF_CANFA	Q29473 canis fam11
32	6	23.1	516	1 LEF9_NPYOP	P41465 autographa
33	6	23.1	516	1 LEF9_NPYOP	P41465 autographa

34	6	23.1	628	1 HCTF_EURCA	Q96F15 eurytelma c
35	6	23.1	715	1 ORC3_MOUSE	Q9JX30 mus musculu
36	6	23.1	892	1 M1S5_SCHPO	P49731 schizosacch
37	6	23.1	911	1 CHSG_ASPFU	P54267 aspergillus
38	6	23.1	1058	1 PMA1_DICDI	P54679 dictyostell
39	6	23.1	1188	1 YEC5_YEAST	P39991 saccharomyc
40	6	23.1	1246	1 YWV2_CAEBL	P34504 caenorhabdi
41	6	23.1	1451	1 SPT6_YEAST	P23515 saccharomyc
42	6	23.1	1636	1 YN37_YEAST	P48363 saccharomyc
43	6	23.1	1877	1 PKC5_RAT	P41413 rattus norv
44	6	23.1	1956	1 ATX1_PLAFA	Q04956 plasmodium
45	6	23.1	4563	1 APB_HUMAN	P04114 homo sapien
46	5	19.2	32	1 PETM_PORPU	P51275 porphyra pu
47	5	19.2	45	1 YSK6_SSV1	P20198 sulfolobus
48	5	19.2	48	1 APP8_HAWII	P48882 hansenula w
49	5	19.2	63	1 TAC1_BOVIN	P01000 bos taurus
50	5	19.2	74	1 YC35_HAETN	P44141 haemophilus
51	5	19.2	84	1 VES_HPV51	P26553 human papil
52	5	19.2	91	1 YVBE_VACCV	P20545 vaccinia vi
53	5	19.2	104	1 DSWC_DESVH	P45573 desulfovibr
54	5	19.2	114	1 GON2_TUPGB	Q95336 tupatia gila
55	5	19.2	117	1 KY5H_MOUSE	P01641 mus musculu
56	5	19.2	119	1 Y128_SYNP6	P05677 synecococc
57	5	19.2	130	1 KY5G_MOUSE	P01639 mus musculu
58	5	19.2	130	1 YQUF_ECOLI	P42619 escherichia
59	5	19.2	131	1 PRDC_ECOLI	P03805 escherichia
60	5	19.2	134	1 TQBL_BACSU	P45928 bacillus su
61	5	19.2	139	1 FXSA_SERMA	P37148 serratia ma
62	5	19.2	140	1 ANF_CHICK	P18908 gallus galli
63	5	19.2	143	1 MK_HUMAN	P21741 homo sapien
64	5	19.2	146	1 AP4A_HUMAN	P50583 homo sapien
65	5	19.2	146	1 AP4A_MOUSE	P56580 mus musculu
66	5	19.2	146	1 AP4A_PIC	P50584 sus scrofa
67	5	19.2	148	1 LYC1_RAT	P00897 rattus norv
68	5	19.2	148	1 LYC2_RAT	P00897 rattus norv
69	5	19.2	150	1 YWEL_STRLN	P55049 streptococ
70	5	19.2	151	1 DTD_LACIA	Q96192 lactococcus
71	5	19.2	156	1 CYNS_ECO57	P58704 escherichia
72	5	19.2	156	1 CYNS_ECOLI	P00816 escherichia
73	5	19.2	157	1 Y7ZF_BACSU	Q32068 bacillus su
74	5	19.2	159	1 COAD_STRCO	Q92bri streptomyce
75	5	19.2	161	1 COAD_AQUAE	O66614 aquilex aeo

ALIGNMENTS

RESULT	ID	STANDARD	PRT	493 AA
1	CERP_HUMAN			
AC	P11577; Q13987; Q13988;			
DT	01-OCT-1989 (Rel. 12; Created)			
DT	01-OCT-1989 (Rel. 12; Last sequence update)			
DT	16-OCT-2001 (Rel. 40; Last annotation update)			
DE	Cholesteryl ester transfer protein precursor (lipid transfer protein I).			
GN	CERP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE-8758172; Pubmed-3600759;			
RA	Drayna D., Jarnagin A.S., McLean J., Henzel W., Kohn W., Fielding C.,			
RT	Lawn R.,			
RT	"Cloning and sequencing of human cholesteryl ester transfer protein			
RT	cDNA."			
RU	Nature 327:632-634(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-90241928; Pubmed-2334701;			
RA	Agellon L.B., Quinet E.M., Gillette T.C., Drayna D.T., Brown M.L.,			

RA Tail A.R.;
RT "Organization of the human cholesterol ester transfer protein gene."
RL Biochemistry 29:1372-1376(1990).
[3]
RP SEQUENCE OF 1-15 FROM N.A.
RX MEDLINE-97112972; PubMed-8943225;
RA Oliveira C.F.O., Chouinard R.A., Agellon L.B., Bruce C., Ma L.,
RA Walsh A., Breslow J.L., Tall A.R.;
RT "Human cholesterol ester transfer protein gene proximal promoter
expression in small intestine and periphery while predominant liver
sequences mapped in transgenic mice."
RT J. Biol. Chem. 271:31831-31838(1996).
[4]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE-97473500; PubMed-9332354;
RA Williams S., Hayes L., Eisenbloss L., Williams A., Andre C.,
RA Abramson R., Thompson J.F., Miles P.M.;
RT "Sequencing of the cholesterol ester transfer protein 5' regulatory
region using artificial transposons."
RL Gene 197:101-107(1997).
[5]
RP SEQUENCE OF 9-493 FROM N.A.
RX TISSUE-Liver;
RC Dinichuk J.E., Hart J.T., Mirak D.O.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
[6]
RP VARIANT GLY-459.
RX MEDLINE-94013514; PubMed-8408659;
RA Takahashi K., Uiang X.-C., Sakai N., Yamashita S., Hirano K., Bujo H.,
RA Yamazaki H., Kusunoki J., Mura T., Kussie P., Matsuzawa Y., Saito Y.,
RA Tall A.;
RT "A missense mutation in the cholesterol ester transfer protein gene
with possible dominant effects on plasma high density lipoproteins."
RL J. Clin. Invest. 92:2060-2064(1993).
[7]
CC -1- FUNCTION: CERP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
TRANSFER OF INSOLUBLE CHOLESTEROL ESTERS IN THE REVERSE TRANSPORT
OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- DISEASE: PROBABLY INVOLVED IN THE DEVELOPMENT OF ATHEROSCLEROSIS.
CC -1- SIMILARITY: BELONGS TO THE BPL/CETP/LBP/PLTP FAMILY.
CC
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CC -----
DR EMBL: M30185; AAA51977.1; -;
DR EMBL: M32998; AAA51978.1; -;
DR EMBL: M32992; AAA51978.1; JOINED.
DR EMBL: M32993; AAA51978.1; JOINED.
DR EMBL: M32994; AAA51978.1; JOINED.
DR EMBL: M32995; AAA51978.1; JOINED.
DR EMBL: M32996; AAA51978.1; JOINED.
DR EMBL: M32997; AAA51978.1; JOINED.
DR EMBL: M32998; AAA51978.1; JOINED.
DR EMBL: AF027656; AB86604.1; -;
DR EMBL: M83573; AA859388.1; -;
DR PIR: A26941; A26941.
DR MIM: 118470; -;
DR InterPro: IPR001124; LBP-BPL_CETP.
DR Pfam: PF01273; LBP-BPL_CETP; 1.
DR Pfam: PF02886; LBP-BPL_CETP_C; 1.
DR SMART: SM00329; BP11; 1.
DR SMART: SM00329; BP12; 1.
DR PROSITE: PS00400; LBP-BPL_CETP; 1.
DR Lipid Transport: Cholesterol metabolism; Glycoprotein; Signal;
DR Atherosclerosis; Disease mutation.

```

FT SIGNAL 1 17 CHOLESTERYL ESTER TRANSFER PROTEIN.
FT CHAIN 18 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 459 459 D -> G (IN CETP DEFICIENCY).
FT VARIANT /FTID=VAR_004172.
FT CONFLICT 251 310 MISSING (IN REF. 5).
FT CONFLICT 422 422 I -> V (IN REF. 2).
FT SEQUENCE 493 AA: 54770 MW: 16D47AC0C99B063C CRC64:

Oy 1 RDGFLQMDGFGPEHLVDFLQSL 26
   |||||||
Db 468 RDGFLQMDGFGPEHLVDFLQSL 493

Query Match 100.0%; Score 26; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 2,5e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RDGFLQMDGFGPEHLVDFLQSL 26
   |||||||
Db 468 RDGFLQMDGFGPEHLVDFLQSL 493

RESULT 2
CETP_MACFA STANDARD; PRT; 493 AA.
ID CETP_MACFA
AC P47896;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
   1).
DE GN CETP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=92051355; PubMed=1931878;
RA Page M.E., Rehberg E.F., Marotti K.R., Melchior G.W.;
RT "Molecular cloning, sequence, and expression of cynomolgus monkey
RT cholesteryl ester transfer protein. Inverse correlation between
RT hepatic cholesteryl ester transfer protein mRNA levels and plasma
RT high density lipoprotein levels.";
RL Arterioscler. Thromb. 11:1759-1771(1991).
CC -1 FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1 SUBCELLULAR LOCATION: Extracellular.
CC -1 TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1 SIMILARITY: BELONGS TO THE BPL/CETP/LBP/PLTP FAMILY.
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CC
DR EMBL: M66343; AAA36840.1; -
DR InterPro: IPR001124; LBP_BPL_CETP.
DR Pfam: PF01273; LBP_BPL_CETP; 1.
DR Pfam: PF02886; LBP_BPL_CETP_C; 1.
DR SMART: SM00328; BP1; 1.
DR SMART: SM00329; BP12; 1.
DR PROSITE: PS00400; LBP_BPL_CETP; 1.
KW Lipid transport; cholesterol metabolism; glycoprotein; signal.
FT SIGNAL 1 17
FT CHAIN 18 493
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 493 AA: 54743 MW: 7682BEC2A8FAE0D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 493;
 Best Local Similarity 100.0%; Pred. No. 2.5e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFFPEHLVDFLOSL 26
 DB 468 RDGFLLLQMDFFPEHLVDFLOSL 493

RESULT 3
 CERP_MESAU STANDARD; PRT; 289 AA.
 AC P25914;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cholesteryl ester transfer protein (Lipid transfer protein I)
 DE (Fragment).
 GN CERP.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91154277; PubMed=1999438;
 RA Jiang X.C., Moulin P., Oulinet E., Goldberg J.J., Yacoub L.K.,
 RA Agellon L.B., Compton D., Schnitzer-Polokoff R., Tall A.R.,
 RT "Mammalian adipose tissue and muscle are major sources of lipid
 RT transfer protein mRNA".
 RL J. Biol. Chem. 266:4631-4639(1991).
 CC -1- FUNCTION: CERP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 CC OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE BPI/CERP/LBP/PLTP FAMILY.
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 CC -----
 CC EMBL: M63992; AAA37065.1; .
 DR PIR: A38700; A38700.
 DR InterPro: IPR001124; LBP_BPI_CERP.
 DR Pfam: PF01273; LBP_BPI_CERP; 1.
 DR SMART: SM00329; BPI2; 1.
 DR SMART: SM00329; BPI2; 1.
 DR PROSITE: PS00400; LBP_BPI_CERP; PARTIAL.
 KW Lipid transport; Cholesterol metabolism; Glycoprotein.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 1 1
 SQ SEQUENCE 289 AA: 32330 MW: CA91A0D83927747 CRC64;

Query Match 96.2%; Score 25; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1.6e-18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFFPEHLVDFLOSL 25
 DB 264 RDGFLLLQMDFFPEHLVDFLOSL 288

RESULT 4
 CERP_RABIT STANDARD; PRT; 497 AA.
 AC P22687;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
 DE I) (Fragment).
 GN CERP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89215620; PubMed=3244015;
 RA Nagashima M., McLean J.W., Lawn R.M.,
 RA "Cloning and mRNA tissue distribution of rabbit cholesteryl ester
 RA transfer protein".
 RL J. Lipid Res. 29:1643-1649(1988).
 CC -1- FUNCTION: CERP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 CC OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
 CC -1- SIMILARITY: BELONGS TO THE BPI/CERP/LBP/PLTP FAMILY.
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 CC -----
 CC EMBL: M27486; AAA11199.1; .
 DR InterPro: IPR001124; LBP_BPI_CERP.
 DR Pfam: PF01273; LBP_BPI_CERP; 1.
 DR SMART: SM00328; BPI1; 1.
 DR SMART: SM00329; BPI2; 1.
 DR PROSITE: PS00400; LBP_BPI_CERP; 1.
 KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
 FT CARBOHYD 497 497
 FT NON_TER 1 1
 FT SIGNAL 1 1
 FT CHAIN 2 497
 FT CARBOHYD 89 89 CHOLESTERYL ESTER TRANSFER PROTEIN.
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 497 AA: 54513 MW: E82944E1821D0332 CRC64;

Query Match 42.3%; Score 11; DB 1; Length 497;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLVDVFLQSL 26
 DB 487 HLVDVFLQSL 497

RESULT 5
 SNA_STRPR STANDARD; PRT; 421 AA.
 ID SNA_STRPR
 NC P34991;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (rel. 35, last annotation update)
 DE Plistinamycin IIA synthase subunit A (PIIA synthase subunit A).
 CC SNA.
 OS Streptomyces pristinaespiralis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RX NCBI_TaxID=38300;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SP92;
 RA MEDLINE=95394837; PubMed=7655509;
 RA Blanc V., Lagneaux D., Didier P., Faucher D., Debussche L., Blanchet F.;
 RT Cloning and analysis of structural genes from Streptomyces
 RT pristinaespiralis encoding enzymes involved in the conversion of
 RT Plistinamycin IIB to pristinamycin IIA (PIIA): PIIA synthase and
 RT NADH:riboflavin 5'-phosphate oxidoreductase.;
 RL J. Bacteriol. 177:5206-5214(1995).
 RL [2]
 RP SEQUENCE OF 1-18 AND 364-383.
 RX MEDLINE=95394836; PubMed=7655508;
 RA Thibaut D., Rabet N., Bisch D., Faucher D., Debussche L., Blanchet F.;
 RT Purification of the two-enzyme system catalyzing the oxidation of
 RT the D-proline residue of pristinamycin IIB during the last step of
 RT pristinamycin IIA biosynthesis.";
 RL J. Bacteriol. 177:5199-5205(1995).
 CC -1- FUNCTION: CATALYZES THE OXIDATION OF THE PROLINE RESIDUE OF
 CC PRISTINAMYCIN IIB (PIIB) TO PRISTINAMYCIN IIA (PIIA).
 CC -1- COFACTOR: FMN.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, SNA AND SNA.
 CC -1- SIMILARITY: BELONGS TO THE NTA/SNA/SOX/DSXA FAMILY OF
 CC MONOOXYGENASES.
 CC -----
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 CC -----
 DR EMBL: U21215; AAA83563.1; -
 DR InterPro: IPR002103; Bac_luciferase.
 DR Pfam: PF00296; bac_luciferase; 1.
 KW Oxidoreductase; Monooxygenase; Flavoprotein; FMN.
 KW INT_MET 0
 SO SEQUENCE 421 AA; 46373 MW; 341AD008A939CECA CRC64;

Query Match 26.9%; Score 7; DB 1; Length 421;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCFEHL 17
 DB 142 GCFEHL 148

RESULT 6
 Y240 ARATH STANDARD; PRT; 825 AA.
 AC 022224;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein At2g41620.
 GN AT2G41620 OR T32G6.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Euphyllophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 RX NCBI_TaxID=3702;
 RX [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CV COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronald C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Trallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT *Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.*;
 RL Nature 402:761-768(1999).
 RL [2]
 RP IDENTIFICATION ON 2D-GELS.
 RC STRAIN-CV COLUMBIA;
 RA Sarzin B., Tonella L., Marques K., Paesano S., Chane-Favre L.,
 RA Heller M., Sanchez J.-C., Hochstrasser D., Thiellement H.;
 RL Unpublished Observations (SEP-2000).
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 CC -----
 DR EMBL: AC002510; AB84345.1; -
 DR SEQUENCE 825 AA; 92304 MW; 1032300E814FDAB CRC64;

Query Match 26.9%; Score 7; DB 1; Length 825;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQSL 26
 DB 155 DFLQSL 161

RESULT 7
 VP2_BTVIA STANDARD; PRT; 961 AA.
 AC P12434;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Outer capsid protein VP2.
 GN S2.
 OS Bluetongue virus (serotype 1 / Isolate Australia).
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 RX NCBI_TaxID=10904;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88203217; PubMed=283466;
 RA Yamaguchi S., Fukusho A., Roy P.;
 RT *Complete sequence of VP2 gene of the bluetongue virus serotype 1
 RT (BTV-1).*;
 RL Nucleic Acids Res. 16:2725-2725(1988).
 RL [2]
 RP REVISIONS.
 RA Marshall J.;
 RL Submitted (FEB-1988) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88180013; PubMed=2833046;
 RX Gould A.R.;
 RT *Conserved and non-conserved regions of the outer coat protein, VP2,
 RT of the Australian bluetongue serotype 1 virus, revealed by sequence
 RT comparison to the VP2 of North American BTV serotype 10.*;
 RL Virus Res. 9:145-158(1988).
 CC -1- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)

CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
 CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
 CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X06464; CAA29772.1; -;
 DR EMBL: M21844; AAA42844.1; -;
 DR PIR: S03654; P2KRAU.
 DR InterPro: IPR001742; Orf1_VP2.
 DR Pfam: PF00898; Orf1_VP2; 1.
 DR Prodom: PD002938; Orf1_VP2; 1.
 KW Coat protein.
 FT CONFLICT 13 13 F -> V (IN REF. 3).
 FT CONFLICT 72 72 L -> V (IN REF. 3).
 FT CONFLICT 186 188 AVA -> LTL (IN REF. 3).
 FT CONFLICT 200 200 E -> D (IN REF. 3).
 FT CONFLICT 557 557 A -> D (IN REF. 3).
 FT CONFLICT 750 750 D -> N (IN REF. 3).
 SQ SEQUENCE 961 AA; 112113 MW; 1D140B03906ACD80 CRC64;
 Query Match 26.9%; Score 7; DB 1; Length 961;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 GPEPHLL 18
 Db 12 GPEPHLL 18
 RESULT 8
 VP2_BTIVS STANDARD; PRT; 961 AA.
 ID VP2_BTIVS
 AC P32508;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Outer capsid protein VP2.
 GN S2
 OS Bluetongue virus (serotype 1 / Isolate South Africa).
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID=10905;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 322-346 AND 492-503.
 RX MEDLINE-90261331; PubMed-2160764;
 RA Made-Evans A.M., Mertens P.P.C.;
 RT "Expression of the outer capsid protein, VP2, from a full length cDNA
 RT clone of genome segment 2 of bluetongue serotype 1 from South Africa,
 RT using both Sp6 and vaccinia expression systems and a comparison of
 RT the nucleic acid sequence of this segment with those of other
 RT serotypes".
 RL Virus Res. 15:213-230(1990).
 CC -1- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)
 CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
 CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
 CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
 CC PIR: A60014; P2KRSA.
 DR InterPro: IPR001742; Orf1_VP2.
 DR Pfam: PF00898; Orf1_VP2; 1.
 DR Prodom: PD002938; Orf1_VP2; 1.
 KW Coat protein
 SQ SEQUENCE 961 AA; 111937 MW; CB7853598EFD197A CRC64;
 Query Match 26.9%; Score 7; DB 1; Length 961;
 Best Local Similarity 100.0%; Pred. No. 9.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 GPEPHLL 18
 Db 12 GPEPHLL 18
 RESULT 9
 VP2_BTIVS STANDARD; PRT; 961 AA.
 ID VP2_BTIVS
 AC 006597;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Outer capsid protein VP2.
 GN S2
 OS Bluetongue virus (serotype 1 / Isolate South Africa-vaccine).
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID=36422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91021485; PubMed-2171239;
 RA Gould A.R., Pritchard L.I.;
 RT "Relationships amongst bluetongue viruses revealed by comparisons of
 RT capsid and outer coat protein nucleotide sequences".
 RT Virus Res. 17:31-52(1990).
 CC -1- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)
 CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
 CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
 CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
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 CC -----
 DR EMBL: X55800; CAA39322.1; -;
 DR PIR: A60017; A60017.
 DR InterPro: IPR001742; Orf1_VP2.
 DR Pfam: PF00898; Orf1_VP2; 1.
 DR Prodom: PD002938; Orf1_VP2; 1.
 KW Coat protein.
 SQ SEQUENCE 961 AA; 111756 MW; 361405246E7E946 CRC64;
 Query Match 26.9%; Score 7; DB 1; Length 961;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 GPEPHLL 18
 Db 12 GPEPHLL 18
 RESULT 10
 YD12_ECOLI STANDARD; PRT; 96 AA.
 ID YD12_ECOLI
 AC P76207;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yd12.
 GN YD12 OR B1724 OR Z2753 OR EC52430.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562; 83334;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-0157:H7 / EDL933 / ATCC 700927;
RX MEDLINE-21074935; PubMed-11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Iln J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-0157:H7 / RIMD 0509952;
RX MEDLINE-21156231; PubMed-11236796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tode T.,
RA Ikida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kohara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN
RP
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```

```

CC -----
CC EMBL: AE000267; AAC74794.1; -
CC DR EMBL: AE005395; AAG56710.1; -
CC DR EMBL: AP002558; BAB35853.1; -
CC DR Ecogene; EG33985; yd12.
CC KW Hypothetical protein; Complete proteome
CC SEQUENCE 96 AA; 10865 MW; 722C0F845B91A855 CRC64;
SQ
```

```

Query Match          23.1%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 1 RDGFL 6
ID 111111
Db 32 RDGFL 37
```

```

RESULT 11
Y638_TREPA STANDARD: PRT; 144 AA.
AC 083645;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein TP0638.
GN TP0638.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLS;
RX MEDLINE-98332770; PubMed-9665876;
```

```

RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
RN
RP -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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```

```

CC -----
CC EMBL: AE001239; AAC65625.1; -
CC DR TIGR; TP0638; -
CC KW Hypothetical protein; Transmembrane; Complete proteome.
CC FT TRANSMEM 7 29 POTENTIAL.
CC FT TRANSMEM 51 73 POTENTIAL.
CC FT TRANSMEM 85 107 POTENTIAL.
CC FT TRANSMEM 122 139 POTENTIAL.
CC SEQUENCE 144 AA; 15394 MW; 7D93DA921FC7699 CRC64;
SQ
```

```

Query Match          23.1%; Score 6; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 17 LAYDFL 22
ID 111111
Db 71 LAYDFL 76
```

```

RESULT 12
MAUF_METFL STANDARD: PRT; 153 AA.
AC 050418; 050419;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Methylamine utilization protein mauF (Fragments).
GN MAUF.
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; beta subdivision; Methylobacillus group.
OC Methylobacillus.
OX NCBI_TaxID=405;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-KT / ATCC 51484 / DSM 6875 / VKM B-1610;
RX MEDLINE-95362696; PubMed-7635847;
RA Gak E.R., Chistoserdov A.Y., Lidstrom M.E.;
RT Cloning, sequencing, and mutation of a gene for azurin in
RT Methylobacillus flagellatum KT-?;
RL J. Bacteriol. 177:4575-4578(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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```

```

CC -----
CC EMBL: L37428; AAC41467.1; -
CC DR EMBL; AF188997; AAC41468.1; -
```

KH Transmembrane. 57
 FT TRANSMEM 58 POTENTIAL.
 FT TRANSMEM 78 POTENTIAL.
 FT TRANSMEM 114
 FT TRANSMEM 127
 FT TRANSMEM 147
 FT TRANSMEM 153 AA: 15761 MW: 20068D9C3A706674 CRC64:

Query Match 23.1% Score 6: DB 1: Length 153:
 Best Local Similarity 100.0% Pred. No. 20:
 Matches 6: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GFLULL 7
 DB 131 GFLULL 136

RESULT 13
 ID NCBI_RHIME STANDARD: PRT: 167 AA.
 AC P56897:
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DE NADH dehydrogenase 1 chain B 2 (EC 1.6.5.3) (NADH-ubiquinone
 oxidoreductase chain B 2).
 GN N00B2 OR RA0833 OR SMA1532.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSMA (megaplasmid 1).
 OC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group:
 OC Rhizobiaceae: Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=41;
 RA Ptenoky P., Jady B., Chellapilla K.P., Bartra F., Kiss E.;
 RT "Rhizobium meliloti carries two sets of nuo genes."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RA MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Bariloy-Hubler F., Bowser L., Capela D., Gilbert F., Gouzy J.,
 RA Gurjel M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kaimen S., Keeling D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 Sinorhizobium meliloti pSMA megaplasmid."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 20 kDa SUBUNIT FAMILY.
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 CC -----
 DR EMBL: AJ245399; CAB51630.1; -
 DR EMBL: AE007270; AAK65491.1; -
 DR EMBL: AF000266; Interferon_1.
 DR Pfam: PF01058; oxidored_96; 1.
 DR Oxidoreductase: NAD: Ubiquinone, Iron-sulfur, 4Fe-4S, Plasmid;
 KW Complete proteome.
 FT METAL 38 38 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 39 39 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 103 103 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 132 132 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 167 167 S -> L (IN REF. 1).
 FT CONFLICT 167 167

SO SEQUENCE 167 AA: 18247 MW: 04D82AAED624D8CF CRC64:

Query Match 23.1% Score 6: DB 1: Length 167:
 Best Local Similarity 100.0% Pred. No. 21:
 Matches 6: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLULL 8
 DB 142 GFLULL 147

RESULT 14
 ID INAA_HUMAN STANDARD: PRT: 189 AA.
 AC P05014; P13358;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interferon alpha-4 precursor (interferon alpha-4b) (interferon
 alpha-M1) (interferon alpha-75).
 GN IFNA4
 OS Homo sapiens (human).
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 OC Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86037205; PubMed=4057246;
 RA Henko K., Brosius J., Fujisawa J., Fujisawa J.-I., Haynes J.R.,
 RA Hochstadt J., Kovacic T., Pasek M., Schamboeck A., Schmid J.,
 RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;
 RT "Structural relationship of human interferon alpha genes and
 pseudogenes."
 RL J. Mol. Biol. 185:227-260(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84307815; PubMed=6089830;
 RA Linane A.W., Bellharz M.W., McMullen G.L., Macreadie I.G.,
 RA Murphy M., Nisbet I.T., Novitski C.E., Woodrow G.C.;
 RT "Nucleotide sequence and expression in E. coli of a human interferon-
 alpha gene selected from a genomic library using synthetic
 oligonucleotides."
 RL Blochm. Int. 8:725-732(1984).
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
 ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
 A PROTEIN KINASE AND AN OLIGONUCLEOTIDE SYNTHETASE.
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X02955; CAA26701.1; -
 DR EMBL: M27318; AAA52726.1; -
 DR PIR: E23753; IYH04B.
 DR HSSP: P01563; ZHE.
 DR MIM: 147564; -
 DR InterPro: IPR000471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; Ifabd; 1.
 DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
 DR Cyclokin; Antiviral; Multigene family; Signal.
 FT SIGNAL 23 23
 FT CHAIN 24 189 INTERFERON ALPHA-4.
 FT DISULFID 24 122 BY SIMILARITY.

FT DISULFID 52 162 BY SIMILARITY.
AC CONFLICT 74 74 T -> A (IN REF. 2).
FT CONFLICT 137 137 V -> E (IN REF. 2).
SO SEQUENCE 189 AA: 21808 MW: 4198P9CC8E2AE80C CRC64;

Query Match 23.1%; Score 6; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DPGFPE 15
DB 58 DPGFPE 63

RESULT 15
KAD_YEREN STANDARD: PRT: 214 AA.
ID P43412;
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK.
OS Versinia enterocolitica.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Versinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=6471/76 / SEROTYPE O:3;
RX MEDLINE=96100456; PubMed=8559076;
RA Skurnik M., Venho R., Toivanen P., Al-Hendy A.;
RT A novel locus of Versinia enterocolitica serotype O:3 involved in
RT lipopolysaccharide outer core biosynthesis.";
RL M01. Microbiol. 17:575-594(1995).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
CC EMBL: Z47767; CAA87696.1; -
DR HSSP: P05082; IAKE.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase.1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin.1.
DR PROSITE: PS00113; ADENYLATE_KINASE; FALSE_NEG.
KW Transferase; Kinase; ATP-binding.
FT NP_BIND 7 15 ATP (BY SIMILARITY).
FT SEQUENCE 214 AA: 23755 MW: 55030EA82BDD04C7 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLL 6
DB 78 RDGFLL 83

RESULT 16

KAD_YERPE STANDARD: PRT: 214 AA.
ID KAD_YERPE
AC O69172;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR YPO3118.
OS Versinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller-Lehmann H.;
RT "Adenylate kinase from Versinia pestis and Escherichia coli:
RT structural relatedness and differences linked to growth properties of
RT these two organisms.";
RT Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
RL [2]

RP SEQUENCE FROM N.A.
RX STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Partridge M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Farraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Hollroyd S., Jørgensen K., Karlyshev A.V.,
RA Leather S., Moutle S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Versinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
CC EMBL: AF065382; AAC17426.1; -
DR EMBL: AJ414155; CAC92354.1; -
DR HSSP: P05082; IAKE.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase.1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin.1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; ATP-binding; Complete proteome.
FT NP_BIND 7 15 ATP (BY SIMILARITY).
FT SEQUENCE 214 AA: 23672 MW: 36D9FD1558E86CA CRC64;

Query Match 23.1%; Score 6; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLL 6
DB 78 RDGFLL 83

RESULT 17
KADB_METTH STANDARD: PRT: 234 AA.
ID KADB_METTH
AC 027728;

```

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA repair and recombination protein radB.
GN RADB OR WH1693.
OS Methanobacterium thermoautotrophicum.
OC Archaea: Euryarchaeota: Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RA MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier R., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDonnell S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT *Complete genome sequence of Methanobacterium thermoautotrophicum
RT delah: functional analysis and comparative genomics.*;
RL J. Bacteriol. 179:7135-7153(1997).
CC -1- FUNCTION: Involved in DNA repair and in homologous recombination.
CC May regulate the cleavage reactions of the branch-structured DNA.
CC Has a very weak ATPase activity that is not stimulated by DNA.
CC Binds DNA but does not promote DNA strand exchange (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC RECA-LIKE PROTEIN FAMILY.
CC RADB SUBFAMILY.
CC -----
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CC -----
DR EMBL: AE000927; AAB86165.1; -
DR HSSP: P03017; 28EB.
DR InterPro: IPR001553; RECA.
DR PRINTS: PR00142; RECA.
DR PROSITE: PS50162; RECA_2; 1.
KW DNA damage; DNA recombination; ATP-binding; DNA-binding;
KW Complete proteome.
FT NP-BIND 37
FT ATP (POTENTIAL).
SQ SEQUENCE 234 AA; 26193 MW; ED4D957A012AADI1 CRC64;

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Query Match 23.1%; Score 6; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 FULLQM 9
DB 150 FULLQM 155

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RESULT 18
FABI_BACSU STANDARD; PRT; 258 AA.
AC P54616; O31621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Enoyl-(acyl-carrier-protein) reductase [NADH] (EC 1.3.1.9) (NMDH-
DE dependent enoyl-ACP reductase) (Cold-shock induced protein 15) (CS115)
DE (Vegetative protein 241) (VEG241).
GN FABI.
OS Bacillus subtilis.
OC Bacteria: Firmicutes: Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.

```

OX NCBI_TaxID=1423;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-21.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT *Cold shock stress-induced proteins in Bacillus subtilis.*;
RL J. Bacteriol. 178:4611-4619(1996).
RN [3]
RP SEQUENCE OF 1-15.
RC STRAIN=1558;
RX MEDLINE=97443988; PubMed=9298659;
RA Anelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT *First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis.*;
RL Electrophoresis 18:1451-1463(1997).
CC -1- CATALYTIC ACTIVITY: Acyl-(acyl-carrier protein) + NAD(+) = trans-
CC 2,3-dehydroacyl-(acyl-carrier protein) + NADH.
CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
CC -1- INDUCTION: BY COLD SHOCK.
CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC -----
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CC -----
DR EMBL: Z99110; CAB3029.1; AL1_INIT.
DR HSSP: Z99132; IDP1.
DR Subtilist; BG13152; FABI.
DR InterPro: IPR002198; ADH-short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00081; GDHRDH.
KW Oxidoreductase; NAD; Fatty acid biosynthesis; Complete proteome.
FT NP-BIND 11
FT CONFLICT 37
FT NAD (BY SIMILARITY).
FT S -> Q (IN REF. 2).
SQ SEQUENCE 258 AA; 27873 MW; 097667168B3F0470 CRC64;

```

Query Match 23.1%; Score 6; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 RDGFLL 6
DB 112 RDGFLL 117

```

RESULT 19
CYST_MESVI STANDARD; PRT; 265 AA.
AC O9MUG;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable sulfate transport system permease protein cyst.
GN CYST.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota: Viridiplantae: Streptophyta: Mesostigmatophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN-NIES-296;
RX MEDLINE-20150907; PubMed-10688199;
RA Lemieux C., Otis C., Tumele M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -1- FUNCTION: COULD BE PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM FOR SULFATE AND THIOSULFATE. PROBABLY RESPONSIBLE FOR THE
TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST; INTEGRAL MEMBRANE PROTEIN
(PROBABLE).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTM
SUBFAMILY.
CC -----
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CC -----
CC EMBL: AF166114; AAF43879.1; -;
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00528; BPD_transp.1;
DR PROSITE: PS00402; BPD_TRANS-1NN_MEMBER; 1;
KW Chloroplast; Sulfate transport; Transp.; Transmembrane.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 130 150 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
SQ SEQUENCE 269 AA; 29674 MW; B20DBFDDP486C59 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSLIS 26
Db 122 FLOSLIS 127
IIIIII
MAUF 20
MAUF METME STANDARD; PRT; 285 AA.
AC OS0230;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Methylamine utilization protein mauF.
GN MAUF.
OS Methylolophilus methylotrophus (Bacterium W3A1).
OC Bacteria; Proteobacteria; beta subdivision; Methylolophilus group;
OC Methylolophilus.
OX NCBI_TaxID=17;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94292427; PubMed-8021186;
RA Chostakov A.Y., McInliffe W.S., Mathews F.S., Lidstrom M.E.;
RT "Organization of the methylamine utilization (mau) genes in
Methylolophilus methylotrophus W3A1-NS";
RL J. Bacteriol. 176:4073-4080(1994).
CC -1- PATHWAY: METHYLAMINE UTILIZATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
CC EMBL: L26407; AAB46947.1; -;
DR Transmembrane-
KW TRANSMEM 39 59 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 145 165 POTENTIAL.
FT TRANSMEM 188 208 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 265 285 POTENTIAL.
SQ SEQUENCE 285 AA; 30429 MW; 7A783207084879AD CRC64;

Query Match 23.1%; Score 6; DB 1; Length 285;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGFLL 7
Db 268 DGFLL 273
IIIIII
RESULT 21
Y74_PSEAE STANDARD; PRT; 286 AA.
ID Y74_PSEAE
AC 068826;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PA3474.
GN PA3474.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RA Xie G., Jensen R.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE-20437357; PubMed-10984043;
RA Slover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Brody L.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Smith K.A., Spencer S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -----
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CC -----
CC EMBL: AF054868; AAC08597.1; -;
DR EMBL: AE004768; AAG06862.1; -;
DR InterPro: IPR000620; DUF6.
DR Pfam: PF00892; DUF6; 2;
CC -----
CC Hypothetical protein; Complete proteome.
FT CONFLICT 27 27 D -> G (IN REF. 1).

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FT CONFLICT 35 35 R -> P (IN REF. 1)
FT CONFLICT 236 236 A -> V (IN REF. 1)
FT CONFLICT 235 235 N -> Y (IN REF. 1)
FT CONFLICT 261 261 P -> L (IN REF. 1)
FT CONFLICT 264 264 A -> V (IN REF. 1)
FT CONFLICT 282 282 R -> G (IN REF. 1)
SQ SEQUENCE 286 AA; 31834 MW; C84001C649BBE9CE CRC64;

Query Match 23.1%; Score 6; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLILO 8
Db 139 GFLILO 144

RESULT 22
ID TF_RAT STANDARD; PRT; 295 AA.
AC P42533;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 36, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III).
GN CF3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RA Rosenfield C., Guba A., Nemerson Y., Taubman M.B.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC
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CC
DR EMBL: U07619; AAA16966.1; -.
DR HSSP: P13726; TRFH.
DR InterPro: IPR000182; Cytok_receptor_2.
DR InterPro: IPR00137; Tissue_fac.
DR Pfam: PF01108; Tissue_fac.1.
DR PRINTS: PR00146; TISSUEFACTOR.
DR PROSITE: PS00621; TISSUE_FACTOR.1.
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 295 TISSUE FACTOR.
FT DOMAIN 29 252 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 253 275 POTENTIAL.
FT DOMAIN 276 295 CYTOPLASMIC (POTENTIAL).
FT SITE 246 248 WKS MOTIF.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT DISULFID 76 84 BY SIMILARITY.
FT DISULFID 219 242 BY SIMILARITY.
FT LIPID 276 276 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 295 AA; 33443 MW; BE4C15B4E362BD48 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLILO 8
Db 19 GFLILO 24

RESULT 23
END4_BACHD
ID END4_BACHD STANDARD; PRT; 298 AA.
AC Q9KD33;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV).
GN NEO OR BHL386.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Endonuclease IV plays a role in DNA repair. It cleaves
CC phosphodiester bonds at apurinic or apyrimidinic sites (AP sites)
CC to produce new 5' ends that are base-free deoxyribose 5-phosphate
CC residues. It preferentially attacks modified AP sites created by
CC bleomycin and neocarzinostatin (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC 3'-phosphooligonucleotide end-products.
CC -1- COFACTOR: Binds 3 zinc ions (By similarity).
CC -1- SIMILARITY: BELONGS TO AP ENDONUCLEASES FAMILY 2.
CC
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CC
DR EMBL: AP001511; BAB05105.1; -.
DR HSSP: P12638; 10TW.
DR InterPro: IPR001719; AP_endonuclease_2.
DR Pfam: PF01261; AP_endonuclease2.1.
DR SMART: SM00518; AP2EC: 1.
DR PROSITE: PS00729; AP_NUCLEASE_F2_1; 1.
DR PROSITE: PS00730; AP_NUCLEASE_F2_2; 1.
DR PROSITE: PS00731; AP_NUCLEASE_F2_3; 1.
KW Hydrolyase; Nuclease; Endonuclease; DNA repair; Metal-binding; Zinc;
KW Complete proteome.
FT METAL 70 70 ZINC 1 (BY SIMILARITY).
FT METAL 111 111 ZINC 1 (BY SIMILARITY).
FT METAL 146 146 ZINC 1 AND 2 (BY SIMILARITY).
FT METAL 180 180 ZINC 2 (BY SIMILARITY).
FT METAL 183 183 ZINC 3 (BY SIMILARITY).
FT METAL 215 215 ZINC 3 (BY SIMILARITY).
FT METAL 228 228 ZINC 3 (BY SIMILARITY).

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FT METAL 230 230 ZINC 3 (BY SIMILARITY).
 FT METAL 260 260 ZINC 2 (BY SIMILARITY).
 SQ SEQUENCE 298 AA: 32997 MW: 9A25ED881A75554B CRC64:

Query Match
 Best Local Similarity 100.0%; Score 6; DB 1; Length 298;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLOS 24
 |||||
 Db 90 VDFLOS 95

RESULT 24
 ID PLSX_BACSU STANDARD: PRT: 333 AA.
 AC P71018; O34561;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fatty acid/phospholipid synthesis protein plsx.
 GN PLSX.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE OF 66-333 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96326321; PubMed=8759840;
 RA Morbidon H.R. de Mendoza D.; Cronan J.E. Jr.;
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
 FT lipid biosynthesis genes."
 RL J. Bacteriol. 178:4794-4800(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Foulger D.; Errington J.;
 RT Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: NOT KNOWN. PROBABLY INVOLVED IN FATTY ACID OR
 CC PHOSPHOLIPID SYNTHESIS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE PLSX FAMILY.
 CC -----
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 CC -----
 CC EMBL: U59433; AAC44305.1; -
 DR EMBL: Y13937; CAB47428.1; -
 DR EMBL: Z99112; CAB13462.1; -
 DR Subtilist; Bg11843; plsx.
 DR InterPro: IPR003664; FA_synthesis.
 DR Pfam: PF02504; FA_synthesis; 1.
 DR Fatty acid biosynthesis; Phospholipid biosynthesis; Complete proteome.
 FT CONFLICT 66 74 DEPRVAVR -> NMRSVPCA (IN REF. 1).
 FT SEQUENCE 333 AA: 35763 MW: 2P66A2E8A034199E CRC64;

Query Match
 Best Local Similarity 100.0%; Score 6; DB 1; Length 333;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFILL 7
 |||||
 Db 133 DGFILL 138

RESULT 25

AUP1_MOUSE
 ID AUP1_MOUSE STANDARD: PRT: 410 AA.
 AC P70295;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ancient ubiquitous protein 1 precursor.
 GN AUP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=96411693; PubMed=8812468;
 RA Tang W.; Weber J.S.; Bashir R.; Bushby K.; Meisler M.H.;
 RT "Aup1, a novel gene on mouse chromosome 6 and human chromosome 2p13."
 RL Genomics 36:366-368(1996).
 CC -!- TISSUE SPECIFICITY: UBQUITOUS.
 CC -!- SIMILARITY: BELONGS TO THE AUP1 FAMILY.
 CC -----
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 CC -----
 CC EMBL: U41736; AAC52839.1; -
 DR MGD; MGI:107789; Aup1.
 DR InterPro: IPR003892; CUE.
 DR Pfam: PF02845; CUE; 1.
 DR SMART: SM00546; CUE; 1.
 KW signal.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 410 ANCIENT UBQUITOUS PROTEIN 1.
 FT SEQUENCE 410 AA: 46121 MW: E7D070CEB296B5B CRC64;

Query Match
 Best Local Similarity 100.0%; Score 6; DB 1; Length 410;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFILL 7
 |||||
 Db 21 DGFILL 26

RESULT 26
 ID AP47_CAEEL STANDARD: PRT: 422 AA.
 AC P35602;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Clathrin coat assembly protein AP47 (clathrin coat associated protein
 DE AP47) (Golgi adaptor Ap-1 47 kDa protein) (HAI 47 kDa subunit)
 DE (clathrin assembly protein assembly protein complex 1 medium chain).
 GN UNC-101.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94116859; PubMed=8288128;
 RA Lee J.; Jongeward G.D.; Sternberg P.W.;
 RT "unc-101, a gene required for many aspects of Caenorhabditis elegans
 development and behavior, encodes a clathrin-associated protein."
 RL Genes Dev. 8:60-73(1994).

--
CC
CC
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOSOLIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC
CC -1- FUNCTION: REQUIRED FOR MANY ASPECTS OF DEVELOPMENT AND BEHAVIOR,
CC INCLUDING NEGATIVE REGULATION OF VULVAL DIFFERENTIATION.
CC
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX I (AP-1) IS A HETEROPENTAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19).
CC
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CC CYTOSOLIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.
CC
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
CC
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CC
CC EMBL: L26291; AAA72418.1;
CC DR InterPro: IPRO01392; Adap_comp_sub;
CC DR Pfam: PF00928; Adap_comp_sub; 1.
CC DR PRINTS: PR00314; CLATHRIADPT.
CC DR PROSITE: PS00990; CLAT_ADAPTOR_M.1; 1.
CC DR PROSITE: PS00991; CLAT_ADAPTOR_M.2; 1.
CC KM Coated pits.
CC SQ SEQUENCE 422 AA: 48297 MW: D57BF5D1EF496D50 CRC64;

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Query Match Similarity      23.1%; Score 6; DB 1; Length 422;
Best Local Similarity      100.0%; Pred. No. 49;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Oy      9 MORGFP 14
          |||||
Db      118 MDGFP 123

RESULT 27
ID      AIM2_HUMAN
AC      G9Y605:
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DE      adaptor-related protein complex 1 mu 2 subunit (Clathrin coat
DE      assembly protein AP47 2) (Clathrin coat associated protein AP47 2)
DE      (soluble adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit 2) (Clathrin
DE      assembly protein assembly protein complex 1 medium chain 2) (AP-mu
DE      chain family member mu1b).
CN      APM2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
[1]
RM      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RA      MIMLINE=9268457; PubMed=10338135;
RA      OMIM H., Tomemori T., Nakatsu F., Okazaki Y., Aguilar R.C.,
RA      Feelsch H., Mellman I., Saito T., Shirasawa T., Bonficio J.S.;
RA      mu1b, a novel adaptor medium chain expressed in polarized epithelial
RA      cells.;
RT      FEELS Lett. 449:215-220(1999).
CC      -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC      TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC      COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC      MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC      AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.

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```
CC CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER  
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN  
CC (APB7) AND A SMALL CHAIN (APB19).  
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SUBROUTING THE  
CC CYTOSOLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.  
CC -1- PTM: AUTOPHOSPHORYLATED (POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS  
CC FAMILY.  
CC -----  
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CC -----  
DR DR EMBL: AF020797; AAD5870.2; -.  
DR InterPro: IPR001392; Adap.comp.sub.  
DR Pfam: PF009528; Adap.comp.sub; 1.  
DR PRINTS: PR00314; CLATHRINADPT.  
DR PROSITE: PS00990; CLAT_ADAPTOR_M_1; 1.  
DR PROSITE: PS00991; CLAT_ADAPTOR_M_2; 1.  
RW Coated pits; Phosphorylation.  
SO SEQUENCE 423 AA; 48108 MW; A3F6FDf8659DDcF7 CRC64;  
  
Query Match 23.1%; Score 6; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 9 MDGFP 14  
|||||  
Db 118 MDGFP 123  
  
RESULT 28  
A1M2_MOUSE  
A1M2_MOUSE STANDARD; PRT: 423 AA.  
AC Q3WVPI; Q39LA4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Adapter-related protein complex 1 mu 2 subunit (Clathrin coat  
DE assembly protein AP47 2) (Clathrin coat associated protein AP47 2)  
DE (Gold adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit 2) (Clathrin  
DE assembly protein assembly protein complex 1 medium chain 2) (AP-mu  
DE chain family member mu1b).  
NM APM2.  
GN Apm2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C37BL/6J;  
RA MEDLINE=99268457; PubMed=10338135;  
RA Ohno H., Tomemori T., Nakatsu F., Okazaki Y., Aguilar R.C.,  
RA Feilsch H., Melman I., Salto T., Shirasawa T., Bonifacio J.S.;  
RT "mlb," a novel adaptor medium chain expressed in polarized epithelial  
RT cells.";  
RL FEBS Lett. 449:215-220(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20108786; PubMed=10640811;  
RA Nakatsu F., Kadohira T., Gilbert D.J., Jenkins N.A., Kakuta H.,  
RA Copeland N.G., Salto T., Ohno H.;  
RT "Genomic structure and chromosome mapping of the genes encoding  
RT clathrin-associated adaptor medium chains mu 1a (Ap1m1) and mu 1b  
RL (Ap1m2)." ;  
RL Cytogenet. Cell Genet. 87:53-58(1999).  
RN [3]  
RP SEQUENCE FROM N.A.
```

Oy	9 MDEGFP 14
Db	118 MDGFPP 123
RESULT:	28
ID	AIM2_MOUSE
TID	AIM2_MOUSE
RC	Q9WVF1; Q99PLA;
Dt	16-OCT-2001 (Rel. 40, Created)
Bt	16-OCT-2001 (Rel. 40, Last sequence update)
De	Adaptor-related protein complex 1 mu 2 subunit (Clathrin coat assembly-related protein AP47 2) (Clathrin adaptor Ap-1 47 kDa protein) [HAI_47 Kda subunit 2] (AP-mu chain family member mu1B).
DE	(solg1 adaptor Ap-1 47 kDa protein) [HAI_47 Kda subunit 2] (Clathrin assembly protein assembly protein complex 1 medium chain 2) (Ap-mu chain family member mu1B).
Gm	APIM2.
O5	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cc Eumetazoa; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_Taxid=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J;
RX	MEDLINE=96268457; PubMed=10338135; RA Ohno H., Tomemori T., Nakatsu F., Okasaki Y., Aguilar R.C., Ra Poelsch H., Mellman I., Salto T., Shirasawa T., Bonfischino J.S.; RT "mlnB, a novel adaptor medium chain expressed in polarized epithelial cells." ; RL FEBS Lett. 449:215-220(1999). RN [2] RP SEQUENCE FROM N.A. RX MEDLINE=20108786; PubMed=10640811; RA Nakatsu F., Kadophila T., Gilbert D.J., Jenkins N.A., Kakuta H., Ra Copeland N.G., Salto T., Ono H.; RT "Genomic structure and chromosome mapping of the gene encoding clathrin associated adaptor medium chains mu 1k (Apiiml) and mu 1b (Apiim2)." ; RL Cytogenet. Cell Genet. 87:53-58(1999). RN [3] RP SEQUENCE FROM N.A.

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DR EMBL: U75930; AAC59064.1; ..
 KM Transcription regulation
 SO SEQUENCE 489 AA; 55590 MW; 999A7699EE7AB0D8 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 489;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 FEPEHL 18
 DB 479 FEPEHL 484

RESULT 31
 A2AP_HUMAN STANDARD; PRT; 491 AA.
 AC P08697;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-P1)
 DE (Alpha-2-Ap).
 GN SERPINE2 OR PLI OR AAP.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TONE M., Kikuno R., Kume T., Kikuno R., Hashimoto-Gotoh T.;
 RT "Structure of human alpha 2-plasmin inhibitor deduced from the cDNA
 RT sequence.";
 RL J. Biochem. 102:1033-1041(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-88320531; PubMed-3166140;
 RA Hirosewa S., Nakamura Y., Mura O., Suni Y., Aoki N.;
 RT "Organization of the human alpha 2-plasmin inhibitor gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:6836-6840(1988).
 RN [3]
 RP ERRATUM.
 RA Hirosewa S., Nakamura Y., Mura O., Suni Y., Aoki N.;
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1612-1613(1989).
 RN [4]
 RP SEQUENCE OF 4-491 FROM N.A.
 RA MEDLINE-87109313; PubMed-2433286;
 RA Holmes W.E., Nelles L., Lijnen H.R., Collen D.;
 RT "Primary structure of human alpha 2-antiplasmin, a serine protease
 RT inhibitor (serpin).";
 RL J. Biol. Chem. 262:1659-1664(1987).
 RN [5]
 RP SEQUENCE OF 218-491 FROM N.A.
 RA MEDLINE-87137400; PubMed-3818581;
 RA Suni Y., Nakamura Y., Aoki N., Sakai M., Muramatsu M.;
 RT "Structure of the carboxyl-terminal half of human alpha 2-plasmin
 RT inhibitor deduced from that of cDNA.";
 RL J. Biochem. 100:1399-1402(1986).
 RN [6]
 RP SEQUENCE OF 40-491.
 RA MEDLINE-87275946; PubMed-2440681;
 RA Lijnen H.R., Holmes W.E., van Hoel B., Wiman B., Rodriguez H.,
 RA Collen D.;
 RT "Amino-acid sequence of human alpha 2-antiplasmin.";
 RL Eur. J. Biochem. 166:565-574(1987).
 RN [7]

RP SEQUENCE OF 40-43.
 RX MEDLINE-78023887; PubMed-21075;
 RA Wiman B., Collen D.;
 RT "Purification and characterization of human antipiasmin, the
 RT fast-acting plasmin inhibitor in plasma.";
 RL Eur. J. Biochem. 78:19-26(1977).
 RN [8]
 RP SEQUENCE OF 28-52.
 RX TISU8E-plasma;
 RX MEDLINE-93050153; PubMed-1385210;
 RA Christensen S., Sottrup-Jensen L.;
 RT "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence.";
 RN FEBS Lett. 312:100-104(1992).
 RN [9]
 RP ACTIVE SITES.
 RX MEDLINE-88290696; PubMed-2456616;
 RA Potempa J., Shieh B.-H., Travis J.;
 RT "Alpha-2-antiplasmin: a serpin with two separate but overlapping
 RT reactive sites.";
 RL Science 241:699-700(1988).
 RN [10]
 RP SEQUENCE OF 481-491, AND SULFATION.
 RX MEDLINE-87137577; PubMed-2434496;
 RA Horton G., Fox K.F., Toren P.C., Straus A.W.;
 RT "Sulfation of a tyrosine residue in the plasmin-binding domain of
 RT alpha 2-antiplasmin.";
 RL J. Biol. Chem. 262:3082-3085(1987).
 CC -1- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND
 CC TRYPSIN, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC *****
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DR EMBL: D00116; BAA0070.1; ..
 DR EMBL: D00174; BAA00124.1; ..
 DR EMBL: M20786; AAA51554.1; ..
 DR EMBL: M20782; AAA51554.1; JOINED.
 DR EMBL: M20783; AAA51554.1; JOINED.
 DR EMBL: M20784; AAA51554.1; JOINED.
 DR EMBL: M20785; AAA51554.1; JOINED.
 DR EMBL: J02654; AAA35543.1; ..
 DR PIR: A24708; A24708.
 DR PIR: A26684; A26684.
 DR PIR: A31402; A31402.
 DR PIR: A32163; A32163.
 DR PIR: A41304; A41304.
 DR PIR: S00068; S00068.
 DR HSSP: P01008; LANT.
 DR SWISS-2DPAGE: P08697; HUMAN.
 DR MIM: 262850; ..
 DR InterPro: IPR000215; Serpin.
 DR Pfam: PF00079; serpin.1.
 DR SMART: SM00093; SERPIN.
 DR PROSITE: PS00284; SERPIN.1.
 KM Serpin: Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 KM Sulfation.

FT SIGNAL 1 27
 FT PROSEP 28 39
 FT CHAIN 40 491
 FT ACT_SITE 403 404
 FT ACT_SITE 404 405
 FT MOD_RES 484 484
 FT CARBOHYD 126 126
 FT CARBOHYD 295 295
 FT CARBOHYD 309 309
 FT CARBOHYD 316 316
 FT CONFLICT 33 33

ALPHA-2-ANTIPLASMIN.
 REACTIVE BOND (FOR PLASMIN).
 REACTIVE BOND (FOR CHYMOTRYPSIN).
 SULFATION.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-> W (IN REF. 1).

FT CONFLICT 49 49 L -> G (IN REF. 6).
 FT CONFLICT 105 105 N -> D (IN REF. 6).
 FT CONFLICT 289 289 H -> D (IN REF. 4).
 FT CONFLICT 408 408 S -> G (IN REF. 6).
 FT CONFLICT 455 455 D -> N (IN REF. 6).
 SO SEQUENCE 491 AA: 54565 MW: 389A1C9B9A53CB CRC64;

Query Match 23.1% Score 6; DB 1; Length 491;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DEFQSL 25
 Db 453 DEFQSL 460

RESULT 32
 CPDF CANFA
 ID CPDF CANFA STANDARD; PRT: 499 AA.
 AC 029473; 002859;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytochrome P450 2D15 (EC 1.14.14.1) (CYP2D15) (P450 DUT2).
 GN CYP2D15.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=98162957; PubMed=7786018;
 RA Sakamoto K., Kitita S., Baba T., Nakamura Y., Yamazoe Y., Kato R.,
 RA Takahara A., Matsubara T.,
 RT "A new cytochrome P450 form belonging to the CYP2D in dog liver
 RT microsomes: purification, cDNA cloning, and enzyme
 RT characterization".
 RL Arch. Biochem. Biophys. 319:372-382(1995).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BEAGLE;
 RX MEDLINE=98162950; PubMed=9504424;
 RA Tasaki T., Nakamura A., Itoh S., Ohashi K., Yamamoto Y., Masuda M.,
 RA Iwata H., Kazusaka A., Kametaki T., Fujita S.;
 RT "Expression and characterization of dog CYP2D15 using baculovirus
 RT expression system".
 RL J. Biochem. 123:162-168(1998).
 RL [3]
 RP CHARACTERIZATION;
 RX MEDLINE=96389575; PubMed=9721180;
 RA Rousset F., Duignan D.B., Lawton M.P., Obach R.S., Strick C.A.,
 RA Tweedie D.J.;
 RT "Expression and characterization of canine cytochrome P450 2D15.";
 RL Arch. Biochem. Biophys. 357:27-36(1998).
 CC -1- FUNCTION: HIGH ACTIVITY FOR THE HYDROXYLATION OF BUNITROL AND
 CC IMPRAMINE: LOW ACTIVITY ON DEBRISOQUINE.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) -> ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: LIVER. ALSO DETECTED IN SEVERAL OTHER TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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 CC -----
 CC EMBL: D17397; BAA04220.1; -

DR EMBL: AB004268; BAA20357.1; -.
 DR HSSP: P00179; IDT6.
 DR InterPro: IPR001128; CYL_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT INIT MET 445 445 HEME (BY SIMILARITY).
 FT BINDING 0
 SO SEQUENCE 499 AA: 56301 MW: 278352B5309E7F1 CRC64;

Query Match 23.1% Score 6; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LIQMDP 11
 Db 48 LIQMDP 53

RESULT 33
 LEF9_NPVAC
 ID LEF9_NPVAC STANDARD; PRT: 516 AA.
 AC P41465;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Late expression factor 9.
 GN LEF-9.
 OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OC NCBI_Taxid=46015;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6;
 RX MEDLINE=94303173; PubMed=8030224;
 RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
 RT "The complete DNA sequence of Autographa californica nuclear
 RT polyhedrosis virus".
 RL Virology 202:586-605(1994).
 CC -1- FUNCTION: INVOLVED IN LATE/VERY LATE GENE ACTIVATION.
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 CC -----
 CC EMBL: L22858; AAA6692.1; -.
 DR TRANSCRIPTION REGULATION;
 KW SEQUENCE 516 AA: 59305 MW: B625F9E623FC058P CRC64;
 SO SEQUENCE 516 AA: 59305 MW: B625F9E623FC058P CRC64;

Query Match 23.1% Score 6; DB 1; Length 516;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PPEHL 18
 Db 506 PPEHL 511

RESULT 34
 BCYF_EURCA
 ID BCYF_EURCA STANDARD; PRT: 628 AA.
 AC 09WFIL5;
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hemocyanin F chain (Hcf).
 GN HCF.
 OS Eurytelma californica (American tarantula).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Aphonopelma.
 RX NCBI_TaxID=23932;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20564303; PubMed=10961996;
 RA "Volte R., Feldmiller-Fuchs G., Schweikardt T., Decker H., Burmester T.;
 RT Complete sequence of the 24-mer hemocyanin of the tarantula Eurytelma
 RT californicum. Structure and intramolecular evolution of the
 RT subunits.";
 RL J. Biol. Chem. 275:39339-39344(2000).
 CC -1- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
 CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
 CC ARTHROPODS.
 CC -1- SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
 CC DIFFERENT CHAINS IDENTIFIED.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A
 CC BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN
 CC ADDITION TO BINDING OXYGEN.
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
 CC SUBFAMILY.

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 DR EMBL: AJ277491; CAB09496.1; -.
 DR HSSP: P04253; ILIA.
 DR InterPro: IPR000896; Hemocyanin.
 DR PRINTS: PR00187; HEMOCYANIN.
 DR PROSITE: PS00209; HEMOCYANIN.1; 1.
 DR PROSITE: PS00210; HEMOCYANIN.2; 1.
 DR PROSITE: PS00498; TYROSINASE.2; 1.
 KW Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
 FT INIT_MET 0
 FT DISULFID 0
 FT METAL 533 581
 FT METAL 171 171
 FT METAL 175 175
 FT METAL 202 202
 FT METAL 323 323
 FT METAL 327 327
 FT METAL 363 363
 FT CARBOHYD 394 394
 FT CARBOHYD 446 446
 FT CARBOHYD 526 526
 FT CARBOHYD 614 614
 FT CARBOHYD 628 AA; 72017 MW; 539C94849CC8D4F4 CRC64;
 SQ SEQUENCE

Query Match 23.1%; Score 6; DB 1; Length 623;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 PETHLV 19
 |||||
 DB 536 PETHLV 541

RESULT 35
 ORC3_MOUSE STANDARD; PRT; 715 AA.
 AC 09JK30;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Origin recognition complex subunit 3 (Origin recognition complex
 DE subunit lathco).
 GN ORC3L OR ORC3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20169198; PubMed=10702681;
 RA Springer J., Nanda I., Hoehn K., Schmid M., Grumme F.;
 RT Identification and chromosomal localization of murine ORC3, a new
 RT member of the mouse origin recognition complex.";
 RL Cytogenet. Cell Genet. 87:245-251(1999).
 CC -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
 CC BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
 CC REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
 CC THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN
 CC ATP-DEPENDENT MANNER.
 CC -1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ORC3 FAMILY.

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 DR EMBL: AJ132830; CAB76399.1; -.
 DR MGD: MGI:1354944; Orc3.
 DR DNA replication; Nuclear protein; DNA-binding.
 KW DNA replication; Orc3.
 SQ SEQUENCE 715 AA; 82341 MW; 1E915A719A2E33B8 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 715;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 LVDFLQ 23
 |||||
 DB 80 LVDFLQ 85

RESULT 36
 MISS_SCHPO STANDARD; PRT; 892 AA.
 AC P49731; 09P7R7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA replication licensing factor m185.
 GN MISS OR SPEC211.04c.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 RX NCBI_TaxID=4896;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95170112; PubMed=7865880;
 RA Takahashi K., Yamada H., Yanagida M.;
 RT "Fission yeast minichromosome loss mutants m18 cause lethal
 RT aneuploidy and replication abnormality.";
 RL Mol. Biol. Cell 5:1145-1158(1994).
 RL (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;

RA WOOD V., Rajandream M.A., Barrell B.G., Davis P., Churcher C.M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
 CC -1- SIMILARITY: BELONGS TO THE MCM FAMILY.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 864
 CC ONWARD AND IS SHORTER (868 AA) DUE TO A FRAMESHIFT.
 CC -----
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 CC -----
 DR EMBL: D31960; BAA06729.1; ALT_FRAME.
 DR EMBL: AL139514; CAB75412.1; -.
 DR InterPro: IPR001208; MCM.
 DR Pfam: PF00493; MCM; 1.
 DR SMART: SM00350; MCM; 1.
 DR PROSITE: PS00847; MCM_1; 1.
 DR PROSITE: PS50051; MCM_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein;
 KW DNA replication; cell cycle; ATP-binding.
 FT DOMAIN 426 483 MCM.
 FT NP_BIND 476 633 ATP (POTENTIAL).
 SO SEQUENCE 892 AA; 99549 MW; 3A00DB552EE08B7 CRC64;
 OY 21 FLOSLS 26 23.1%; Score 6; DB 1; Length 892;
 Db 405 FLOSLS 410 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 RESULT 37
 CHSG-ASPFU STANDARD: PRT: 911 AA.
 AC P54267: 009031: 009032:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chitin synthase G (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
 DE transferase G) (Class-III chitin synthase G).
 GN CHSG
 OS Aspergillus fumigatus (Sartorya fumigata).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H237;
 RX MEDLINE=96347138; PubMed=8736545;
 RA Mellado E., Aufauvre-Brown A., Gow N.A.R., Holden D.W.;
 RT "The Aspergillus fumigatus chsc and chsg genes encode class III
 RT chitin synthases with different functions.";
 RL Mol. Microbiol. 20:667-679(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S10001;
 RA Borgia P.T., Iatichouk N., Riggle P.J., Winter K.R., Koltin Y.,
 RA Butawa C.E.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + [(1,4)-(N-acetyl-
 CC beta-D-glucosaminyl)](N) -> UDP + [(1,4)-(N-acetyl-beta-D-
 CC glucosaminyl)](N+1).
 CC -1- SUBCELLULAR LOCATION: Plasma membrane-bound.
 CC -1- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY. SUPERFAMILY CLASS
 CC III.

```

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CC or send an email to license@isb-slb.ch).
CC -----
CC EMBL: X34244; CA63928.1; -
CC DR EMBL: U39478; AAB07678.1; -
CC DR EMBL: U39479; AAB07679.1; -
CC DR InterPro: IPR002923; Chitin_synth.
CC DR Pfam: PF01644; Chitin_synth; 1.
CC DR Prodom: PD002998; Chitin_synth; 1.
CC KW Transferrase; Glycosyltransferase; Transmembrane; Cell wall;
CC Multiene family.
CC FT TRANSMEM 579 599 POTENTIAL.
CC FT TRANSMEM 628 644 POTENTIAL.
CC FT TRANSMEM 639 679 POTENTIAL.
CC FT TRANSMEM 711 731 POTENTIAL.
CC FT TRANSMEM 840 860 POTENTIAL.
CC FT TRANSMEM 879 899 POTENTIAL.
CC FT CONFLICT 334 337 PPVO -> LPSK (IN REF. 1).
CC FT CONFLICT 537 537 R -> C (IN REF. 2; AAB07679).
CC FT CONFLICT 628 629 IV -> MM (IN REF. 2; AAB07679).
CC FT CONFLICT 892 892 F -> N (IN REF. 2; AAB07679).
CC FT CONFLICT 911 AA: 101669 MW: BC933F8BA00BE48D CRC64;
CC SEQUENCE
CC -----
CC
CC Query Match 23.1%; Score 6; DR 1; Length 911;
CC Best Local Similarity 100.0%; Pred. No. 96;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Oy 3 GFLLD 8
CC Db 635 GFLLD 640
CC
CC RESULT 38
CC PVAL.DICDI STANDARD; PRT: 1058 AA.
CC ID PVAL.DICDI STANDARD; PRT: 1058 AA.
CC AC P34679;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Probable plasma membrane ATPase (EC 3.6.3.6) (Proton pump) (PATZ).
CC GN PATB.
CC OS Dictyostelium discoideum (Slime mold).
CC OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostellum.
CC NCBI_TaxID=44689;
CC RX MEDLINE=98083743; PubMed=9421912;
CC RX Coukell M.B., Moniakis J., Cameron A.M.;
CC RA "The patB gene of Dictyostelium discoideum encodes a P-type H(+)-
CC RT ATPase isoform essential for growth and development under acidic
CC RT conditions.";
CC RL Microbiology 143:3877-3888(1997).
CC CC -I- FUNCTION: THE PLASMA MEMBRANE ATPASE IS A HYDROGEN ION PUMP. THE
CC PROTON GRADIENT IT GENERATES DRIVES THE ACTIVE TRANSPORT OF
CC NUTRIENTS BY H+ SYMPORT. THE RESULTING EXTENSIVE ACIDIFICATION
CC AND/OR INTERNAL ALKALIZATION MAY MEDIANE GROWTH RESPONSES.
CC -I- CATALYTIC ACTIVITY: ATP + H(2O) + H(+)(IN) = ADP + PHOSPHATE +
CC H(+)(OUT).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES). SUBFAMILY IITA.
CC -----
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EMBL: X8286; CA66931.1; -

DICtyDb: DD00061; patB.

InterPro: IPR004014; Cation_ATPase.

InterPro: IPR001757; El-E2_ATPase.

InterPro: IPR006695; HATPase.

InterPro: IPR001454; Hydrolyase.

Pfam: PF00690; Cation_ATPase_N; 1.

Pfam: PF00122; El-E2_ATPase; 1.

Pfam: PF00702; Hydrolyase; 1.

PRINTS: PR00119; CATAPASE.

PRINTS: PR00120; HATPASE.

PROSITE: PS00154; ATPase_El_E2; 1.

Hydrolyase: Hydrogen ion transport; Transmembrane; Phosphorylation; Magnesium; ATP-binding.

DOMAIN 1 212 CYTOPLASMIC (POTENTIAL).

TRANSMEM 213 232 POTENTIAL.

TRANSMEM 233 237 EXTRACELLULAR (POTENTIAL).

TRANSMEM 238 258 POTENTIAL.

DOMAIN 259 387 CYTOPLASMIC (POTENTIAL).

TRANSMEM 388 407 POTENTIAL.

DOMAIN 408 417 EXTRACELLULAR (POTENTIAL).

TRANSMEM 426 447 POTENTIAL.

DOMAIN 448 783 CYTOPLASMIC (POTENTIAL).

TRANSMEM 784 805 POTENTIAL.

DOMAIN 806 810 EXTRACELLULAR (POTENTIAL).

TRANSMEM 811 833 POTENTIAL.

DOMAIN 834 849 CYTOPLASMIC (POTENTIAL).

TRANSMEM 850 870 POTENTIAL.

DOMAIN 871 889 EXTRACELLULAR (POTENTIAL).

TRANSMEM 890 910 POTENTIAL.

DOMAIN 911 922 CYTOPLASMIC (POTENTIAL).

TRANSMEM 923 943 POTENTIAL.

DOMAIN 944 967 EXTRACELLULAR (POTENTIAL).

TRANSMEM 968 988 POTENTIAL.

DOMAIN 989 1058 CYTOPLASMIC (POTENTIAL).

MOD_RES 480 480 PHOSPHORYLATION (BY SIMILARITY).

METAL 728 728 MAGNESIUM (BY SIMILARITY).

DOMAIN 732 732 MAGNESIUM (BY SIMILARITY).

DOMAIN 44 55 POLY-SER.

DOMAIN 113 116 POLY-SER.

DOMAIN 246 249 POLY-LEU.

SEQUENCE 1058 AA; 117373 MW; C80E5AB9BDEB9AF2 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 1058;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 17 LTVDFL 22
|||||

DB 403 LTVDFL 408

RESULT 39
ID YECS_YEAST STANDARD; PRT; 1188 AA.
AC P39991;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 136.1 kDa protein in VMA3-RIP1 Intergenic region.
GN YEL025C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.

STRAIN-S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Hyman R., Duncan M., Guzman E., Hartzell G., Hunke-Smith S.,
RA Hymn R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogen T., Smith V.,
RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.,
RA Submitted (DRC-1994) to the EMBL/GenBank/DBJ databases.

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CC or send an email to license@isb-sdb.ch).

EMBL: U18530; AB64502.1; -

SGD: S0000751; SRI1.

Hypothetical protein; Transmembrane.

TRANSMEM 73 93 POTENTIAL.

TRANSMEM 878 898 POTENTIAL.

TRANSMEM 1089 1109 POTENTIAL.

SEQUENCE 1188 AA; 136068 MW; 82C3F04D1F78AD3D CRC64;

Query Match 23.1%; Score 6; DB 1; Length 1188;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 19 VDFLQS 24
|||||

DB 523 VDFLQS 528

RESULT 40
ID YMW2_CAEEL STANDARD; PRT; 1246 AA.
AC P34504; P34505; P34506; P09097;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 130.6 kDa protein K04H4.2 in chromosome III.
GN K04H4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnenhammer E., Staden R.,
RA Sutcliffe J., Thierly-Mieg J., Thomas K., Vaund M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wolldman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.*;
RL Nature 368:32-38(1994).
[2]
REVIEWS:
RP Durbin R.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: K04H4.2A (SHOWN HERE) AND
CC K04H4.2B; ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.

RC STRAIN-S288C / FY1679;
 RX MEDLINE=96132033; PubMed=8553702;
 RA Maurer K.C.T., Urbanus J.H.M., Planeta R.J.;
 RT Sequence analysis of a 30 Kb DNA segment from yeast chromosome XIV
 RT carrying a ribosomal protein gene cluster, the genes encoding a
 RT plasma membrane protein and a subunit of replication factor C, and a
 RT novel putative serine/threonine protein kinase gene.";
 RL Yeast 11:1303-1310(1995).
 CC -1- SIMILARITY: SOME, TO S.POMBE SPAC303.13C.
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 CC -----
 DR EMBL: U23084; AAC49101.1; -;
 DR EMBL: Z71573; CAAG6214.1; -;
 DR SGD: S0005241; YNL297C.
 KW Hypochemical protein.
 SO SEQUENCE 1636 AA; 186834 MW; F0B3D8E6BD0994D6 CRC64;
 QY 20 DFLQSL 25
 D5 936 DFLQSL 941
 Query Match 23.18; Score 6; DB 1; Length 1636;
 Best Local Similarity 100.08; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 43:
 PCK5_RAT
 ID PCK5_RAT STANDARD; PRT: 1877 AA.
 AC P41413; Q62914;
 DT 01-NOV-1995 (rel. 32, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Proprotein convertase PCS) (Subtilisin/kexin-like protease PCS)
 DE (Convertase PCS) (PC5) (PC6) (Fragments).
 GN PCSK5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM), AND TISSUE-SPECIFICITY.
 RC TISSUE-Adrenal gland;
 RX MEDLINE=93342056; PubMed=8341687;
 RA Lussan J., Viteau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT *CDNA structure of the mouse and rat subtilisin/kexin-like PCS: a
 RT candidate proprotein convertase expressed in endocrine and
 RT nonendocrine cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [2]
 RP SEQUENCE OF 1676-1877 FROM N.A. (LONG ISOFORM).
 RC TISSUE-Adrenal gland;
 RA De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
 RL Submitted (Jan-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=20214819; PubMed=10749928;
 RA Xiang Y., Molloy S.S., Thomas L., Thomas G.;
 RT *The PC6B cytoplasmic domain contains two acidic clusters that direct
 RT sorting to distinct trans-Golgi network/endosomal compartments.";
 RL Mol. Biol. Cell 11:1257-1273(2000).
 RN [4]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97166043; PubMed=9013936;

RA Zheng M., Seidah N.G., Platar J.E.;
 RT "The developmental expression in the rat CNS and peripheral tissues of
 RT proteases PCS and PACE4 mRNAs: comparison with other proprotein
 RT processing enzymes.";
 RL Dev. Biol. 181:268-283(1997).
 CC -1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 CC OF CLEAVAGE AT THE RX/K/R/R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 CC FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 CC IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 CC OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 CC PROPEPTIC BY CLEAVAGE OF ARG-XAA-TYA-ARG-1-ZNA BONDS, WHERE XAA
 CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: PCS4 IS SECRETED THROUGH THE REGULATED
 CC SECRETORY PATHWAY. PCS5 IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
 CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 CC EARLY ENDOSOMES (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PCSB/LONG (SHOWN HERE)
 CC AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE INTESTINE, BRAIN, ADRENAL
 CC GLAND, ANTERIOR PITUITARY, THYROID, OVARIES, TESTIS AND LUNG.
 CC EXPRESSION IS HIGHER IN FEMALE THAN IN MALE REPRODUCTIVE ORGANS.
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT E3 IN HIGHLY RESTRICTED
 CC REGIONS OF THE NEURAL TUBE, IN CAUDAL MYOTOMES, AND AT THE
 CC MATERNO-EMBRYONIC JUNCTION OF THE UTERUS. AT E10, RESTRICTED
 CC EXPRESSION IS DETECTED IN THE OPTIC AND OTIC VESICLES, THE ROOF OF
 CC MIDBRAIN, AND TRUNK MYOTOMES. BY MIDGESTATION (E13-E16),
 CC EXPRESSION IN THE DEVELOPING NERVOUS SYSTEM HAS EXPANDED TO
 CC MULTIPLE REGIONS INCLUDING HIPPOCAMPUS, THALAMUS, HYPOTHALAMUS,
 CC BRAIN STEM, AND SPINAL CORD. EXPRESSION IS ALSO DETECTED IN
 CC SEVERAL PERIPHERAL ORGAN SYSTEMS, INCLUDING GUT, LUNG, ADRENAL AND
 CC KIDNEY PRIMORDIA.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZIMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 CC SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 CC WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
 CC SUBTILASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
 CC -----
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 CC -----
 DR EMBL: L14933; AAA99906.1; -;
 DR EMBL: U47014; AAA87888.1; -;
 DR PIR: B48225; B48225.
 DR HSSP: Q99405; IMPT.
 DR MEROPS: S08_076; -;
 DR InterPro: IPR002174; Furin-like.
 DR InterPro: IPR002884; P_domain.
 DR InterPro: IPR000209; Peptidase_S8.
 DR Pfam: PF01483; P_1.
 DR Pfam: PF00082; Peptidase_S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR ProDom: PD000717; P_domain; 1.
 DR SMART: SM00261; FU; 6.
 DR PROSITE: PS00136; SUBTILASE_ASP; 1.
 DR PROSITE: PS00137; SUBTILASE_HIS; 1.
 DR PROSITE: PS00138; SUBTILASE_SER; 1.
 KW Hydrolyse. Serine protease. Glycoprotein; zymogen; signal;
 KW cleavage on pair of basic residues; Alternative splicing; Repeat;
 KW Transmembrane.
 FT SIGNAL 1 34 BY SIMILARITY.
 FT PROPEP 35 116 BY SIMILARITY.

RX MEDLINE-87008488; PubMed-3759943;
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
 RA Gotto A.M. Jr., Chan L.;
 RT "The complete cDNA and amino acid sequence of human apolipoprotein
 RT B-100.";
 RL J. Biol. Chem. 261:12918-12921(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87041416; PubMed-3464946;
 RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Leckner K.J.,
 RA Lee N., Brewer H.B. Jr.;
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
 RT derived amino acid sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87161758; PubMed-3030729;
 RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
 RA Zannis V.I.;
 RT "The complete sequence and structural analysis of human
 RT apolipoprotein B-100: relationship between apob-100 and apob-48
 RT forms.";
 RL EMBO J. 5:3495-3507(1986).
 RN [6]
 RP SEQUENCE OF 709-906 FROM N.A.
 RX MEDLINE-85270450; PubMed-3860836;
 RA Deep S.S., Motulsky A.G., Albers J.J.;
 RT "A partial cDNA clone for human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
 RN [7]
 RP SEQUENCE OF 3056-3159 FROM N.A.
 RX MEDLINE-86041888; PubMed-3903660;
 RA Mehlman M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
 RA Kirchessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
 RT "Human apolipoprotein B: identification of cDNA clones and
 RT characterization of mRNA.";
 RL Nucleic Acids Res. 13:6937-6953(1985).
 RN [8]
 RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.
 RX MEDLINE-86093680; PubMed-3841204;
 RA Carlsson P., Olafsson S.O., Bondjers G., Darnfors C., Wiklund O.,
 RA Bjursell G.;
 RT "Molecular cloning of human apolipoprotein B cDNA.";
 RL Nucleic Acids Res. 13:8813-8826(1985).
 RN [9]
 RP SEQUENCE OF 3109-4563 FROM N.A.
 RX MEDLINE-85300528; PubMed-2994225;
 RA Knott T.J., Ball S.C. Jr., Innerarity T.L., Jacobson S.F.,
 RA Urdea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Edy R.,
 RA Nakai H., Byers M., Priestley L.M., Robertson E., Ball T.B.,
 RA Bernholz C., Shows T.B., Mahley R.W., Scott J.;
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains,
 RT sites of gene expression, and chromosomal localization.";
 RL Science 230:37-43(1985).
 RN [10]
 RP SEQUENCE OF 1-291 FROM N.A.
 RX MEDLINE-86149325; PubMed-3513177;
 RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
 RA Chen G.C., Kirsher S.W., McIntee G., Kane J.P.;
 RT "Isolation of a cDNA clone encoding the amino-terminal region of
 RT human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
 RN [11]
 RP SEQUENCE OF 1-1670 FROM N.A.
 RX MEDLINE-86287319; PubMed-346154;
 RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,
 RA Yamanaoka M., Hort Y.-Y., Hjertild K.A., Chen G.C., Kane J.P.;
 RT "Analysis of cDNA clones encoding the entire B-26 region of human
 RT apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
 RN [12]
 RP PARTIAL SEQUENCE, AND IDENTIFICATION (APO-B48).
 RX MEDLINE-88018019; PubMed-3659919;
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Wang S.-H.,
 RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
 RA Gotto A.M. Jr., Li W.-H., Chan L.;
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
 RT specific in-frame stop codon.";
 RL Science 238:363-366(1987).
 RN [13]
 RP DOMAINS.
 RX MEDLINE-87039351; PubMed-3773997;
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Ball S.C. Jr.,
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
 RA Levy-Wilson B., Scott J.;
 RT "Complete protein sequence and identification of structural domains
 RT of human apolipoprotein B.";
 RL Nature 323:734-738(1986).
 RN [14]
 RP DOMAINS.
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
 RA Tanimura M., Li W.-H., Sparrow D.A., Paloo H., Rosseneu M.,
 RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.;
 RT "Sequence, structure, receptor-binding domains and internal repeats
 RT of human apolipoprotein B-100.";
 RL Nature 323:738-742(1986).
 RN [15]
 RP CALCULUM-BINDING DATA.
 RX MEDLINE-86242245; PubMed-3087360;
 RA Dashti N., Lee D.M., Mok T.;
 RT "Apolipoprotein B is a calcium binding protein.";
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
 RN [16]
 RP VARIANT SER-4338.
 RX MEDLINE-91071750; PubMed-1979313;
 RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
 RA Cuny G., Cambien F., Roizes G.;
 RT "Detection by denaturing gradient gel electrophoresis of a new
 RT polymorphism in the apolipoprotein B gene.";
 RL Hum. Genet. 86:91-93(1990).
 RN [17]
 RP VARIANT FDB GLN-3527.
 RX MEDLINE-89098975; PubMed-2563166;
 RA Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
 RA McCarthy B.J.;
 RT "Association between a specific apolipoprotein B mutation and
 RT familial defective apolipoprotein B-100.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
 RN [18]
 RP VARIANT LEU-2739.
 RX MEDLINE-91016974; PubMed-2216805;
 RA Huang L.-S., Gavish D., Breslow J.L.;
 RT "Sequence polymorphism in the human apob gene at position 8344.";
 RL Nucleic Acids Res. 18:5922-5922(1990).
 RN [19]
 RP VARIANT FDB CYS-3558.
 RX MEDLINE-95190020; PubMed-7883971;
 RA Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
 RT "Familial lipand-defective apolipoprotein B. Identification of a new
 RT mutation that decreases LDL receptor binding affinity.";
 RL J. Clin. Invest. 95:1225-1234(1995).
 RN [20]
 RP VARIANTS L-1437, S-1914, K-2566, T-3121, A-3945, M-4128 AND T-4481.
 RX MEDLINE-97044521; PubMed-8889592;
 RA Poirier O., Richard S., Behague I., Souriau C., Evans A.E.,
 RA Avetier D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
 RT PCR-SSCP.";
 RL Hum. Mutat. 8:282-285(1996).
 RN [21]
 RP VARIANTS FDB GLN-3527 AND CYS-3558.
 RX MEDLINE-97403938; PubMed-9259199;
 RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
 RA Krempf M., Giraudet P., Junien C., Boileau C.;

RT *Familial ligand-defective apolipoprotein B-100: simultaneous
RT detection of the ARG3500-->Gln and ARG3531-->Cys mutations in a
RT French population.*
RT Hum. Mutat. 10:160-163(1997).
RN [22]
RN VARIANTS S-1914; R-1923; L-2739; D-3319; T-3427; Q-3432 AND I-3923.
RX MEDLINE-98141125; PubMed-9490296;
RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.
RT *Screening for mutations of the apolipoprotein B gene causing
RT hypocholesterolemia.*
RL Hum. Genet. 102:44-49(1998).
CC -1- FUNCTION: APOLIPOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF
CC CHROMIDIONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL
CC FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY
CC THE APOB/E RECEPTOR.
CC -1- DISEASE: DEFECTS IN APOB ARE A CAUSE OF FAMILIAL LIGAND-DEFECTIVE
CC APOLIPOPROTEIN B-100 (FDB). IT IS A DOMINANTLY INHERITED DISORDER
CC OF LIPOPROTEIN METABOLISM LEADING TO HYPERCHOLESTEROLEMIA AND
CC INCREASED PRONESS TO CORONARY ARTERY DISEASE (CAD).
CC THE PLASMA CHOLESTEROL LEVELS ARE DRAMATICALLY ELEVATED DUE TO
CC IMPAIRED CLEARANCE OF LDL PARTICLES BY DEFECTIVE APOB/E RECEPTORS.
CC -1- DISEASE: DEFECTS IN APOB ASSOCIATED WITH OTHER GENE DEFECTS
CC (POLYGENIC) CAN BE THE CAUSE OF HYPOCHOLESTEROLEMIA.
CC -1- MISCELLANEOUS: APO B-48 WHICH IS SYNTHESIZED ONLY BY THE
CC INTESTINE, AND FOUND IN CHYLOMICRONS, IS A SHORTENED FORM OF APO
CC B.
Query Match 23.18; Score 6; DB 1; Length 4563;
Best Local Similarity 100.0%; Pred. No. 4; 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 LILLOND 10
DB 1146 LILLOND 1151
RESULT 46
PRTM_PORPU STANDARD; PRT: 32 AA.
AC P51275;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome B6-F complex subunit VII (Cytochrome b6f complex subunit
DE petM).
GN PRTM OR YCF31.
OS Porphyra purpurea.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=2787;
RN [1]
RP SPOUNCE FROM N.A.
RC STRAIN=AYONPORT;
RA Reich M.E., Runkholland J.;
RT Complete nucleotide sequence of the Porphyra purpurea chloroplast
RT genome.*
RL Plant Mol. Biol. Rep. 13:333-335(1995).
CC -1- FUNCTION: CYTOCHROME B6-F COMPLEX SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Thylakoid membrane-associated (by
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE PRTM FAMILY.
CC -----
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CC -----
DR EMBL; U38804; AAC08161.1; -
DR Mendel; 10379; PORPU; ycf31.1.
KW Electron transport; Chloroplast; Respiratory chain; Thylakoid;
KW Transmembrane.

FT TRANSMEM 5 25 POTENTIAL.
SQ SEQUENCE 32 AA; 3313 MW; 3F220BB834379FDA CRC64;
Query Match 19.28; Score 5; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 GFFLL 7
DB 23 GFFLL 27
RESULT 47
Y5K6_SSV1 STANDARD; PRT: 45 AA.
AC P20198;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 5.6 kDa protein (ORF A-45).
OS Sulfolobus virus-like particle SSV1.
CC Viruses; dsDNA viruses, no RNA stage; Fuselloviridae; Fusellovirus.
OX NCBI_TaxID=10476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92024080; PubMed-1926776;
RA Palm P., Schleper C., Grapp B., Yeats S., McWilliam P., Reiter W.-D.,
RA Zillig W.;
RT "Complete nucleotide sequence of the virus SSV1 of the
RT archaeobacterium Sulfolobus shibatae.*"
RL Virology 185:242-250(1991).
CC -----
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CC -----
DR EMBL; X07234; CAA30195.1; -
DR PIR; S03227; S03227.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Hypothetical protein; Zinc-finger; Metal-binding.
FT ZN.FING 2 25
SQ SEQUENCE 45 AA; 5559 MW; 38BF487EDDCA308B CRC64;
Query Match 19.28; Score 5; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15 EHLLV 19
DB 19 EHLLV 23
RESULT 48
ATP8_HAMWI STANDARD; PRT: 48 AA.
AC P48862;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN ATP8.
OS Hansenula wingel (Yeast).
KW Mitochondrion.

```

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4907;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=21;
RA Sekito T., Okamoto K., Kitano H., Yoshida K.;
RT "Yeast Hansenula wingel mitochondria genome's complete DNA sequence
demonstrated unique characteristics."
RL Nucleic Acids Symp. Ser. 31:233-234(1994).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NOMEMENYATIC COMPONENT
(CC) (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC -----
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CC -----
DR EMBL: D31785; BAA0565.1; -;
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 13 33
SQ SEQUENCE 48 AA; 5879 MW; 2714F6968DB8DC CRC64;

Query Match 19.2%; Score 5; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GELLT 7
DB 16 GFLLL 20

RESULT 49
TAC1_BOVIN STANDARD; PRT; 63 AA.
ID TAC1_BOVIN
AC P01000;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acrosin inhibitor I (BUST-1).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN
RP SEQUENCE.
RX MEDLINE=84133805; PubMed=6365719;
RA Meloun B., Cechova D., Jonakova V.;
RT "Homologies in the structures of bull seminal plasma acrosin
inhibitors and comparison with other homologous proteinase inhibitors
of the kazal type."
RL Hoppe-Seyler's Z. Physiol. Chem. 364:1665-1670(1983).
CC -1- FUNCTION: THIS PROTEIN IS A STRONG INHIBITOR OF ACROSIN.
CC -1- SIMILARITY: CONTAINS 1 KAZAL-LIKE DOMAIN.
DR HSP: A01234; XTBO1.
DR HSP: P01004; ISGP.
DR InterPro: IPR001239; Kazal_inhib.
DR InterPro: IPR002350; kazal.
DR Pfam: PR00050; Kazal.1.
DR PRINTS; PR00290; KAZALINHBT.
DR SMART; SM00280; KAZAL.1.
DR PROSITE; PS00282; KAZAL.1.
KW Serine protease inhibitor; Semen.
FT DISULFID 14 43 BY SIMILARITY.
FT DISULFID 21 40 BY SIMILARITY.
FT DISULFID 29 61 BY SIMILARITY.

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FT ACT_SITE 23 24 REACTIVE BOND.
SQ SEQUENCE 63 AA; 7379 MW; A02668698ABDE2 CRC64;

Query Match 19.2%; Score 5; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DEGFP 14
DB 7 DEGFP 11

RESULT 50
VC55_HAEBN STANDARD; PRT; 74 AA.
ID VC55_HAEBN
AC P44141;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein H11255.
GN H11255.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=9530630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirtnes E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd."
RL Science 269:496-512(1995).
CC
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CC -----
DR EMBL: U32805; AAC22910.1; -;
DR TIGR: H11255; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 74 AA; 8446 MW; CC22E0A6C0C98D3 CRC64;

Query Match 19.2%; Score 5; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLQ 23
DB 70 VDFLQ 74

```

Search completed: June 19, 2002, 11:11:22
Job time: 201 sec

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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:07:41 ; Search time 25.27 seconds
(without alignments)
177.992 million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26
Sequence: 1 RDSFLLIQMDFGFPEHLVDFLQSLIS 26

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 segs, 17294929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

SPTREMBL_19:*

1: SP_archaea:*

2: SP_bacteria:*

3: SP_fungi:*

4: SP_human:*

5: SP_invertebrate:*

6: SP_mammal:*

7: SP_mhc:*

8: SP_organelle:*

9: SP_phage:*

10: SP_plant:*

11: SP_protent:*

12: SP_virus:*

13: SP_vertebrate:*

14: SP_unclassified:*

15: SP_virus:*

16: SP_bacteriap:*

17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	61.5	485	6	Q9BG59
2	7	26.9	210	11	Q9WVJ8
3	7	26.9	213	11	Q9WVJ7
4	7	26.9	221	11	Q9WVJ7
5	7	26.9	227	11	Q9WU32
6	7	26.9	227	16	Q9ZKY0
7	7	26.9	238	11	Q9WU39
8	7	26.9	244	11	Q9Z202
9	7	26.9	253	11	Q9WU31
10	7	26.9	253	10	Q9W8S3
11	7	26.9	260	16	Q9K8S9
12	7	26.9	373	2	Q9J3LN5
13	7	26.9	405	10	Q9JLMT6
14	7	26.9	547	16	Q9K1J7
15	7	26.9	846	2	Q9S6R3
16	7	26.9	861	10	Q94CF2

17	7	26.9	903	5	Q9XX09	Q9XX09 caenorhabd
18	7	26.9	1300	2	Q32555	Q32555 escherichia
19	7	26.9	1300	2	Q32591	Q32591 escherichia
20	6	23.1	81	2	Q9L719	Q9L719 styechoococ
21	6	23.1	88	6	Q95108	Q95108 styechoococ
22	6	23.1	111	9	Q9MC72	Q9MC72 steles belz
23	6	23.1	112	11	Q9DBU1	Q9DBU1 bacterioph
24	6	23.1	115	16	Q9K317	Q9K317 mus musculu
25	6	23.1	130	16	Q67666	Q67666 aquifex aeo
26	6	23.1	150	11	Q9JMH5	Q9JMH5 mus musculu
27	6	23.1	155	11	Q9DB70	Q9DB70 mus musculu
28	6	23.1	156	10	Q9SKX1	Q9SKX1 arabidopsi
29	6	23.1	163	17	Q97V16	Q97V16 sulfolobus
30	6	23.1	166	2	Q52661	Q52661 rhodobacter
31	6	23.1	166	3	Q9P380	Q9P380 schizosacch
32	6	23.1	204	16	Q55840	Q55840 schizosacch
33	6	23.1	210	16	Q9A706	Q9A706 synecocyst
34	6	23.1	222	11	Q9D6M8	Q9D6M8 mus musculu
35	6	23.1	235	10	Q9ST53	Q9ST53 malus domes
36	6	23.1	241	2	Q86738	Q86738 streptomyce
37	6	23.1	260	16	Q9K909	Q9K909 bacillus ha
38	6	23.1	275	16	Q99UJ1	Q99UJ1 staphylococ
39	6	23.1	279	5	Q87858	Q87858 streptomyce
40	6	23.1	279	5	Q9W535	Q9W535 caenorhabd
41	6	23.1	283	16	Q07011	Q07011 bacillus su
42	6	23.1	283	16	Q9K6A7	Q9K6A7 bacillus su
43	6	23.1	289	10	Q9F085	Q9F085 nicotiana t
44	6	23.1	298	16	Q9KD33	Q9KD33 bacillus ha
45	6	23.1	303	16	Q85704	Q85704 staphylococ
46	6	23.1	305	4	Q9HBL5	Q9HBL5 homo sapien
47	6	23.1	311	3	Q9PE00	Q9PE00 candida alb
48	6	23.1	311	11	Q9DB26	Q9DB26 mus musculu
49	6	23.1	313	16	Q99RY9	Q99RY9 staphylococ
50	6	23.1	324	10	Q9F084	Q9F084 nicotiana t
51	6	23.1	324	16	Q98109	Q98109 rhizobium l
52	6	23.1	335	13	Q9DES4	Q9DES4 fuqu rubrip
53	6	23.1	351	4	Q13539	Q13539 homo sapien
54	6	23.1	354	4	Q96LJ5	Q96LJ5 homo sapien
55	6	23.1	354	4	Q96EM0	Q96EM0 homo sapien
56	6	23.1	354	11	Q99KX5	Q99KX5 mus musculu
57	6	23.1	354	11	Q99KX5	Q99KX5 mus musculu
58	6	23.1	365	10	Q9FC06	Q9FC06 nicotiana t
59	6	23.1	378	5	Q9VME8	Q9VME8 drosophila
60	6	23.1	380	5	Q9VH17	Q9VH17 drosophila
61	6	23.1	380	13	Q9DE06	Q9DE06 cyprinus ca
62	6	23.1	390	10	Q9F090	Q9F090 nicotiana t
63	6	23.1	393	17	Q97VG1	Q97VG1 sulfolobus
64	6	23.1	394	10	Q9AVY2	Q9AVY2 guillardi
65	6	23.1	397	16	Q26006	Q26006 helicobacte
66	6	23.1	406	16	Q9ZJF8	Q9ZJF8 helicobacte
67	6	23.1	414	5	Q9XUC7	Q9XUC7 caenorhabd
68	6	23.1	416	2	Q9H154	Q9H154 streptomyce
69	6	23.1	419	4	Q9UG83	Q9UG83 homo sapien
70	6	23.1	422	5	Q02282	Q02282 caenorhabd
71	6	23.1	425	4	Q9BS18	Q9BS18 homo sapien
72	6	23.1	425	10	Q9FO91	Q9FO91 nicotiana t
73	6	23.1	425	11	Q9CMP7	Q9CMP7 mus musculu
74	6	23.1	426	3	Q9HFE5	Q9HFE5 schizosacch
75	6	23.1	439	5	Q965V6	Q965V6 caenorhabd

ALIGNMENTS

RESULT 1

Q9BG59

Q9BG59; PRELIMINARY; PRT: 485 AA.

AC 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

DE CHOLESTERYL ESTER TRANSFER PROTEIN (FRAGMENT).

OS Tupala gilis (Tree shrew).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupai.
 OX NCBI_TaxID=9395;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Zeng W.W., Chen B.S., Zhang J.;
 RT Cloning and sequencing of tree shrew cholesterol ester transfer
 protein (CETP) cDNA.*;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF34033; AAK08086.1; -
 DR InterPro: IPR001124; LBP_BPI_CETP.
 DR Pfam: PF01273; LBP_BPI_CETP; 1.
 DR Pfam: PF02866; LBP_BPI_CETP_C; 1.
 DR SMART: SM00326; BPI1; 1.
 DR SMART: SM00329; BPI2; 1.
 DR PROSITE: PS00400; LBP_BPI_CETP; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 485 AA; 53993 MW; 2605E76D2635C367 CRC64;

Query Match 61.5%; Score 16; DB 6; Length 485;
 Best Local Similarity 100.0%; Pred. No. 16e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLIQMDFGPEHL 17
 DB 461 DGFLLIQMDFGPEHL 476

RESULT 2
 O9WVJ8 PRELIMINARY; PRT; 210 AA.
 AC O9WVJ8;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE NATURAL KILLER CELL PROTEIN GROUP 2-A2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RC MEDLINE=929364; PubMed=10369936;
 RA Silver E.T., Lau J.C., Kane K.P.;
 RT Molecular cloning of mouse NK2A and C.*;
 RL Immunogenetics 49:727-730(1999).
 DR EMBL; AF106009; AAD40222.1; -
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 SQ SEQUENCE 210 AA; 24210 MW; 0E7F9C3903F34E97 CRC64;

Query Match 26.9%; Score 7; DB 11; Length 210;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
 DB 139 DFLQSL 145

RESULT 3
 O9WVJ7 PRELIMINARY; PRT; 213 AA.
 AC O9WVJ7;
 DT 03-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE NATURAL KILLER CELL PROTEIN GROUP 2-C2.
 GN KIRC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RC MEDLINE=929364; PubMed=10369936;
 RA Silver E.T., Lau J.C., Kane K.P.;
 RT Molecular cloning of mouse NK2A and C.*;
 RL Immunogenetics 49:727-730(1999).
 DR EMBL; AF106011; AAD40224.2; -
 DR MGD: MGI:136162; KIRC2.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 SQ SEQUENCE 213 AA; 23951 MW; 6633CB9DFC46C4DD CRC64;

Query Match 26.9%; Score 7; DB 11; Length 213;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
 DB 142 DFLQSL 148

RESULT 4
 O9QXN7 PRELIMINARY; PRT; 221 AA.
 AC O9QXN7;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE NATURAL KILLER CELL GROUP 2E CELL RECEPTOR NK2E.
 GN KIRC3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RC MEDLINE=20069888; PubMed=10601355;
 RA Vance R.E., Jamieson A.M., Raulic D.H.;
 RT Recognition of the class Ib molecule Qa-1b by putative activating
 receptors CD94/NKG2C and CD94/NKG2E on mouse natural killer cells.*;
 RL J. Exp. Med. 190:1801-1812(1999).
 DR EMBL; AF195779; AAF24982.1; -
 DR MGD: MGI:1929720; KIRC3.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 SQ SEQUENCE 221 AA; 24925 MW; F4521B9017BD0473 CRC64;

Query Match 26.9%; Score 7; DB 11; Length 221;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
 DB 150 DFLQSL 156

RESULT 5
 O9WJ32

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ID 09WU32 PRELIMINARY; PRT; 227 AA.
AC 09WU32;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE NATURAL KILLER CELL RECEPTOR NKG2B.
GN KLRK1 OR NKG2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA LeDwasser S., Hande P., Mager D.L., Takel F.;
RA LeDwasser S., Hande P., Mager D.L., Takel F.;
RT Cloning of murine NKG2A, B and C: second family of C-type lectin
RT receptors on murine NK cells.
RL Eur. J. Immunol. 29:755-761(1999).
DR EMBL: AF109784; AAD24970.1; -.
DR MGD: MGI:133616; Klrcl.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 227 AA; 25746 MW; 1651968539C28C86 CRC64;

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Query Match 26.9%; Score 7; DB 11; Length 227;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 20 DFLQSLIS 26
DB 156 DFLQSLIS 162
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RESULT 6 PRELIMINARY; PRT; 227 AA.
AC 092KY0;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PUTATIVE CARBONIC ANHYDRASE PROTEIN (EC 4.2.1.1).
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RA MEDLINE=21368234; PubMed=11474104;
RA Gallibert F., Finan T.W., Long S.R., Puenhler A., Abola F., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Bolstad P., Boche G.,
RA Bouly M., Bowser L., Bunmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Goux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Hultzer L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ransperger U., Surzycki R., Thebaud P., Vandebol M.,
RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yen K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti.";
RL Science 293:668-672(2001).
DR EMBL: AL591793; CAC47897.1; -.
KW lysate; Complete proteome.
SQ SEQUENCE 227 AA; 25244 MW; D34001C07F69D76F CRC64;

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Query Match 26.9%; Score 7; DB 16; Length 227;
Best Local Similarity 100.0%; Pred. No. 13;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 12 GPEPHLL 18
DB 17 GPEPHLL 23
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RESULT 7 PRELIMINARY; PRT; 238 AA.
AC 09WTJ9;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE NATURAL KILLER CELL PROTEIN GROUP 2-C1.
GN KLRK2 OR NKG2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=9929364; PubMed=10369936;
RA Silver E.T., Lau J.C.Y., Kane K.P.;
RT "Molecular cloning of mouse NKG2A and C.";
RL Immunogenetics 49:727-730(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=99190498; PubMed=10092077;
RA LeDwasser S., Hande P., Mager D.L., Takel F.;
RT Cloning of murine NKG2A, B and C: second family of C-type lectin
RT receptors on murine NK cells.
RL Eur. J. Immunol. 29:755-761(1999).
DR EMBL: AF106010; AAD40223.1; -.
DR MGD: MGI:1336162; Klrcl.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 238 AA; 26811 MW; 8C3EDAA22D50451 CRC64;

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Query Match 26.9%; Score 7; DB 11; Length 238;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 20 DFLQSLIS 26
DB 167 DFLQSLIS 173
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RESULT 8 PRELIMINARY; PRT; 244 AA.
AC 09Z202;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE NATURAL KILLER CELL RECEPTOR NKG2A.
GN KLRK1 OR NKG2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=99034608; PubMed=9815261;
RA Vance R.E., Kraft J.R., Altman J.D., Jensen P.E., Raulat D.H.;

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"Mouse CD94/NGG2A is a natural killer cell receptor for the nonclassical major histocompatibility complex (MHC) class I molecule 0a-1(b).";
 J. Exp. Med. 188:1841-1848(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE=9929364; PubMed=10369936;
 RA Silver E.T., Lau J.C.Y., Kane K.P.;
 RT "Molecular cloning of mouse NKG2A and C.";
 RL Immunogenetics 49:727-730(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE=99190498; PubMed=10092077; Takei F.;
 RA Lotwasser S., Hande P., Mager D.L., Takei F.;
 RT "Cloning of murine NKG2A, B and C: second family of C-type lectin receptors on murine NK cells";
 RL Eur. J. Immunol. 29:755-761(1999).
 DR EMBL: AF095447; AAD03419.1; -;
 DR EMBL: AF106008; AAD40221.1; -;
 DR EMBL: AF109782; AAD24968.1; -;
 DR MGD: MGI:1336161; KIRCL
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PSS0041; C_TYPE_LECTIN_2; 1.
 RV Receptor.
 SQ SEQUENCE 244 AA; 27675 MW; 187E7A8439FBF68A CRC64;

Query Match 26.9%; Score 7; DB 11; Length 244;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
 |||||
 DB 173 DFLQSL 179

RESULT 9
 O9MUJ1 PRELIMINARY; PRT; 244 AA.
 AC O9MUJ1;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE NATURAL KILLER CELL RECEPTOR NKG2A.
 GN KIRCL OR NKG2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=99190498; PubMed=10092077;
 RA Lotwasser S., Hande P., Mager D.L., Takei F.;
 RT "Cloning of murine NKG2A, B and C: second family of C-type lectin receptors on murine NK cells";
 RL Eur. J. Immunol. 29:755-761(1999).
 DR EMBL: AF109783; AAD24969.1; -;
 DR MGD: MGI:1336161; KIRCL
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PSS0041; C_TYPE_LECTIN_2; 1.
 RV Receptor.
 SQ SEQUENCE 244 AA; 27605 MW; 072003BD7F5A4D9E CRC64;

Query Match 26.9%; Score 7; DB 11; Length 244;
 Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 20 DFLQSL 26
 |||||
 DB 173 DFLQSL 179

RESULT 10
 ID O9M9S3 PRELIMINARY; PRT; 263 AA.
 AC O9M9S3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE F14L17.18 PROTEIN (HYPOTHETICAL 29.1 KDA PROTEIN).
 GN F14L17.18.
 OS Arabidopsis thaliana (mouse-ear cress). Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots; Rosidae;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Liu S., Sakano H., Yu G., Lee J., Lenz C., Pham P., Toriumi M.,
 RA Chin C., Chlou J., Choi E., Chung M., Gonzalez A., Hwang B., Liu A.,
 RA Vaysberg M., Altali H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C., Shinn P., Southwick A., Davis R.,
 RA Ecker J., Federspiel N., Theologis A.;
 RT "The sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Ertu P., Lee J.M.,
 RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene F14L17.18 (GI:7262683).";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
 RA Lee J.M., Onodera C.S., Quach H.U., Tang C., Toriumi M., Wu H.C.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carlini P., Chen H., Cheuk R.,
 RA Hayashiraki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene F14L17.18 (GI:7262683).";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.U., Tang C., Toriumi M., Yu G.,
 RA Bowser L., Carlini P., Chen H., Cheuk R., Hayashiraki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,

RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
 RT *Full length cDNA of gene FILL17.18 (GI:726283).
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC012188; AAF3941.1; -
 DR EMBL: AF332452; AAG4815.1; -
 DR EMBL: AY059097; AAL15203.1; -
 DR EMBL: AF370156; AAK43971.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 263 AA; 29058 MW; E90F85763198C614 CRC64;

Query Match 26.9%; Score 7; DB 10; Length 363;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLQ 8
 DB 116 DGFLLQ 122

RESULT 11
 ID O9K8S9 PRELIMINARY; PRT; 280 AA.
 AC O9K8S9;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE MALTOSE/MALTODEXTRIN TRANSPORT SYSTEM (PERMEASE).
 GN BH2924.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=8665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE=20512582; Pubmed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kunara S.,
 RA Horikoshi K.,
 RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.;
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
 CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
 DR EMBL: AP001517; BAB0643.1; -
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp. 1.
 DR PROSITE: PS00402; BPD_TRANSP_INN_MEMBER; 1.
 KW Complete proteome: Transmembrane; Transport.
 SQ SEQUENCE 280 AA; 31670 MW; E7CBF59591B95C4 CRC64;

Query Match 26.9%; Score 7; DB 16; Length 280;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLLQ 9
 DB 112 GFLLLQ 118

RESULT 12
 ID O93LN5 PRELIMINARY; PRT; 373 AA.
 AC O93LN5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE OUTER PROTEIN J.
 OS Xanthomonas campestris (pv. vesicatoria).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xanthomonas.
 OX NCBI_TaxID=341;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Noel L.D., Thieme F., Neenstiel D., Bonus U.,
 RT *cDNA-AFLP analysis unravels a genome-wide hsp90-regulon in the plant
 RT pathogen Xanthomonas campestris pv. vesicatoria.*;
 RL Mol. Microbiol. 0:0-0(2001).
 DR EMBL: AY036108; AAK72486.1; -
 SQ SEQUENCE 373 AA; 40600 MW; 6AFE76783ACE642 CRC64;

Query Match 26.9%; Score 7; DB 2; Length 373;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
 DB 146 DFLQSL 152

RESULT 13
 ID O9LMT6 PRELIMINARY; PRT; 405 AA.
 AC O9LMT6;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE F2H15.16.
 GN F2H15.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA.
 RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Tortum M.,
 RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
 RA Alraei H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federspiel N.A., Theologis A.,
 RT *The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1.*;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC034106; AAF97273.1; -
 SQ SEQUENCE 405 AA; 45080 MW; B6814769864805D CRC64;

Query Match 26.9%; Score 7; DB 10; Length 405;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLOSL 25
 DB 37 VDFLOSL 43

RESULT 14
 ID O9KLJ7 PRELIMINARY; PRT; 547 AA.
 AC O9KLJ7;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ANAEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE, SUBUNIT A.
 GN VCA0747.

OS *Vibrio cholerae*.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
 CX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ET TOR N16961 / SEROTYPE O1;
 RA MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tellein H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McAnulla L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT *DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT *cholerae*.
 RL Nature 406:477-483(2000).
 DR EMBL: AEO04403; AAF96645.1; -.
 DR TIGR: VCA0747; -.
 DR InterPro: IPR000447; FAD_GLY3P_dh.
 DR InterPro: IPR001345; PG_mutase.
 DR PRINTS: PR01001; FADG3PDH.
 DR PROSITE: PS00978; FAD_G3PDH_2; 1.
 DR PROSITE: PS00175; PG_MUTASE; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 547 AA; 59915 MW; ACS942DEDD04165A8 CRC64;

Query Match 26.9%; Score 7; DB 16; Length 547;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLYDFL 22
 |||||
 DB 495 HLYDFL 501

RESULT 15
 ID O9S6R3 PRELIMINARY; PRT; 846 AA.
 AC O9S6R3.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ESPP PROTEIN (FRAGMENT).
 GN ESPP.
 OS *Escherichia coli*.
 OC Plasmid p0157.
 OC *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 CX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99303308; PubMed=10376815;
 RA Brunder W., Schmidt H., Frosch M., Karch H.;
 RT *The large variable of *Shiga-toxin*-producing *Escherichia coli* (STEC)
 RT are highly variable genetic elements.*;
 RL Microbiology 145:1005-1014(1999).
 DR EMBL: AJ010390; CAB42538.1; -.
 DR InterPro: IPR000710; IGA_S6.
 DR Pfam: PF02395; IGA1; 1.
 KW Plasmid.
 RT none;
 FT NON_TER 1 1
 SQ SEQUENCE 846 AA; 91894 MW; 124C9E23421CDCEB CRC64;

Query Match 26.9%; Score 7; DB 2; Length 846;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 HLYDFLQ 23
 |||||
 DB 479 HLYDFLQ 485

RESULT 16
 ID O94CF2 PRELIMINARY; PRT; 861 AA.
 AC O94CF2.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHEICAL 96.6 KDA PROTEIN.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
 RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki T., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Kosemura E.,
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shin P., Southwick A.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT *Full length cDNA of gene T3266.14/At2g41620 (GI:2618698).*;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDI databases.
 DR EMBL: AY034907; AAK59414.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 861 AA; 96615 MW; 9F53F0BF013D673 CRC64;

Query Match 26.9%; Score 7; DB 10; Length 861;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DELOSUS 26
 |||||
 DB 146 DELOSUS 152

RESULT 17
 ID O9XX09 PRELIMINARY; PRT; 903 AA.
 AC O9XX09.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Y39A1A.15C PROTEIN.
 GN Y39A1A.15C.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 CX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wall M.;
 RT submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99069613; PubMed=9851916;
 RT none;
 FT "Genome sequence of the nematode *C. elegans*: A platform for
 RT investigating biology.*;
 RL Science 282:2012-2018(1998).
 DR EMBL: AL031633; CA21032.1; -.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001806; Ras_transferring.
 DR InterPro: IPR003575; Small_GTPase.
 DR InterPro: IPR001164; Znf_GCS.
 DR Pfam: PF00023; ank; 2.
 DR Pfam: PF01412; ArtGap; 1.
 DR Pfam: PF00169; PH; 1.

DR PRINTS: PR00449; RASTRNSFRNG.
 DR PRINTS: PR00405; REVINTRACTING.
 DR SMART: SM00248; ANK; 2.
 DR SMART: SM00105; ArfGap; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00010; small_GTPase; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 1.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR ANK repeat; GTP-binding; Repeat.
 KW ANK repeat; GTP-binding; Repeat.
 SO SEQUENCE 903 AA; 99830 MW; A9D5EE112AFDC66 CRC64;

Query Match 26.9%; Score 7; DB 5; Length 903;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 LTVDFLQ 23
 |||||
 Db 7 LTVDFLQ 13

RESULT 18
 ID 032555 PRELIMINARY; PRT; 1300 AA.
 AC 032555.

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE PUTATIVE EXOPROTEIN-PECURSOR.

GN Espp.
 OS Escherichia coli O157:H7.

OC Bacteri; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Plasmid p0157.

OC Escherichia
 OX NCBI_TaxID=83334;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-EDL933;
 RX MEDLINE=9738033; PubMed=9194704;

RA Brunder W., Schmidt H., Karch H.;
 *Espp, a novel extracellular serine protease of enterohaemorrhagic
 RT Escherichia coli O157:H7 cleaves human coagulation factor V.*;

RL Mol. Microbiol. 24:767-778(1997).

RN [2]
 RP SEQUENCE FROM N.A.

RC MEDLINE=98290540; PubMed=9628576;
 RA Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,

Yatsudo H.C., Kubota Y., Yamachi Y., Iida T., Yamamoto K., Honda T.,
 Han C., Ohtsubo A., Kasamatsu M., Hayashi T., Kuhara S., Shinagawa H.;

*Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an
 RT enterohaemorrhagic Escherichia coli O157:H7 derived from Sakai

outbreak.*;

RL DNA Res. 5:1-9(1998).

RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN-EDL933;
 RX MEDLINE=98391744; PubMed=9722640;
 RA Brund V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,

Blattner F.R.;
 *The complete DNA sequence and analysis of the large virulence plasmid
 RT of Escherichia coli O157:H7.*;

RL Nucleic Acids Res. 26:4196-4204(1998).

DR EMBL: X97542; CA66144.1; -;
 DR EMBL: AB011549; BA31836.1; -;

DR EMBL: AF074613; AAC70088.1; -;
 DR MEROPS: S06.002; -;

DR InterPro: IPR000710; IGA_S6.

KM Pfam: PF03395; IGA1; 1.

DR Signal; Plasmid; Protease.
 FT SIGNAL 1 35
 FT CHAIN 56 1023 POTENTIAL.
 SO SEQUENCE 1300 AA; 141757 MW; E34D3F037DRC672F CRC64;

Query Match 26.9%; Score 7; DB 2; Length 1300;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 LTVDFLQ 23
 |||||
 Db 933 LTVDFLQ 939

RESULT 19
 ID 032591 PRELIMINARY; PRT; 1300 AA.
 AC 032591.

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PROTEASE.

GN PSSA.

OS Escherichia coli.
 OC Bacteri; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.
 OX NCBI_TaxID=562;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=413/89-11;
 RX MEDLINE=98025473; PubMed=9379905;

RA Djafarzadeh S., Ebel F., Deibel C., Kramer S., Hudel M., Chakraborty T.;
 *Characterization of an exported protease from Shiga toxin-producing

RT Escherichia coli.*;

RL Mol. Microbiol. 25:771-784(1997).

DR EMBL: Y13614; CA73935.1; -;
 DR MEROPS: S06.002; -;

DR InterPro: IPR000710; IGA_S6.

DR Pfam: PF03395; IGA1; 1.
 SO SEQUENCE 1300 AA; 141710 MW; F84D24086DE77C24 CRC64;

Query Match 26.9%; Score 7; DB 2; Length 1300;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 LTVDFLQ 23
 |||||
 Db 933 LTVDFLQ 939

RESULT 20
 ID 09L719 PRELIMINARY; PRT; 81 AA.
 AC 09L719.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE CPGB (FRAGMENT).

GN CPGB.

OS Synechococcus sp. PS672.
 OC Bacteri; Cyanobacteria; Chroococcales; Synechococcus.

OX NCBI_TaxID=115754;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=PS672;
 RX MEDLINE=21304427; PubMed=11411708;

RA Robertson B.R., Tezuka N., Watanabe M.M.;
 *Phylogenetic analyses of Synechococcus strains (cyanobacteria) using

RT multiple evolutionary lines and part of the phyococyanin operon reveal
 RT sequences of 16S rDNA and part of the phyococyanin content.*;

RL Int. J. Syst. Evol. Microbiol. 51:861-871(2001).

DR EMBL: AF223433; AAF60094.1; -;
 DR HSSP: P00311; IPHN.

DR InterPro: IPR001659; Phycobillisoem.
 PFam: PF00502; Phycobillisoem; 1.

FT NON_TER 1 1
 SO SEQUENCE 81 AA; 8455 MW; 606190A7C5B0CB76 CRC64;

Query Match 23.1%; Score 6; DB 2; Length 81;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFILL 7
 |||||
 Db 9 DGFILL 14

RESULT 21

O95L08 PRELIMINARY; PRT; 88 AA.

AC O95L08; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE APOLOPROTEIN B (FRAGMENT).
 OS Ateles belzebuth chamek (Chamek spider monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
 OX NCBI_TaxID=118643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Senarez H.N., Lima C.R., Lemos B., Bonvicino C.R., Moreira M.M.,
 RA Canavez F.C.;
 RT "Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).
 RT Allocation of 18 markers of human syntenic groups 1, 2, 7, 14, 15, 17,
 RT and 22.";
 RL Chromosome Res. 9:631-639(2001).
 DR EMBL: AY040549; AAK82940.1; -
 KW Lipo-protein.
 FT NON_TER 1 1
 FT NON_TER 88 88
 SO SEQUENCE 88 AA; 9981 MW; 95E7947A3DB73142 CRC64;

Query Match 23.1%; Score 6; DB 6; Length 88;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMD 10
 |||||
 Db 15 LLLQMD 20

RESULT 22

O9MC72 PRELIMINARY; PRT; 111 AA.

AC O9MC72; 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ORE50.
 CN ORE50.
 OS Bacteriophage D3.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda phage group.
 OX NCBI_TaxID=31535;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20042341; PubMed=10572124;
 RT Cloning and analysis of the capsid morphogenesis genes of Pseudomonas
 RT aeruginosa bacteriophage D3: another example of protein chain mal17";
 RL J. Bacteriol. 181:7221-7227(1999).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20485557; PubMed=11029426;
 RX Kropinski A.M.;

RT "Sequence of the Genome of the Temperate, Serotype-Converting,
 RT Pseudomonas aeruginosa Bacteriophage D3.";
 RL J. Bacteriol. 182:6066-6074(2000).
 DR EMBL: AF165214; AAF80809.1; -
 SO SEQUENCE 111 AA; 12720 MW; 426E2DD0BAAD7413 CRC64;

Query Match 23.1%; Score 6; DB 9; Length 111;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFILL 7
 |||||
 Db 37 DGFILL 42

RESULT 23

O9DBU1 PRELIMINARY; PRT; 112 AA.

AC O9DBU1; 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE 1810033P05SRK PROTEIN.
 GN 1810033P05SRK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SYRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamana I.,
 RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Matchioni L., Mashima J., Mazzarelli J., Kombeerts P.,
 RA Norcone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK007685; BAB25150.1; -
 DR MGD; MGI:1916434; 1810033P05SRK.
 SO SEQUENCE 112 AA; 12043 MW; D97AAE4236659EEF CRC64;

Query Match 23.1%; Score 6; DB 11; Length 112;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLILL 8
 |||||
 Db 39 GFLILL 44

RESULT 24

O9R317 PRELIMINARY; PRT; 115 AA.

AC O9R317; 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE HYPOTHETICAL 12.9 KDA PROTEIN (HYPOTHETICAL PROTEIN PA0634).
 GN PA0634.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision: Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01. AND PML14;
 RA Nakayama K., Kashihara K., Ishihara H., Shinomiya T., Kageyama M.,
 Kanaya S., Ohnishi M., Murata T., Terahashi Y., Mori H., Hayashi T.,
 RT "Genetic relationship between bacteriocins and bacteriophages."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Ervin A.L., Mizoguchi S.D., Warrenner P.,
 Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
 Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen."
 RL Nature 406:959-964 (2000).
 DR EMBL: AB030825; BAA83173.1; -;
 DR EMBL: AB030826; BAA83141.1; -;
 DR EMBL: AB004495; AAC04023.1; -;
 KW EMBL: AB004495; AAC04023.1; -;
 SO SEQUENCE 115 AA; 12870 MW; BB69B6D3D19E49 CRC64;

Query Match 23.1%; Score 6; DB 16; Length 115;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLIQLQ 8
 Db 96 GFLIQLQ 101
 ID 067666 PRELIMINARY; PRT; 130 AA.
 AC 067666;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE HYPOTHETICAL 15.6 KDA PROTEIN.
 GN AQ.1797.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RA MEDLINE=9819666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Warren R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus."
 RL Nature 392:353-358 (1998).
 DR EMBL: AEO00756; AAC07630.1; -;
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 130 AA; 15626 MW; 45CF04E5F6D90DDF CRC64;

Query Match 23.1%; Score 6; DB 16; Length 130;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLYDFL 22
 Db 80 LLYDFL 85
 ID 09JM85 PRELIMINARY; PRT; 150 AA.
 AC 09JM85;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE D64 PROTEIN.
 GN ETOS1 OR DD64.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ikegawa S., Nakamura Y.,
 RT "DD64, a novel mouse gene implicated in the early stage of ectopic
 RT ossification."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB036742; BAA95410.1; -;
 DR MGD, MGI:2149837; Etos1
 SO SEQUENCE 150 AA; 17248 MW; 23309C51DB484C7 CRC64;

Query Match 23.1%; Score 6; DB 11; Length 150;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLIQLQ 8
 Db 120 GFLIQLQ 125
 ID 09DB70 PRELIMINARY; PRT; 155 AA.
 AC 09DB70;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE 1500005J14RIK PROTEIN (RIKEN CDNA 1500005J14 GENE).
 GN 1500005J14RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TTSUB=CERE8BLUM;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka S.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiava H.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,
 RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,

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RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cdna collection.";
RL Nature 409:685-690(2001).
RM [2]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005163; BAB23854.1; -
DR EMBL; BC012515; AAH12515.1; -
DR MGD; MGI:1919268; 150000514R1k.
SQ SEQUENCE 155 AA; 17158 MW; 8AA46566714ED80 CRC64;

Query Match          23.1%; Score 6; DB 11; Length 155;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLUQ 8
   |||||
DB 82 GFLUQ 87

RESULT 28
Q9SKX1 PRELIMINARY; PRT; 156 AA.
ID Q9SKX1;
AC Q9SKX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE At2g43060 PROTEIN.
GN At2g43060.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.; Kaul S.; Rounsley S.D.; Shea T.P.; Benito M.-I.; Town C.D.;
RA Fujii C.Y.; Mason T.M.; Bowman C.L.; Barnstead M.E.; Feldblyum T.V.;
RA Buelli C.R.; Ketchum K.A.; Lee J.J.; Ronning C.M.; Koo H.; Moffat K.S.;
RA Cronin L.A.; Shen M.; Vanaken S.F.; Mayhew L.; Tallon L.J.; Gill J.E.;
RA Adams M.D.; Carrera A.J.; Creasy T.H.; Goodman H.M.; Somerville C.R.;
RA Salzberg S.L.; Fraser C.M.; Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana."
RT thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006224; AAD2125.1; -
SQ SEQUENCE 156 AA; 17825 MW; 7DBCT5BE4047A48A CRC64;

Query Match          23.1%; Score 6; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLQSL 26
   |||||
DB 22 FLQSL 27

RESULT 29
Q97VI6 PRELIMINARY; PRT; 163 AA.
ID Q97VI6;
AC Q97VI6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)

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DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE, SMALL CHAIN, AMINO-END FRAGMENT
DE (CUTC-2) (EC 1.2.99.2).
GN CUTC-2.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RA MEDLINE=21332296; PubMed=11427726;
RA She Q.; Singh R.K.; Confalonieri F.; Zivanovic Y.; Allard G.;
RA Awaizer M.J.; Chan-Welher C.C.-Y.; Clausen I.G.; Curtis B.A.;
RA De Moors A.; Erauso G.; Fletcher C.; Gordon P.M.K.;
RA Heikamp-de Jong I.; Jeffries A.C.; Kozera C.J.; Medina N.; Peng X.;
RA Thi-Ngoc H.P.; Redder P.; Schenk M.B.; Theriault C.; Tolstrup N.;
RA Charlebois R.L.; Doollittle W.F.; Duguet M.; Gaasterland T.;
RA Garrett R.A.; Ragan M.A.; Sengen C.W.; Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus p2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006859; AAK42758.1; -
DR InterPro; IPR002888; 2Fe-2S-BD.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF01111; fer2; 1.
DR Pfam; PF01799; fer2.2; 1.
DR Prodom; PD186071; 2Fe-2S-BD; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 163 AA; 17953 MW; FDCDD218ECFDF0F5F6 CRC64;

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Query Match          23.1%; Score 6; DB 17; Length 163;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LWDPL 22
   |||||
DB 30 LWDPL 35

RESULT 30
ID 052661 PRELIMINARY; PRT; 166 AA.
ID 052661;
AC 052661;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PRIMARY SIGMA FACTOR RPOD (RPOD) AND UNKNOWN ORF 1 GENES, AND UNKNOWN
DE ORF 2.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;
OC Rhodospirillum.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SH1003;
RA Zheng S.; Scappino L.; Haselkorn R.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28162; AAA70412.1; -
SQ SEQUENCE 166 AA; 18009 MW; 95AF53474634B9DB CRC64;

Query Match          23.1%; Score 6; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQSL 25
   |||||
DB 154 DFLQSL 159

RESULT 31
Q9P3B0

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ID 09P380 PRELIMINARY; PRT: 166 AA.
 AC 09P380:
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE VERY HYPOTHEICAL PROTEIN.
 GN SPAC1565.03.
 OS Schizosaccharomyces pombe (Pisalion yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H.
 RA Seeger K., Harris D., Wood V., Rajandream M.A., Barrett B.G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL390274; CAB99270.1;
 DR InterPro: IPR001230; Pfam: P00440; TrEMBL: P00440.
 DR PROSITE: PS00294; Pfam: P00440; TrEMBL: P00440.
 KW Hypothetical protein.
 SQ SEQUENCE 166 AA; 18985 MW; D52D50C4DCB02297 CRC64;

Query Match 23.1%; Score 6; DB 3; Length 166;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSLS 26
 Db 135 FLOSLS 140

RESULT 32
 ID 055840 PRELIMINARY; PRT: 204 AA.
 AC 055840:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE HYPOTHEICAL 23.4 KDA PROTEIN.
 GN SLR0517.
 OS Synchocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-96127529; PubMed-8590279;
 RA Kaneo T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 * Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synchocystis sp. strain PCC6803. I. Sequence features on the 1 Mb
 RL region from map positions 644 to 924 of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-97061201; PubMed-8905231;
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Haruo K., Okumura S.,
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.;
 * Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
 RL entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-116(1996).
 DR EMBL; D64004; BAA10596.1;
 DR InterPro: IPR000182; Acetyltransferase-GCN5.
 DR Pfam: PFO0583; Acetyltransferase; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 204 AA; 23376 MW; 4A60C87CCDDA6B4 CRC64;

Query Match 23.1%; Score 6; DB 16; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDFPL 22
 Db 23 LVDFPL 28

RESULT 33
 ID 09A706 PRELIMINARY; PRT: 210 AA.
 AC 09A706:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE TRANSCRIPTIONAL REGULATOR, TETR FAMILY.
 GN CC1664.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCBI_TaxID=69394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 19089 / CB15;
 RA MEDLINE-21173698; PubMed-11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.R., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouli H., Shetty J., Berry K.,
 RA Uitterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc Natl Acad Sci U S A. 98:4136-4141(2001)
 CC - SIMILARITY: BELONGS TO THE TETR/ACR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC EMBL; AF005841; AAK23642.1;
 DR TIGR; CC1664;
 DR InterPro: IPR001647; HTH_Tetr.
 DR Pfam: PFO0440; Tetr. 1.
 DR PRINTS: PR00455; HTH_Tetr.
 KW Complete proteome; DNA-binding; Transcription regulation.
 SQ SEQUENCE 210 AA; 22742 MW; B181CDD406C2CFA1 CRC64;

Query Match 23.1%; Score 6; DB 16; Length 210;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLOLS 24
 Db 182 VDFLOLS 187

RESULT 34
 ID 09D68 PRELIMINARY; PRT: 222 AA.
 AC 09D68:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 2310075612R1K PROTEIN.
 GN 2310075612R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-TONGUE;
 RA MEDLINE-21085660; PubMed-11217851;
 KW Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Oikio T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Hyslav-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK010175; BAB26748.1; -
 DR MGD: MG1:1916924; 2310075G12R1K.
 DR InterPro: IPR003890; EIP4G_cent.
 DR SMART: SM00543; MIF4G; 1.
 SQ SEQUENCE 222 AA; 25493 MW; 2A0D56790F33701E CRC64;

Query Match 23.1%; Score 6; DB 11; Length 222;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 |||||
 Db 178 RDGFLL 183

RESULT 35
 09ST53 PRELIMINARY; PRT; 235 AA.
 AC 09ST53;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MADS-box PROTEIN 4.
 OS Malus domestica (apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids I; Rosales; Rosaceae; Maloideae; Malus.
 OC NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV: FULL; TISSUE=FLOWER BUDS;
 RX MEDLINE=20246725; PubMed=10787044.
 RA Sung S.K., Yu G.H., Nam J., Jeong D.H., An G.,
 RT "Developmentally regulated expression of two MADS-box genes, MdMADS3
 RT and MdMADS4, in the morphogenesis of flower buds and fruits in
 RT apple.",
 RL Planta 210:519-528(2000).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL: U78950; AAD51423.1; -
 DR HSSP: P11831; ISRS.
 DR TRANSFAC: T04732;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PRO0432; MADSBOX.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00356; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR DN3-binding; Nuclear protein; Transcription regulation.
 KM DN3-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 235 AA; 26690 MW; 6613CA8601CA8F1B CRC64;

Query Match 23.1%; Score 6; DB 10; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GPEHL 17
 |||||
 Db 193 GPEHL 198

RESULT 36
 086738 PRELIMINARY; PRT; 241 AA.
 AC 086738;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HYPOTHETICAL 26.3 KDA PROTEIN.
 GN SC6A9.06.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Murphy L., Harris D.,
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denaparte D., Eichner A., Cullum J.,
 RA Kinash H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.",
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL031035; CAI19891.1; -
 DR InterPro: IPR004129; GDP.
 DR InterPro: IPR000909; PL_PLC_X.
 DR Pfam: PF03009; GDP.
 DR PROSITE: PS50007; PLPLC_X_DOMAIN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 241 AA; 26349 MW; D238AC642110406A CRC64;

Query Match 23.1%; Score 6; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 |||||
 Db 193 RDGFLL 198

RESULT 37
 09K909 PRELIMINARY; PRT; 260 AA.
 AC 09K909;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE.
 GN BH2843.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OC NCBI_TaxID=86655;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RX MEDLINE-20512582; PubMed-11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL, AP001516; BAB06562.1; -.
DK HSSP; P29132; 1DFT.
KM Complete proteome.
SQ SEQUENCE 260 AA; 28101 MW; 155D849A9AF40C03P CRC64;

Query Match 23.1%; Score 6; DB 16; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFL 6
DB 113 RDGFL 118

RESULT 38
O99UJ1 PRELIMINARY; PRT; 275 AA.
ID O99UJ1.
AC 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DR 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN SAI124 (HYPOTHETICAL PROTEIN SAV1281).
GN SAI124 OR SAV1281.
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain M50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879, 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus (strain N315), and S.aureus (strain M50);
RX MEDLINE-21311952; PubMed-11418146;
RA Kuroda M., Ohta T., Uchiyama I., Babe T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hsuyama A.,
RA Mizutani-U I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Karihisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shida T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL, AP003333; BAB42376.1; -.
DK EMBL, AP003361; BAB57443.1; -.
DR InterPro; IPR002912; ACT.
PF pfam; PF01842; ACT; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 275 AA; 31478 MW; AD7A1FCEADB69CAE CRC64;

Query Match 23.1%; Score 6; DB 16; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LLYDFL 22
DB 114 LLYDFL 119

RESULT 39
O87858 PRELIMINARY; PRT; 279 AA.
ID O87858

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AC 087858;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DR 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE TRANSMEMBRANE SUGAR TRANSPORT PROTEIN.
GN SC8A6.24.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Parkhill J., Barrett B.G., Rajandream M.A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE=97000351; PubMed-8843436;
RA Redenbach M., Kleser H.M., Denaplatte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Microbiol. 21:77-96(1996).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM.
CC -1- PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE SUBSTRATE ACROSS
CC THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL, AL031013; CAI9796.1; -.
DK InterPro; IPR000515; BPD_transp.
DR InterPro; IPR000531; TONB_boxC.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMB; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Sugar transport; Transmembrane; Transport.
SQ SEQUENCE 279 AA; 30335 MW; 886063385E8F3BFA CRC64;

Query Match 23.1%; Score 6; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLQ 8
DB 261 GFLLQ 266

RESULT 40
O9N535 PRELIMINARY; PRT; 279 AA.
ID O9N535
AC 09N535;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DR 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 31.8 KDA PROTEIN.
GN Y32H12A.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for

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RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Holmes A., Elliott G., Cloud J.;
RT "The sequence of C. elegans cosmid Y32H12A.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006733; AAF60484.1; -
KW Hypothetical protein.
SQ SEQUENCE 279 AA; 31829 MW; 47286DB425912264 CRC64;

Query Match 23.1%; Score 6; DB 5; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FLLQMD 10
DB 236 FLLQMD 241

RESULT 41
O07011 PRELIMINARY; PRT; 283 AA.
AC O07011;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHELICAL 31.3 KDA PROTEIN.
GN YFM.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
[1]
RP SEQUENCE FROM N.A.
RA Denizot F.C.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA MEDLINE-98044033; PubMed-9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel N.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Ghim S.Y., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Grand G.,
RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasehara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koeltter P., Konigstein G., Krogh S., Kumano M.,
RA Kunita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ojawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Popollik S., Prescott A.M.,
RA Preece E., Fujic P., Punnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Saito T., Scallan E., Schleich S., Schroeter R., Scoffone F.,
RA Spkiguchi J., Sekowska A., Seror S.J., Serrito P., Shin B.S., Soldo B.,
RA Sorokin A., Taccoti E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

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RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viéri A., Wambolt R., Wedler E., Wedler H., Weitenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; Z96043; CAB08007.1; -
DR EMBL; Z99121; CAB15419.1; -
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp.1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR.1.
KW Complete proteome: Hypothetical protein; Transmembrane; Transport.
SQ SEQUENCE 283 AA; 31305 MW; 168D39BC8721CE2E CRC64;

Query Match 23.1%; Score 6; DB 16; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLQMD 9
DB 116 FLLQMD 121

RESULT 42
O9KBA7 PRELIMINARY; PRT; 283 AA.
ID O9KBA7;
AC O9KBA7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MALTOSE/MALTODEXTRIN TRANSPORT SYSTEM (PERMEASE).
GN BH2021.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RA MEDLINE-20512562; PubMed-11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; AP001514; BAB05740.1; -
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp.1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR.1.
KW Complete proteome: Transmembrane; Transport.
SQ SEQUENCE 283 AA; 31353 MW; 2072AFBFC7C00FP8 CRC64;

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Query Match 23.1%; Score 6; DB 16; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FILLQ 9
DB 116 FILLQ 121

RESULT 43
09R085 PRELIMINARY; PRT: 289 AA.

AC 09F085;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE CHLOROPLAST RNA HELICASE VDL' ISOFORM 5 (FRAGMENT).
GN VDL'.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, SRL;
RX MEDLINE=20541613; PubMed=11090214;
RA Wang Y., Dudy G., Purnelle B., Bouvry M.;
RT "Tobacco VDL Gene Encodes a Plastid DEAD Box RNA Helicase and Is
Involved in Chloroplast Differentiation and Plant Morphogenesis.";
RL Plant Cell 12:2129-2142(2000).
DR EMBL: AF261032; AAC8497.1; -;
DR InterPro: IPR001410; DEAD.
DR Pfam: PF00270; DEAD. 1.
DR SMART: SMO0487; DEXDC. 1.
KW ATP-binding; Helicase.
FT NON_TER 289
SQ SEQUENCE 289 AA; 31822 MW; FE5AA248C78FF4F2 CRC64;

Query Match 23.1%; Score 6; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDPL 22
DB 271 LVDPL 276

RESULT 44
09KD33 PRELIMINARY; PRT: 298 AA.

AC 09KD33;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ENDONUCLEASE IV.
GN BH1386.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001511; BAB05105.1; -;

DR HSSP: P12638; 10TW.
DR InterPro: IPR001719; AP_endonuclease_2.
DR Pfam: PF01261; AP_endonuclease2; 1.
DR SMART: SM00518; AP2ec; 1.
DR PROSITE: PS00729; AP_NUCLEASE_F2_1; 1.
DR PROSITE: PS00730; AP_NUCLEASE_F2_2; UNKNOWN_1.
DR PROSITE: PS00731; AP_NUCLEASE_F2_3; 1.
KW Complete proteome.
SQ SEQUENCE 298 AA; 32997 MW; 9A25ED881A755B4B CRC64;

Query Match 23.1%; Score 6; DB 16; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLOS 24
DB 90 VDFLOS 95

RESULT 45
085704 PRELIMINARY; PRT: 303 AA.

AC 085704;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE HEME A SYNTHASE (SA0964 PROTEIN) (HYPOTHETICAL PROTEIN
SAV1115).
GN CTA A OR SA0964 OR SAV1115.
OS Staphylococcus aureus;
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain Mu50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280; 158879, 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=8325-4;
RA Clements M.O., Watson S.P., Foster S.J.;
RT "Starvation-survival and recovery of Staphylococcus aureus require
CTA, a putative heme A synthase.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iken J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Matsuyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AF072726; AAD09875.1; -;
DR EMBL: AP003132; BAB42212.1; -;
DR EMBL: AP003361; BAB57277.1; -;
DR InterPro: IPR003780; COX15_CtaA.
DR Pfam: PF02628; COX15-CtaA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 303 AA; 34059 MW; 21D3ECC1812C260 CRC64;

Query Match 23.1%; Score 6; DB 16; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLQ 8
DB 100 GFLQ 105

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RESULT 46
Q9HBL5 PRELIMINARY; PRT; 305 AA.
ID Q9HBL5
AC Q9HBL5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE AD023.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RA Xiao H., Song H., Gao G., Ren S., Chen Z., Han Z.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF225422; AAC09724.1;
SQ SEQUENCE 305 AA; 34261 MW; 452D9FB5F9F70F CRC64;

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Query Match 23.1%; Score 6; DB 4; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DGFLL 6
DB 178 DGFLL 183

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RESULT 47
Q9P800 PRELIMINARY; PRT; 311 AA.
ID Q9P800
AC Q9P800;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NTG1 (FRAGMENT).
GN NTG1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RA Dicken S., Koetter P., Ertian K.;
RT *Characterization of CAT8 of Candida albicans.*;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222908; AAF35322.1;
DR HSSP; P20625; ZABK.
DR InterPro; IPR004036; Endonuclease_IIT_HhH.
DR InterPro; IPR003265; Endo_3c.
DR Pfam; PF00730; HhH-GPD; 1.
DR SMART; SM00478; Endo3c; 1.
DR PROSITE; PS01155; ENDONUCLEASE_IIT_2; UNKNOWN_1.
FT NON_TER 311
SQ SEQUENCE 311 AA; 35180 MW; 59908B8959C0B71 CRC64;

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Query Match 23.1%; Score 6; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 GFLILQ 8
DB 199 GFLILQ 204

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RESULT 48
Q9DB26 PRELIMINARY; PRT; 311 AA.
ID Q9DB26

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AC Q9DB26;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADULT MALE CEREBELLUM CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:1500019N11, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Balov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carpinici P., de Ronaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guertincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Matzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL; AK005293; BAB23937.1;
SQ SEQUENCE 311 AA; 34614 MW; D89EBF6A84D2C5 CRC64;

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Query Match 23.1%; Score 6; DB 11; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 DGFLL 7
DB 35 DGFLL 40

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RESULT 49
Q99RY9 PRELIMINARY; PRT; 313 AA.
ID Q99RY9
AC Q99RY9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SA2078 PROTEIN (HYPOTHETICAL PROTEIN SAV2283).
GN SA2078 OR SAV2283.
OS staphylococcus aureus (strain N315), and
OS staphylococcus aureus (strain Mu50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879, 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX MEDLINE=21311952; Pubmed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yanuzaki J.,
RA Kanehisa M., Yamashita A., Oshuma K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
RT *Whole genome sequencing of methicillin-resistant Staphylococcus

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RT aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003136; BAB4375.1; -;
 DR EMBL: AP003364; BAB58445.1; -;
 DR InterPro: IPR001910; IUNH.
 DR Pfam: PF01156; I0_nuc_hydro; 1.
 DR ProDom: PD007736; IUNH; 1.
 KW Complete proteome: Hypothetical protein.
 SQ SEQUENCE 313 AA; 35362 MW; E335FAF497CH755A CRC64;

Query Match 23.1%; Score 6; DB 16; Length 313;
 Best Local Similarity 100.0%; Pred.No.1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FILLQM 9
 |||||
 DB 20 FILLQM 25

RESULT 50
 O9FQ84 PRELIMINARY: PRT; 324 AA.
 AC O9FQ84;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PUTATIVE CHLOROPLAST RNA HELICASE VDL ISOFORM 4 (FRAGMENT).
 GN VDL.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SR1;
 RX MEDLINE=20341613; PubMed=11090214;
 RA Wang Y., Dudy G., Purnelle B., Boult M.;
 RT "Tobacco VDL Gene Encodes a Plastid DEAD Box RNA Helicase and Is
 RT Involved in Chloroplast Differentiation and Plant Morphogenesis.";
 RL Plant Cell 12:2129-2142(2000).
 DR EMBL: AF261032; AAG38496.1; -;
 DR InterPro: IPR001410; DEAD.
 DR Pfam: PF00270; DEAD; 1.
 DR SMART: SM00487; DEXDC; 1.
 KW ATP-binding; Helicase.
 FT NON_TER 324
 SQ SEQUENCE 324 AA; 36250 MW; C3118BCBDC8A53BC CRC64;

Query Match 23.1%; Score 6; DB 10; Length 324;
 Best Local Similarity 100.0%; Pred.No.1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LTVDFL 22
 |||||
 DB 306 LTVDFL 311

Search completed: June 19, 2002, 11:11:05
 Job time: 204 sec

10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:05:35 : Search time 29.84 seconds
(without alignments)
96,780 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26
Sequence: 1 RDGFLQMDPFCPEHLVDFLOSLIS 26

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

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22: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result: being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	26	17	AAW06128 Human cholesteryl
2	26	100.0	26	21	AAV13801 Rabbit CERP immuno
3	26	100.0	26	21	AAV91228 Human cholesteryl
4	26	100.0	46	21	AAV91233 Modified MYP Th ep
5	26	100.0	46	21	AAV91233 Modified MYP Th ep
6	26	100.0	476	17	AAW06127 Human cholesteryl
7	26	100.0	476	18	AAW64446 Human mature chole
8	26	100.0	476	20	AAV02466 Human cholesteryl
9	26	100.0	493	15	AAW63442 Partial human LipI
10	26	100.0	493	20	AAV49556 Human cholesteryl
11	26	100.0	493	20	AAV49556 Human cholesteryl

12	26	100.0	493	22	AAW65636 Human cholesteryl
13	22	84.6	22	20	AAV13815 Rabbit CERP immuno
14	22	84.6	22	20	AAV13821 Human CERP immuno
15	22	84.6	496	20	AAV02469 Human used rabbit c
16	22	84.6	16	21	AAV91229 Human cholesteryl
17	16	61.5	16	21	AAV91229 Anti-cholesteryl e
18	16	61.5	31	17	AAW06129 Fusion of a tetanu
19	16	61.5	35	21	AAV91236 Modified HBVSufac
20	16	61.5	36	21	AAV91234 Modified MYP Th ep
21	16	61.5	36	21	AAV91235 Modified MYP Th ep
22	16	61.5	30	21	AAV91237 Modified MYP Th ep
23	16	61.5	36	21	AAV91237 Anti-cholesteryl e
24	11	42.3	11	18	AAW24294 Human/Rabbit CERP
25	11	42.3	16	21	AAV91230 Human cholesteryl
26	11	42.3	22	20	AAV13803 Rabbit CERP immuno
27	11	42.3	26	20	AAV13802 Rabbit CERP immuno
28	11	42.3	26	21	AAV91231 Human cholesteryl
29	11	42.3	36	21	AAV91238 Modified MYP Th ep
30	11	42.3	36	21	AAV91239 Modified MYP Th ep
31	11	42.3	46	21	AAV91240 Modified MYP Th ep
32	11	42.3	46	21	AAV91241 Anti-cholesteryl e
33	11	42.3	50	17	AAW06132 CERP B cell epitop
34	11	42.3	50	18	AAW6447 Modified rabbit ch
35	11	42.3	477	20	AAV02468 Rabbit cholesteryl
36	11	42.3	496	17	AAW06133 Mature rabbit chol
37	11	42.3	496	18	AAW6445 Rabbit cholesteryl
38	11	42.3	51	20	AAV02467 Rabbit cholesteryl
39	7	26.9	51	22	AAW1886 Novel human respir
40	7	26.9	186	22	ABG07716 Novel human diagno
41	7	26.9	401	22	ABG15752 Novel human diagno
42	7	26.9	417	22	ABG07733 Novel human diagno
43	7	26.9	422	15	AAW54202 snA4 gene product
44	7	26.9	466	22	ABG16251 Novel human diagno
45	7	26.9	478	22	ABG15687 Novel human diagno
46	7	26.9	1501	22	AAW82878 S. epidermidis ope
47	6	23.1	14	20	AAV27814 Human secreted pro
48	6	23.1	31	21	AAW51836 Human secreted pro
49	6	23.1	42	21	AAW51836 Human secreted pro
50	6	23.1	56	22	ABW03312 Human musculoskele
51	6	23.1	65	22	ABW44219 Peptide #11725 enco
52	6	23.1	65	22	ABW27096 Protein #9095 enco
53	6	23.1	65	22	AAW65251 Human brain expres
54	6	23.1	65	22	AAW77956 Human bone marrow
55	6	23.1	65	22	AAW21850 Peptide #8284 enco
56	6	23.1	65	22	AAW38174 Peptide #12211 enc
57	6	23.1	69	22	AAW73544 Human colon cancer
58	6	23.1	70	20	AAV19484 Amino acid sequenc
59	6	23.1	75	22	ABW44253 Peptide #11759 enc
60	6	23.1	75	22	ABW27126 Protein #9125 enco
61	6	23.1	75	22	AAW65292 Human brain expres
62	6	23.1	75	22	AAW77990 Human bone marrow
63	6	23.1	75	22	AAW21883 Peptide #8317 enco
64	6	23.1	75	22	AAW38210 Peptide #12247 enc
65	6	23.1	77	20	AAV00283 Human secreted pro
66	6	23.1	86	22	AAU20330 Human novel endocr
67	6	23.1	99	22	AAU29655 Human polypeptide
68	6	23.1	112	22	AAU29655 Novel human secret
69	6	23.1	116	22	ABW27938 Novel human diagno
70	6	23.1	121	21	AAW01114 Human secreted pro
71	6	23.1	121	21	AAV53001 Human secreted pro
72	6	23.1	155	22	AAW39518 Human polypeptide
73	6	23.1	166	6	AAW50023 Sequence of new mo
74	6	23.1	166	6	interferon-alpha-7
75	6	23.1	166	16	

ALIGNMENTS

RESULT 1
AAW06128 standard; Peptide: 26 AA.
XX

AC	AAM06128;
XX	
DT	07-FEB-1997 (first entry)
XX	
DE	Human cholesteryl ester transfer protein C-terminal B-cell epitope.
KM	Cholesteryl ester transfer protein; CETP; antigen; vaccine;
KW	cardiovascular disease; atherosclerosis; B-cell epitope.
XX	
OS	Homo sapiens.
PN	MO9634888-A1.
PD	
XX	07-NOV-1996.
XX	
PF	01-MAY-1996; 96MO-US06147.
XX	
PR	01-MAY-1995; 95US-0432483.
XX	
PA	(TCCL-) T CELL SCI INC.
XX	
PI	Rittershaus CM, Thomas LJ;
XX	
DR	WPI; 1996-506103/50.
XX	
PT	Cholesteryl ester transfer protein B cell epitope linked to T cell
PT	epitope used to generate vaccine to regulate CETP activity for
PT	decreasing the risk of developing a cardiovascular disease e.g.
XX	atherosclerosis
XX	
PS	Claim 5; Page 41; 72pp; English.
XX	
CC	A B-cell epitope (AAM06128) comprising the C-terminal 26 amino acids
CC	of human liver mature cholesteryl ester transfer protein (CETP)
CC	(see also AAM06127) is involved in a neutral lipid binding or a
CC	transfer activity of CETP. It can be linked to a universal or
CC	broad range immunogenic T-cell epitope, such as that found at amino
CC	acids 830-843 of tetanus toxoid protein, to produce a synthetic
CC	vaccine (see also AAM06129) that elicits an immune response against
CC	endogenous CETP activity, thereby treating or preventing
CC	cardiovascular disease, such as atherosclerosis. It may also be
CC	incorporated into a multivalent vaccine (see also AAM06131)
CC	including another CETP B-cell epitope.
XX	
SQ	Sequence 26 AA:
	Query Match 100.0%; Score 26; DB 17; Length 26;
	Best local similarity 100.0%; Pred. No. 3.1e-17;
	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 RDGFLIOMDFGFPEHLIVDFLOSLS 26
DB	1 rdgfillqmdfgyipehlvdfllqs 26
RESULT 2	
ID	AAV13801
XX	AAV13801 standard; peptide; 26 AA.
AC	
XX	AAV13801;
DT	08-JUL-1999 (first entry)
XX	
DE	Rabbit CETP immunogenetic fragment.
XX	
CETP	cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW	antibody production; cholesteryl ester transfer; therapy;
KW	high density lipoprotein; HDL cholesterol concentration;
KW	pro-atherogenic dyslipoproteinaemia.
OS	Oryctolagus sp.
XX	

XX	PN	MO9915655-A1.
XX	PD	01-APR-1999.
XX	PX	
PF	17-SEP-1998:	98WO-US19366.
PR	19-SEP-1997;	97US-0934367.
PS	(MONS) MONSANTO CO.	
PT	Glenn K. Needleman P;	
DR	WPI; 1999-276984/23.	
PT	New recombinant DNA vaccines	
PS	Claim 15; Page 85; 99pp; English.	
XX	This sequence represents an immunogenic fragment of the rabbit	
CC	cholesteryl ester transferase protein (CEP).	
CC	The invention relates to recombinant DNA vaccines that contain DNA	
CC	encoding CEP, which can be used for producing antibodies to lessen the	
CC	transfer of cholesteryl esters from high density lipoprotein (HDL). The	
CC	method can provide an autogenic immunological process for lessening the	
CC	transfer of cholesteryl esters from HDL particles and for increasing the	
CC	HDL cholesterol concentration of a mammal whose blood also contains	
CC	CEP. The method may be useful in treating human pro-atherogenic	
CC	dyslipoproteinemias characterised by low HDL/LDL cholesterol ratios. The	
CC	method can have an effect that lasts for months as compared to the	
CC	short-term effects of the small molecule drugs now available.	
XX	Sequence 26 AA;	
SQ		
OY	Query Match	100.0%; Score 26; DB 20; Length 26;
	Best Local Similarity	100.0%; Pred. No. 3.1e-17;
Matches	26; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
Db	1 RDGFLUOMDFGPPEHLVDPLOSLS 26	
	1 rdgflldqmdfgfpehlvdftqsls 26	
RESULT	3	
ID	AA91228	
AC	AA91228 standard; peptide; 26 AA.	
XX		
DT	22-MAY-2000 (first entry)	
XX		
DE	Human cholesteryl transport protein (CEP) peptide, SEQ ID NO:106.	
XX		
KM	Promiscuous T-cell epitope; measles virus F protein; MFV;	
KM	hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;	
KM	luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;	
KM	somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;	
KM	foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;	
KM	Plasmodium falciparum; circumsporozoite; antimalarial; CEP;	
KM	cholesterol ester transport protein; anti-arteriosclerotic.	
OS	Homo sapiens.	
XX		
PN	WO9966957-A2.	
PD		
XX	29-DEC-1999.	
PF	21-JUN-1999;	99WO-US13975.
PR	20-JUN-1998;	98US-0100412.
XX		
PA	(UNBI-) UNITED BIOMEDICAL INC.	
XX		

PI Wang CY;
XX WPI: 2000-160564/14.
XX
XX New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
XX Claim 10: Page 49; 129pp: English.
XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response.
CC Specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AA91121 represents a promiscuous T helper epitope
CC from the measles virus F (WVF) protein and sequences AA91122-Y91142,
CC AA91226 and AA91245-Y91246 represent synthetic Th epitopes based on the
CC WVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AA91208 is a
CC human CD4 CDR2-like domain antigenic site, and AA91209-Y90211 are MVA Th
CC epitopes/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AA91212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AA91213-Y90219 are Th epitopes/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AA91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AA91221-Y91222 comprise this peptide and a Th
CC epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AA91224-Y91225 comprise the CS antigen and an MVA Th
CC epitope, and may be used in a malaria vaccine. AA91228-Y91231 represent
CC CEP-derived peptides and AA91232-Y91241 are immunogens comprising a
CC CEP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AA91248-Y91251 and
CC AA91258-Y91273 are antigenic peptides comprising WVF Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AA91198 and AA91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the invention.
CC Note: Sequence AA91227 is also designated SEQ ID NO:166 in the
CC specification.
XX
XX
SQ Sequence 26 AA:
Query Match 100.0%; Score 26; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RDGFTLLMDRGPERHLLVDFLOSLS 26
DB 1 rdgftllmdrgperhllvdflosls 26

RESULT 4
AA91232
ID AA91232 standard; peptide: 46 AA.
XX
XX AA91232:
AC
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Modified WVF Th epitope/CEP peptide, SEQ ID NO:110.
DE
XX
XX Promiscuous T-cell epitope; measles virus F protein; WVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; anti-HIV; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CEP;
KW cholesterol ester transport protein; anti-arteriosclerotic.
XX
XX Chimeric - Measles virus.
OS Chimeric - Homo sapiens.
XX
XX WO966957-A2.
XX
XX 29-DEC-1999.
PD
XX
XX 21-JUN-1999: 99NO-US13975.
PF
XX
XX 20-JUN-1998: 98US-0100412.
PR
XX
XX (UNB1-) UNITED BIOMEDICAL INC.
PA
XX
XX Wang CY;
XX
XX WPI: 2000-160564/14.
XX
XX New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
XX Claim 11: Page 104; 129pp: English.
XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes and peptide immunogens
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response.
CC Specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AA91121 represents a promiscuous T helper epitope
CC from the measles virus F (WVF) protein and sequences AA91122-Y91142,
CC AA91226 and AA91245-Y91246 represent synthetic Th epitopes based on the
CC WVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AA91208 is a
CC human CD4 CDR2-like domain antigenic site, and AA91209-Y90211 are MVA Th

CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AA9Y0212 is a modified version of a human IGE
CC (immunoglobulin E) CH3 domain, and AA9Y0213-Y0219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AA9Y1220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AA9Y1221-Y1222 comprise this peptide and a Th
CC epitope. AA9Y1223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AA9Y1224-Y1225 comprise the CS antigen and an MVE Th
CC epitope and may be used in a malaria vaccine. AA9Y1228-Y1231 represent
CC CMTP-derived peptides and AA9Y1232-Y1241 are immunogens comprising a
CC CMTP peptide and a Th epitope which may be used to prevent or treat a
CC allergic dermatitis and cardiovascular disease. AA9Y1247 and AA9Y1252-Y1257
CC are HIV-1 neutralising B-cell epitopes, and AA9Y1248-Y1251 and
CC AA9Y1258-Y1273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AA9Y1198 and AA9Y1199 are respectively an immunostimulatory invasin
CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

Sequence	46 AA;
5Q	

Query Match	100.0%;	Score 26;	DB 21;	Length 46;
Best Local Similarity	100.0%;	Pred. No. 5.1e-17;		
Matches 26; Conservative	0;	Mismatches	0;	Indels 0; Caps 0

```
Oy      1 RDGELLLOWDFGPEHLLVDFLOSL 26
         |||||
Db      21 rdgfl1lqmdfgfpehllvdf1qsls 46
```

RESULT	5
AA91233	
ID	AA91233 standard; peptide; 46 AA

AC AA91233

DT 22-MAY-2000 (first entry)

Modified MVF Th epitope/CETP peptide, SEQ ID NO:111.

KM Promiscuous T-cell epitope: measles virus F protein; MBV;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin-6 hormone releasing hormone; LHRH; contraceptive; antitumor
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM plasmidum falciparum; circumsporozoite; antimalarial; CDP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.

OS	chimeric -	Measles virus
OS	chimeric -	Homo sapiens.

PN W09966957-A2

PD 29-DEC-1999

PF 21-JUN-1999; 99WO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY

DR WPI; 2000-160564/14

PT New artificial T helper cell epitope and derived immunogens with large
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus -
XX
PS Claim 11: Page 104-105; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th),
 and immunogenic peptides comprising the Th epitopes of the invention
 along with B cell epitopes. The Th epitopes and peptide immunogens
 containing them, are used to induce a T helper cell response,
 specifically against Plasmodium falciparum, cholesteryl ester transport
 protein (CEMP) or HIV epitopes, but more generally against any pathogen,
 immunoreactive self-antigen or tumour antigen. The Th epitopes and
 peptide immunogens may be used for prevention and/or treatment of
 infections (HIV, foot-and-mouth disease or malaria); for cancer
 immunotherapy; for inhibition of the action of interleukin hormone
 releasing hormone (LHRH) for contraception, treatment of hormone-
 dependent cancer, prevention of boar taint in meat, and
 immunosuppression; for promoting the growth of animals; or for
 treating allergies or arteriosclerosis. Incorporation of a promiscuous
 Th (functional) in genetically diverse subjects into an immunogen
 improves capacity to induce a strong T helper cell mediated immune
 response, resulting in production of antibodies against a target
 antigen. Th can replace carrier proteins and pathogen-derived T helper
 epitopes. Sequence AA91121 represents a promiscuous T helper epitope
 from the measles virus F (WNV) protein and sequences AA91112-911142,
 AA911226 and AA911245-911246 represent synthetic Th epitopes based on the
 WNV Th epitope. Sequence AA911143 represents a promiscuous Th epitope
 from hepatitis B virus (HBV) surface antigen, and sequences
 AA911144-911155 are synthetic epitopes derived from this HBV epitope.
 AA911156-911195, AA911227 and AA912442-912444 are antigenic peptides
 comprising an LHRH sequence joined to a promiscuous Th epitope. AA911197
 is the LHRH target antigenic peptide used in these LHRH antigenic
 peptides. AA911200 is somatostatin, and AA911201-911207 are antigenic
 peptides comprising somatostatin and a Th epitope. Somatostatin
 immunogens may be used to promote growth in livestock. AA911208 is a
 human CD4 CD82-like domain antigenic site, and AA911209-911211 are MVA Th
 epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV
 infection of T cells. AA91212 is a modified version of a human Ige
 (Immunoglobulin E) CH3 domain, and AA9120213-9120219 are Th epitope/19E CH3
 antigenic peptides which may be used in the treatment of allergies.
 AA911220 is a peptide derived from foot and mouth disease virus (FMDV)
 VP1 capsid protein and AA911221-911222 comprise this peptide and a Th
 epitope. AA911223 is a Plasmodium falciparum circumsporozoite (CS) target
 antigen, and AA911224-911225 comprise the CS antigen and an MVA Th
 epitope, and may be used in a malaria vaccine. AA911228-911231 represent
 CEMP-derived peptides and AA911232-911241 are immunogens comprising a
 CEMP peptide and a Th epitope which may be used to prevent or treat
 arteriosclerosis and cardiovascular disease. AA912447 and AA91252-91257
 are HIV-1 neutralising B-cell epitopes, and AA912448-912451 and
 AA9125158-9125173 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 epitope which may be used as a component in an anti-HIV-1 vaccine.
 AA911198 and AA911199 are respectively an immunostimulatory invasion
 protein epitope from Yersinia species, and hinge spacer peptide, both of
 which may optionally be used in the antigenic peptides of the
 invention.

SQ Sequence 46 AA

Query Match	100.0%;	Score 26;	DB 21;	Length 46;
Best Local Similarity	100.0%;	Pred. No. 5.1e-17;		
Matches 26; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1 RDGELLQMDFGPEHLLVDFLQSL 26
         |||||
Db      21 rdgflllqmdfgfpehllvdfllqsl 46
```

RESULT	6
AAW06127	
ID	AAW06127 standard; Protein; 476 AA

AC AAW06127;

DT 07-FEB-1997 (first entry)

DE Human cholesteryl ester transfer protein

XX

KM		Cholesteryl ester transfer protein; CERP; antigen; vaccine;
KM		cardiovascular disease; atherosclerosis.
XX		
OS	Homo sapiens.	
FR	Key	Location/Qualifiers
FT	Region	/label= B-cell epitope
FT	Region	/label= B-cell epitope
FT	Region	/note= "C-terminal epitope involved in neutral lipid binding or a transfer activity of CERP (Claim 5)."
XX		
PN	M09634888-A1..	
XX		
PD	07-NOV-1996.	
XX		
PP	01-MAY-1996; 96WO-US06147.	
XX		
PR	01-MAY-1995; 95US-0432483.	
XX		
PA	(CECU) T CELL SCI INC.	
PI	Rittershaus CW, Thomas LJ;	
DR	WPI; 1996-506103/50.	
XX		
PT	Cholesteryl ester transfer protein B cell epitope linked to T cell epitope - used to generate vaccine to regulate CERP activity for decreasing the risk of developing a cardiovascular disease e.g. atherosclerosis	
PS	Claim 2; Page 44-47; 72pp; English.	
CC	Human liver mature cholesteryl ester transfer protein (CERP) (AAW06127)	
CC	plays a role in altering the relative profile of circulating lipoproteins to one associated with an increased risk of cardiovascular disease. B-cell epitopes (see also AAW06128) of CERP can be used in novel peptide vaccines (see also AAW06119, AAW06131) that elicit an immune response against endogenous CERP activity, thereby treating or preventing cardiovascular disease, such as atherosclerosis.	
SQ	Sequence 476 AA:	
OY	Query Match	100.0%; Score 26; DB 17; Length 476;
	Best Local Similarity	100.0%; Pred. No. 3.9e-16;
	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	1 RDGFIILQMDFGPEHLLVDLFLOSLS 26	
	451 rdgfillqmdfgfpehlvdlflqsas 476	
RESULT 7		
ID	AAW46446 standard; Peptide; 476 AA.	
AC	AAW46446;	
DT	18-MAY-1998 (first entry)	
DE	Human mature cholesteryl ester transfer protein (CERP).	
KM	Cholesteryl ester transfer protein; CERP; cholesteryl ester; high density lipoprotein; HDL; very low density lipoprotein; VLDL; low density lipoprotein; LDL; atherosclerosis; neutral lipid binding; transfer activity; immunogenic; B cell epitope; antibody; TPZ; DNA plasmid-based vaccine; broad range helper T cell epitope; treatment; cardiovascular disease.	

OS	Homo sapiens.
XX	
PN	W09741227-A1.
PD	06-NOV-1997.
PF	01-MAY-1997; 97WC-US07294.
PX	21-FEB-1997; 97US-0802967.
PR	01-MAY-1996; 96US-0640713.
PA	(TCELL-) T CELL SCI INC.
PI	Thomas LJ;
DR	WPI: 1997-549731/50.
N-PDB:	AAV05127.
PT	DNA plasmid-based vaccine encodes CERP B cell and helper T cell epitope(s) - used for elevating high density lipoprotein levels, and for treating cardiovascular disease
PS	Claim 6; Pages 36-38; 67pp; English.
XX	
CC	The present sequence represents a human mature cholesterol ester transfer protein (CERP). CERPs mediate the transfer of cholesterol esters from CC high density lipoprotein (HDL) to very low density lipoprotein (VLDL), and CC produces an atherogenic lipoprotein profile and induces atherosclerosis. CC A 13 amino acid stretch in the human CERP (Phe463 to Leu475), and also possibly Asp460, are particularly important for neutral lipid binding and CC transfer activity. This region has been shown to be immunogenic as a B CC cell epitope of CERP, and a monoclonal antibody (7P2) directed at this CC region has been shown to inhibit neutral lipid transfer. A second B cell CC epitope is defined by Arg349 to Ile367. Antibodies to this second epitope CC would allow the formation of immune complexes involving CERP, and promote CC the removal of the complexed CERP. This peptide region was selected for CC its potential antigenicity and high possibility for surface expression CC on native CERP. Sequences encoding these 2 epitopes can be used in a DNA CC plasmid-based vaccine which comprises sequences encoding at least 1 B CC cell epitope of CERP linked in frame with at least one segment encoding CC a broad range helper T cell epitope. The vaccines can be used to elevate CC the ratio of circulating HDL to circulating LDL, VLDL or total CC cholesterol in a human. It can also be used for decreasing the level of CC endogenous CERP activity in a human. The vaccine can be used to produce CC anti-CERP antibodies in vivo and for treating cardiovascular disease.
SO	Sequence 476 AA;
XX	
Query Match	100.0%; Score 26; DB 18; Length 476;
Best Local Similarity	100.0%; Pred. No. 3.9e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 RDGELLQDMFGFPHLLVDPLQSLS 26 ##### 451 rdgelllqdmfgfphllvdtlqsls 476
Db	
RESULT 8	
AAV02466	AAV02466 standard; protein; 476 AA.
AC	AAV02466;
DT	14-JUL-1999 (first entry)
XX	
DE	human cholesterol ester transfer protein (CERP).
XX	
KM	Vaccine; antibody; endogenous; cholesterol ester transfer protein; CERP,
KM	high-density lipoprotein associated Cholesterol; metabolism;
KM	low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
KM	cholesterol; atherosclerosis; heart disease.

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XX OS Homo sapiens.
XX PN W09920302-A1.
XX PD 29-APR-1999.
XX PF 20-OCT-1998; 98WO-US22145.
XX PR 20-OCT-1997; 97US-0954643.
XX PA (AVANT-) AVANT IMMUNOTHERAPEUTICS INC.
XX PI Rittershaus CW, Thomas LJ;
XX DR WPI: 1999-302645/25.
XX N-PSDB: AAX35807.
XX PT Vaccine against cholesterol ester transfer protein
XX PS Disclosure; Page 44-46; 61pp; English.
XX CC The specification describes a vaccine that promotes the production of
XX CC antibodies that bind endogenous cholesterol ester transfer protein
XX CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
XX CC used to increase the ratio of circulating high-density lipoprotein
XX CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
XX CC cholesterol; to decrease the level of endogenous CETP activity in humans
XX CC or other animals; to alter metabolism of LDL-associated cholesterol; for
XX CC inhibiting development of atherosclerotic lesions; to lower circulating
XX CC levels of LDL and total cholesterol; and to treat or prevent
XX CC atherosclerosis (or more generally heart disease). The present sequence
XX CC represents human CETP.
XX SQ Sequence 476 AA;

Query Match 100.0%; Score 26; DB 20; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILQMDGFPPEHLVDFLOSLIS 26
DB 451 rdgflilqmdgfppehlvdfloslis 476

RESULT 9
AAR60342
ID AAR60342 standard; protein; 491 AA.
XX AC AAR60342;
XX DT 01-MAR-1995 (first entry)
XX DE Partial human lipid transfer protein.
XX KW Lipid transfer protein; LTP; monoclonal antibody; immunoassay;
XX KW antigen determining group.
XX OS Homo sapiens.
XX PH Key
XX FT Location/Qualifiers
XX FT 16..43
XX FT /label= peptide 1
XX FT /note="claim 1; antigen determining group"
XX FT 209..221
XX FT /label= peptide 2
XX FT /note="claim 1; antigen determining group"
XX FT 275..288
XX FT /label= peptide 3
XX FT /note="claim 1; antigen determining group"
XX FT 303..322
XX FT /label= peptide 4

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FT FT /note="claim 1; antigen determining group"
FT FT 360..370
FT FT /label= peptide 5
FT FT /note="claim 1; antigen determining group"
XX PN JP06169793-A.
XX PD 21-JUN-1994.
XX PF 02-DEC-1992; 92JP-0349842.
XX PR 02-DEC-1992; 92JP-0349842.
XX PA (EIKE ) EIKEN KAGAKU KK.
XX DR WPI: 1994-237601/29.
XX PT A monoclonal antibody recognising human lipid transfer protein -
XX PT useful for immunoassay
XX PS Disclosure; Fig 1: 14pp; Japanese.
XX CC This sequence shows a partial human lipid transfer protein,
XX CC containing specific peptide groups that are antigen determining. The
XX CC monoclonal antibody of the invention recognises any of these
XX CC peptides. The MAb can be used in an immunoassay for HLTP.
XX SQ Sequence 491 AA;

Query Match 100.0%; Score 26; DB 15; Length 491;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILQMDGFPPEHLVDFLOSLIS 26
DB 466 rdgflilqmdgfppehlvdfloslis 491

RESULT 10
AAV49556
ID AAV49556 standard; Protein; 493 AA.
XX AC AAV49556;
XX DT 13-JAN-2000 (first entry)
XX DE Human cholesterol ester transfer protein sequence.
XX KW Human; coding sequence polymorphism; vascular pathology gene;
XX KW polymorphic site; phenotype correlation; forensic; paternity testing;
XX KW medicine; genetic analysis; vascular disease.
XX OS Homo sapiens.
XX PN W09950454-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US06473.
XX PR 01-APR-1998; 98US-0054272.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
XX DR WPI: 1999-620066/53.
XX N-PSDB: AA232165.
XX PT Determination of polymorphisms in genes, especially those identifying
XX PT predisposition to vascular disease

```

PS Disclosure: Fig 9; 134pp; English.
 XX
 CC AA232159 to AA232194 represent reference alleles for specifically
 CC claimed nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected
 CC from 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic
 CC analysis. AAY49550 to AAY49573 represent the proteins which correspond
 CC to some of the reference alleles.
 XX
 SQ Sequence 493 AA:
 Query Match 100.0%; Score 26; DB 20; Length 493;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFTLLQMDGFPFHHLYVDFQSL 26
 Db 468 rdgftllqmdgfpfhhlyvdfqsls 493
 RESULT 11
 ID AAY49568 standard; Protein; 493 AA.
 XX
 AC AAY49568;
 XX
 DT 13-JAN-2000 (first entry)
 XX
 DE Human cholesterol ester transfer protein sequence.
 XX
 KW Human; coding sequence polymorphism; vascular pathology; gene;
 KW polymorphic site; phenotype correlation; forensic; paternity testing;
 KW medicine; genetic analysis; vascular disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9950454-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WC-US06473.
 XX
 PR 01-APR-1998; 98US-0054272.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Lander ES, Daley GO, Cargill M, Ireland JS, Rozen SG,
 DR N-PSDB; AA232188.
 XX
 WPI: 1999-620066/53.
 XX
 PT Determination of polymorphisms in genes, especially those identifying
 PT predisposition to vascular disease -
 XX
 PS Disclosure: Fig 32; 134pp; English.
 XX
 CC AA232159 to AA232194 represent reference alleles for specifically
 CC claimed nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected
 CC from 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic
 CC analysis. AAY49550 to AAY49573 represent the proteins which correspond
 CC to some of the reference alleles.

XX
 SQ Sequence 493 AA:
 Query Match 100.0%; Score 26; DB 20; Length 493;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFTLLQMDGFPFHHLYVDFQSL 26
 Db 468 rdgftllqmdgfpfhhlyvdfqsls 493
 RESULT 12
 ID AAG5636 standard; Protein; 493 AA.
 XX
 AC AAG5636;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE Human cholesterol ester transfer protein (CETP).
 XX
 KW CETP; arteriosclerosis; cholesterol ester transfer protein; HDL;
 KW high density lipoprotein; human.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 XX
 FT Peptide 1..17
 FT /note= "signal peptide"
 FT Protein 18..493
 FT /note= "mature protein indicated as Seq Id No. 2"
 XX
 PN WO200171032-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-GP02327.
 XX
 PR 24-MAR-2000; 2000JP-0084264.
 XX
 PA (BMLB-) BML INC.
 XX
 PI Nagano M, Ito M, Sageshashi Y, Hattori H, Egaashira T, Yamashita S,
 PI Matsuzawa Y;
 XX
 DR WPI: 2001-611516/70.
 XX
 DR N-PSDB; AAI6654.
 XX
 PT Determining a risk factor for arteriosclerosis comprises detecting
 PT mutations in genes for cholesterol ester transfer protein.
 XX
 PS Disclosure: Page 43-47; 58pp; Japanese.
 XX
 CC The invention relates to detecting the risk factor for arteriosclerosis
 CC in a subject that involves detecting mutations in the gene for
 CC cholesterol ester transfer protein (CETP) related to the degree of risk
 CC of arteriosclerosis. The mutant proteins alter the level of HDL in the
 CC blood. The high frequency mutations can be detected for prevention and
 CC treatment of arteriosclerosis. The present sequence represents a
 CC human CETP.
 XX
 SQ Sequence 493 AA:
 Query Match 100.0%; Score 26; DB 22; Length 493;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFTLLQMDGFPFHHLYVDFQSL 26
 Db 468 rdgftllqmdgfpfhhlyvdfqsls 493

RESULT 13
 ID AAY13815 standard; peptide; 22 AA.
 XX
 AC AAY13815;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Rabbit CERP immunogenic fragment.
 XX
 KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Oryctolagus sp.
 XX
 PN WO9915655-A1.
 XX
 PD 01-APR-1999.
 XX
 PE 17-SEP-1998; 98MO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI; 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 XX
 PS Disclosure; Page 75; 99pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 SO Sequence 22 AA:

Query Match 84.68; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDGFPEHLVDFLOSLIS 26
 ||||||||||||||||||
 DB 1 LLLQMDGFPEHLVDFLOSLIS 22

RESULT 14
 ID AAY13821 standard; peptide; 22 AA.
 XX
 AC AAY13821;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Human CERP immunogenic fragment.
 XX
 KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;

KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO9915655-A1.
 XX
 PD 01-APR-1999.
 XX
 PE 17-SEP-1998; 98MO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI; 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 XX
 PS Disclosure; Page 88; 99pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the human
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 SO Sequence 22 AA:

Query Match 84.6%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDGFPEHLVDFLOSLIS 26
 ||||||||||||||||||
 DB 1 LLLQMDGFPEHLVDFLOSLIS 22

RESULT 15
 ID AAY02469 standard; protein; 496 AA.
 XX
 AC AAY02469;
 XX
 DT 14-JUL-1999 (first entry)
 XX
 DE Humanised rabbit cholesteryl ester transfer protein (CERP).
 XX
 KW Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CERP;
 KW high-density lipoprotein-associated cholesterol; metabolism;
 KW low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
 KW cholesterol; atherosclerosis; heart disease.
 XX
 OS Synthetic.
 XX
 PN WO9920302-A1.
 XX
 PD 29-APR-1999.
 XX
 PE 20-OCT-1998; 98MO-US22145.
 XX

PR 20-OCT-1997; 97US-0954643.
 XX
 PA (AVANT) AVANT IMMUNOTHERAPEUTICS INC.
 PI Rittershaus CM, Thomas LJ;
 XX
 DR WPI: 1999-302645/25.
 XX
 PT Vaccine against cholesteryl ester transfer protein
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein
 CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents a humanised rabbit CETP.
 XX
 SO Sequence 496 AA:
 Query Match 84.6%; Score 22; DB 20; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1,8e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 LLLQMDGFEHLVDFLOSLs 26
 |||||
 Db 475 LLLQMDGFEHLVDFLOSLs 496
 RESULT 16
 AAY91229
 ID AAY91229 standard; peptide; 16 AA.
 AC AAY91229;
 XX
 DT 22-MAY-2000 (first entry)
 DE Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:107.
 XX
 KW Promiscuous T-cell epitope; measles virus F protein; WVF;
 KW Hepatitis B virus surface antigen; HBV; Immunogenic; B-cell epitope;
 KW Interleukin-6; IL6; Interleukin-6; IL6; Interleukin-6; IL6;
 KW Somatostatin; growth promoting; CD4 receptor; HIV-1; antiviral; FMDV;
 KW Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO9966957-A2.
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI: 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus

XX
 PS Claim 10; Page 50; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (WVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC WVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CD82-like domain antigenic site, and AAY91209-Y90211 are MVH Th
 CC epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SO Sequence 16 AA:
 Query Match 61.5%; Score 16; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2,8e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 11 FGFPEHLVDFLOSLs 26
 |||||
 Db 1 fgfpehlivdflosls 16
 RESULT 17
 AAY06129
 ID AAY06129 standard; Peptide; 31 AA.
 AC AAY06129;
 XX
 DT 07-FEB-1997 (first entry)

XX 21-JUN-1999; 99WO-US13975.
 PF
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Claim 11; Page 106; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes and peptide immunogens along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CTP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of interleukin hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AA9Y1121 represents a promiscuous T helper epitope from the measles virus F (WVF) protein and sequences AA9Y1122-9Y1142, AA9Y1226 and AA9Y1245-9Y1246 represent synthetic Th epitopes based on the WVF Th epitope. Sequence AA9Y1143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AA9Y1144-9Y1195 are synthetic epitopes derived from this HBV epitope. AA9Y1156-9Y1196, AA9Y1227 and AA9Y1242-9Y1244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AA9Y1197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AA9Y1200 is somatostatin, and AA9Y1201-9Y1207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AA9Y1208 is a human CD4 CDR2-like domain antigenic site, and AA9Y1209-9Y0211 are HIV Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AA9Y0212 is a modified version of a human IGE (immunoglobulin E) CH3 domain, and AA9Y0213-9Y0219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AA9Y1220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AA9Y1221-9Y1222 comprise this peptide and a Th epitope. AA9Y1223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AA9Y1224-9Y1225 comprise the CS antigen and an MWF Th epitope and may be used in a malaria vaccine. AA9Y1228-9Y1231 represent CTRP-derived peptides and AA9Y1232-9Y1241 are immunogens comprising a CTRP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AA9Y1247 and AA9Y1252-9Y1257 are HIV-1 neutralising B-cell epitopes, and AA9Y1246-9Y1251 and AA9Y1256-9Y1273 are antigenic peptides comprising MWF Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AA9Y1198 and AA9Y1199 are respectively an immunostimulatory invasin protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptide of the invention.

50	Sequence	35 AA;
	Query Match	61.5%; Score 16; DB 21; Length 35;
	Best Local Similarity	100.0%; Pred. No. 5.6e-08;

	Matches	16; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	11	FGPEHLLVDFLOSLS	26						
Db	20	fgfepenhllvdflosls	35						

```

RESULT 20
AA191234 ID AA191234 standard; peptide; 36 AA.
XX
XX
MC AA191234;
XX
DT 22-MAY-2000 (first entry)
XX
XX Modified MYF 7h epitope/CERP peptide, SEQ ID NO:112

```

KM Promiscuous T-cell epitope; measles virus E protein; MVE;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM Interleukin-6; IL-6; interleukin 6; IL6; interleukin-6; IL-6;
 KM Interleukin-6; IL-6; interleukin 6; IL6; interleukin-6; IL-6;
 KM Somatostatin; growth promotion; CD4 receptor; HIV-1; antitumor; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.

OS	Chimeric - Measles virus.
OS	Chimeric - Homo sapiens.
XX	
PN	W09966957-A2.

PD 29-DEC-1999.

21-JUN-1999; 99MO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

Wang CY;

DR WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus -

PS Claim 11; Page 105; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against plasmodium falciparum, cholesterol ester transport protein (CEMP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of uterine-inhibiting hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AA91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AA91122-91142, AA91126 and AA91245-91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AA91144-91155 are synthetic epitopes derived from this HBV epitope. AA91156-91196, AA91127 and AA91242-91244 are anti-tumour peptides

CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope, and AAY91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

CC Sequence 36 AA:

SO

Query Match 61.5%; Score 16; DB 21; Length 36;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGPEHLVDLFGSLSS 26
 |||||||||
 Db 21 fgfpehlvdfgls 36

RESULT 21
 AAY91235
 ID AAY91235 standard; peptide: 36 AA.

XX
 AC AAY91235;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Modified MVA Th epitope/CERP peptide, SEQ ID NO:113.

XX
 KW Promiscuous T-cell epitope; measles virus F protein; MVA;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin-6 releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 PN WO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99MO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNB1-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI: 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus -
 PS Claim 11: Page 105; 129pp; English.

XX
 XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVA) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVA Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope, and AAY91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX
 XX Sequence 36 AA:

SO

Query Match 61.5%; Score 16; DB 21; Length 36;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGPEHLVDLFGSLSS 26
 |||||||||
 Db 21 fgfpehlvdfgls 36

RESULT 22
 AAY91237
 ID AAY91237 standard; peptide: 36 AA.

AAV91237:
 22-MAY-2000 (first entry)
 Modified MVF 7th epitope/CERP peptide, SEQ ID NO:115.

Promiscuous T-cell epitope; measles virus F protein; MVF;
 hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
 somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 cholesterol ester transport protein; anti-arteriosclerotic.

Chimeric - Measles virus.
 Chimeric - Homo sapiens.
 WO966957-A2.

29-DEC-1999.
 21-JUN-1999: 99WO-US13975.
 20-JUN-1998: 98US-0100412.
 (UNB1-) UNITED BIOMEDICAL, INC.

Mang CY;
 WPI; 2000-160564/14.

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus -

Claim 11: Page 106: 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CERP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinizing hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and for immunosuppression; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper antigens. Sequence AAV91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AAV91122-Y91142, AAV91226 and AAV91245-Y91246 represent synthetic Th epitopes based on the MVF Th epitope. Sequence AAV91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAV91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAV91156-Y91196, AAV91227 and AAV91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. CC AAV91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAV91200 is somatostatin, and AAV91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAV91208 is a human CD4 CDR2-like domain antigenic site, and AAV91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAV90212 is a modified version of a human IGE (immunoglobulin E) CH3 domain, and AAV90213-Y90219 are Th epitope/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AAV91220 is a peptide derived from foot and mouth disease virus (FMDV)

CC VP1 capsid protein and AAV91221-Y91222 comprise this peptide and a Th
 CC epitope. AAV91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAV91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAV91228-Y91231 represent
 CC CERP-derived peptides and AAV91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAV91247 and AAV91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAV91248-Y91251 and
 CC AAV91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAV91198 and AAV91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

Sequence 36 AA:
 SQ

Query Match 61.58; Score 16; DB 21; Length 36;
 Best Local Similarity 100.08; Pred. No. 5.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGPEHLVDFQLSLS 26
 Db 21 fgfpehlvdfqls1s 36

RESULT 23
 ID AAM06131 standard; Peptide: 50 AA.
 AC AAM06131;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Anti-cholesterol ester transfer multivalent vaccine peptide.
 XX
 KW Cholesterol ester transfer protein; CERP; antigen; vaccine;
 KW cardiovascular disease; atherosclerosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 1 /note- "C-terminal Cys residue is present for use
 FT in linking the peptide to itself or other
 FT molecules"

Region
 FT 2..15
 FT /label- "T-cell epitope
 FT /note- "T-cell epitope comprises amino acids
 FT 830-843 of tetanus toxoid protein"

Region
 FT 16..34
 FT /label- "B-cell-epitope
 FT /note- "B-cell epitope comprises amino acids
 FT 349-367 of human CERP"

Region
 FT 35..50
 FT /label- "B-cell epitope
 FT /note- "B-cell epitope comprises the C-terminal 16
 FT amino acids of human CERP, involved in
 FT neutral lipid binding or transfer activity"

PN WO9634888-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 01-MAY-1996: 96WO-US06147.
 XX
 PR 01-MAY-1995: 95US-0432483.
 XX
 PA (TCBL-) T CELL SCI INC.
 XX
 PI Rittershaus CW, Thomas LJ;

[illegible]

CC	a region of CERP which is common to both human and rabbit proteins.
XX	
S0	Sequence 11 AA;
OY	Query Match 42.3%; Score 11; DB 16; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00076; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
D8	16 HLLVDLFQSLSS 26 1 hllvdfqsls 11
RESULT 25	
AAV91230	
XX	AAV91230 standard; peptide; 16 AA.
AC	
XX	AAV91230;
DT	22-MAY-2000 (first entry)
DE	
XX	Human cholesterol transport protein (CERP) peptide, SEQ ID NO:108.
XX	
KW	Promiscuous T-cell epitope; measles virus F protein; MYF;
KW	hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW	luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
KW	somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW	foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM	Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
KW	cholesterol ester transport protein; anti-arteriosclerotic.
XX	
OS	Homo sapiens.
PN	
PD	WC9966957-A2.
XX	
PD	29-DEC-1999.
XX	
PE	21-JUN-1999; 99MO-US13975.
PR	20-JUN-1998; 98DS-0100412.
PA	(UNBI-) UNITED BIOMEDICAL INC.
PI	
XX	Mang CY;
DR	
XX	WPI: 2000-160564/14.
PT	
PT	New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus -
PS	Claim 10; Page 62; 12pp; English.
XX	
CC	The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CERP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone releasing hormone (LHRH) for contraception, treatment of hormone- dependent cancer, prevention of boar taint in meat, and immunosuppression); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAV91121 represents a promiscuous T helper epitope
CC	

from the measles virus F (MFV) protein and sequences AA91122-Y91142, AA911226 and AA91245-Y91246 represent synthetic Th epitopes based on the MFV Th epitope. Sequence AA91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AA91144-Y91155 are synthetic epitopes derived from this HBV epitope. AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides comprising an IHRH sequence joined to a promiscuous Th epitope. AA91197 is the IHRH target antigenic peptide used in these IHRH antigenic peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AA91208 is a human CD4 CD82-like domain antigenic site, and AA91209-Y90211 are HIV Th epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV infection of T cells. AA92012 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AA92021-Y90219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AA91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AA91221-Y91222 comprise this peptide and a Th epitope. AA91223 is a plasmodium falciparum circumsporozoite (CS) target antigen, and AA91224-Y91225 comprise the CS antigen and an MVE Th epitope and may be used in a malaria vaccine. AA91228-Y91231 represent CTRP-derived peptides and AA91232-Y91241 are immunogens comprising a CTRP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AA91248 Th and HIV-1 B-cell epitope AA91255-Y91273 are antigenic peptides comprising MVE Th and HIV-1 epitope which may be used as a component in an anti-HIV-1 vaccine. AA91196 and AA91199 are respectively an immunostimulatory invasive protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

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Query Match 42.3%; Score 11; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 HLVDFLOSLS 26
          |||||
Db       6 hlvdfips 16

RESULT 26
AY13809
ID  AY13809 standard; peptide; 22 AA.
XX
AC  AY13809;
XX
DT  08-JUL-1999 (first entry)
XX
DE  Rabbit CERP immunogenic fragment.
XX
CE  CERP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW  antibody production; cholesteryl ester transfer; therapy;
KW  high density lipoprotein; HDL cholesterol concentration;
KW  pro-atherogenic dyslipoproteinemia.
XX
OS  Oryctolagus sp.
XX
PN  W09915655-A1.
XX
PD  01-APR-1999.
XX
PF  17-SEP-1998; 98MO-US19366.
XX
PR  19-SEP-1997; 97US-0934367.
XX
PA  (MONS ) MONSANTO CO.
XX
PI  Glenn K, Needleman P;
XX

```

DR WP1; 1999-276984/23.
XX
XX
PP New recombinant DNA vaccines
XA
PS
XX
XX
CC This sequence represents an immunogenic fragment of the rabbit
CC cholesteryl ester transferase protein (CEPT).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CEPT, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CEPT. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
SQ Sequence 22 AA;

```

Query Match: 42.3%; Score 11; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. Nb. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 16 HLVDPLQSLVS 26
   |||||
DB 12 hlvdfllqsls 22

RESULT 27
AAV13802
ID AAV13802 standard; peptide; 26 AA.
XX
AC AAV13802;
XX
DT 08-JUL-1999 (first entry)
DE
DE Rabbit CERP immunogenic fragment.
XX
DE CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
XX antibody production; cholesteryl ester transfer; therapy;
XX high density lipoprotein; HDL cholesterol concentration;
XX pro-atherogenic dyslipoproteinemia.
XX
OS Oryctolagus sp.
XX
PN W09915655-A1.
XX
PD 01-APR-1999.
XX
PF 17-SEP-1998; 98WC-US19366.
XX
PR 19-SEP-1997; 97US-0934367.
XX
PA (MONS ) MONSANTO CO.
XX
PI Glenn K, Needleman P;
XX
DR WPI: 1999-276984/23.
XX
PT New recombinant DNA vaccines
XX
PS Claim 15: Page 94: 99pp; English.
XX
CC This sequence represents an immunogenic fragment of the rabbit
CC cholesteryl ester transferase protein (CERP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CERP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the

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CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX Sequence 26 AA;

Query Match 42.3%; Score 11; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSLIS 26
 16 hllvdfllgslls 26

RESULT 28
 AAY91231
 ID AAY91231 standard; peptide; 26 AA.

XX AAY91231;
 XX 22-MAY-2000 (first entry)

DE Human cholesterol transport protein (CERP) peptide, SEQ ID NO:109.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Homo sapiens.

OS MO9966957-A2.

PN 29-DEC-1999.

XX 21-JUN-1999; 99MO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

WP1; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus

PS Claim 10; Page 62; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen

CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CD82-like domain antigenic site and AAY91209-Y90211 are MVF Th
 CC epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 26 AA;

Query Match 42.3%; Score 11; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSLIS 26
 16 hllvdfllgslls 26

RESULT 29

XX AAY91238
 ID AAY91238 standard; peptide; 36 AA.

XX AAY91238;

XX 22-MAY-2000 (first entry)

DE Modified MVF Th epitope/CERP peptide, SEQ ID NO:116.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Chimeric - Measles virus.

OS Chimeric - Homo sapiens.

PN MO9966957-A2.

XX 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13975.
 XX 20-JUN-1998; 98US-0100412.
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA Wang CY;
 XX WPI: 2000-160564/14.
 DR New artificial T helper cell epitope and derived immunogens with target
 XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 PS Claim 11; Page 106; 129pp; English.
 The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals, or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AA91121 represents a promiscuous T helper epitope
 CC from the measles virus F (WVF) protein and sequences AA91122-Y91142,
 CC AA91226 and AA91245-Y91246 represent synthetic Th epitopes based on
 CC WVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AA91208 is a
 CC human CD4 CD82-like domain antigenic site, and AA91209-Y90211 are MVA Th
 CC epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AA90212 is a modified version of a human IGE
 CC (Immunoglobulin E) CH3 domain, and AA90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AA91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AA91221-Y91222 comprise this peptide and a Th
 CC epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AA91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope, and may be used in a malaria vaccine. AA91228-Y91231 represent
 CC CEP-derived peptides and AA91232-Y91241 are immunogens comprising a
 CC CEP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AA91248-Y91251 and
 CC AA91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AA91198 and AA91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX Sequence 36 AA;
 SQ

Query Match 42.3%; Score 11; DB 21; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFIQSLS 26
 |||||
 Db 26 hllvdfiqs 36
 RESULT 30
 AA91239
 ID AA91239 standard; peptide; 36 AA.
 XX
 AC AA91239;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Modified MVA Th epitope/CEP peptide. SEQ ID NO:117.
 XX
 KW Promiscuous T-cell epitope: measles virus F protein; WVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CEP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 FN W09966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX Wang CY;
 XX WPI: 2000-160564/14.
 DR New artificial T helper cell epitope and derived immunogens with target
 XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 PS Claim 11; Page 107; 129pp; English.
 The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals, or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AA91121 represents a promiscuous T helper epitope
 CC from the measles virus F (WVF) protein and sequences AA91122-Y91142,
 CC AA91226 and AA91245-Y91246 represent synthetic Th epitopes based on
 CC WVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197

CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IGE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MWF Th
CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CEMP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CEMP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

XX Sequence 36 AA;

Query Match 42.3%; Score 11; DB 21; Length 36;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLVDFTQSLT 26
| | | | | | | | | |
Db 26 hlvdfllgls 36

RESULT 31

AAY91240
ID AAY91240 standard; peptide; 46 AA.

AC AAY91240;

XX 22-MAY-2000 (first entry)

DE Modified MWF Th epitope/CEMP peptide, SEQ ID NO:118.

XX Promiscuous T-cell epitope; measles virus F protein; MWF;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesterol ester transport protein; anti-arteriosclerotic.

XX Chimeric - Measles virus.
OS Chimeric - Homo sapiens.

PN W05966957-A2.

XX 29-DEC-1999.

PD 21-JUN-1999; 99MO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target

PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus -
XX
XX Claim 11; Page 107; 129pp; English.

CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CEMP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (WVF) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MWF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IGE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MWF Th
CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CEMP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CEMP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

XX Sequence 46 AA;

Query Match 42.3%; Score 11; DB 21; Length 46;

Best Local Similarity 100.0%; Pred. No. 0.0026;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLVDFTQSLT 26
| | | | | | | | | |
Db 36 hlvdfllgls 46

RESULT 32

AAY91241
ID AAY91241 standard; peptide; 46 AA.

AC AAY91241;

XX 22-MAY-2000 (first entry)
 DT Modified MvF Th epitope/CEPP peptide, SEQ ID NO:119.
 XX
 DE
 XX Promiscuous T-cell epitope; measles virus F protein; MvF.
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin-6; growth promoting; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CEPP.
 XX cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 PN WO966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 XX 21-JUN-1999; 99MO-US13975.
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI: 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Claim 11; Page 107-108; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes and the invention
 CC along with B cell epitopes. The Th epitopes and peptides immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CEPP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infectious (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin-6 hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper
 CC epitope from the measles virus F (MvF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MvF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91166, AAY91227 and AAY91247-Y91248 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MvF Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th

CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MvF Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CEPP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CEPP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MvF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SQ Sequence 46 AA;
 XX
 OY 16 HLVDPLQSLG 26
 DB 36 hllvdfqlqsls 46
 XX
 RESULT 33
 AAW06132
 ID AAW06132 standard; Peptide; 50 AA.
 XX
 AC AAW06132;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Anti-cholesterol ester transfer multivalent vaccine peptide.
 KW Cholesterol ester transfer protein; CEPP; antigen; vaccine;
 KW cardiovascular disease; atherosclerosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Region 2..15
 FH /label= "T-cell epitope
 FH /note= "T-cell epitope comprises amino acids
 FH Region 16..34
 FH /label= "B-cell epitope
 FH /note= "B-cell epitope comprises amino acids
 FH Region 35..50
 FH /label= "B-cell epitope
 FH /note= "B-cell epitope comprises the C-terminal 16
 FH amino acids of rabbit CEPP, involved in
 FH neutral lipid binding or transfer activity"
 XX
 PM W09634888-A1.
 XX
 PD 07-NOV-1996.
 XX
 PR 01-MAY-1996; 96MO-US06147.
 XX
 PR 01-MAY-1995; 95US-0432483.
 XX
 PA (TCEL-) T CEL SCI INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI: 1996-506103/50.
 XX
 PT Cholesterol ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CEPP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.

PT atherosclerosis
XX
XX Disclosure; Page 7; 72pp; English.
XX
CC A multivalent vaccine comprises an immunogenic helper T-cell
CC epitope of tetanus toxoid protein covalently linked to the B-cell
CC epitopes of rabbit cholesteryl ester transfer protein (CETP) (see
CC also AAM6133). The vaccine elicits an immune response against
CC endogenous CETP activity, and is used to treat or prevent a
CC cardiovascular disease, such as atherosclerosis.
XX
SQ Sequence 50 AA;

Query Match 42.3%; Score 11; DB 17; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDPLQSLG 26
|||
Db 40 hllvdfqls 50

RESULT 34
AAM6447
ID AAM6447 standard; Peptide: 50 AA.
XX
AC AAM6447;
XX
DT 18-MAY-1998 (first entry)
XX
DE CETP B cell epitope/tetanus toxoid construct for a plasmid vaccine.
XX
KM Cholesteryl ester transfer protein; CETP; cholesteryl ester;
KM low density lipoprotein; HDL; very low density lipoprotein; VLDL;
KM low density lipoprotein; LDL; atherosclerosis; neutral lipid binding;
KM transfer activity; immunogenic; B cell epitope; antibody;
KM DNA plasmid-based vaccine; broad range helper T cell epitope;
KM treatment; cardiovascular disease; chimeric.
XX
OS Chimeric - Clostridium tetani.
OS Chimeric - Oryctolagus sp.
XX
FM Key Location/Qualifiers
FT Peptide 2..15
FT /note- "tetanus toxoid broad range helper T cell
FT epitope"
FT Peptide 16..34
FT /note- "CETP epitope of amino acids 350-368 of
FT AAM6445"
FT Peptide 35..50
FT /note- "CETP epitope of amino acids 481-496 of
FT AAM6445"
XX
PM WO9741227-A1.
XX
PD 06-NOV-1997.
XX
PF 01-MAY-1997; 97MO-US07294.
XX
PR 21-FEB-1997; 97US-0802967.
PR 01-MAY-1996; 96US-0640713.
XX
PA (TCELL-) T CELL SCI INC.
XX
PI Thomas LJ;
XX
DR WPI: 1997-549731/50.
DR N-PSDB; AAV05128.
XX
PT DNA plasmid-based vaccine encodes CETP B cell and helper T cell
epitope(s) - used for elevating high density lipoprotein levels, and

PT for treating cardiovascular disease
XX
XX Claim 8; Page 22; 67pp; English.
XX
CC The present sequence represents a construct containing a helper T cell
CC epitope from the toxoid tetanus protein, and 2 B cell epitopes of rabbit
CC mature cholesteryl ester transfer protein (CETP). CETPs mediate the
CC transfer of cholesteryl esters from high density lipoprotein (HDL) to
CC very low density lipoprotein (VLDL) and low density lipoprotein (LDL),
CC and vice versa. An increased CETP activity produces an atherogenic
CC lipoprotein profile and induces atherosclerosis. A 13 amino acid stretch
CC in the rabbit CETP (AAM6445) (Phe483 to Leu495) is important for
CC neutral lipid binding and transfer activity. This region has been shown
CC to be immunogenic as a B cell epitope of CETP. A second B cell epitope
CC is defined by Arg350 to Ile368. Antibodies to this second epitope would
CC allow the formation of immune complexes involving CETP, and promote
CC the removal of the complexed CETP. The present sequence is encoded by a
CC DNA plasmid-based vaccine which comprises sequences encoding at least 1
CC B cell epitope of CETP linked in frame with at least one segment
CC encoding a broad range helper T cell epitope. The vaccines can be used to
CC elevate the ratio of circulating HDL to circulating LDL, VLDL or total
CC cholesterol in a human. It can also be used for decreasing the level of
CC endogenous CETP activity in a human. The vaccine can be used to produce
CC anti-CETP antibodies in vivo and for treating cardiovascular disease.
XX
SQ Sequence 50 AA;

Query Match 42.3%; Score 11; DB 18; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDPLQSLG 26
|||
Db 40 hllvdfqls 50

RESULT 35
AAV02468
ID AAV02468 standard; protein; 477 AA.
XX
AC AAV02468;
XX
DT 14-JUL-1999 (first entry)
XX
DE Modified rabbit cholesteryl ester transfer protein (CETP).
XX
KM vaccine; antibody; endogenous; cholesteryl ester transfer protein; CETP;
KM high density lipoprotein-associated cholesterol; metabolism;
KM low density lipoprotein-associated cholesterol; atherosclerotic lesion;
KM cholesterol; atherosclerosis; heart disease.
XX
OS Synthetic.
OS Oryctolagus sp.
XX
PM WO9920302-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98MO-US22145.
XX
PR 20-OCT-1997; 97US-0954643.
XX
PA (AVANT) AVANT IMMUNOTHERAPEUTICS INC.
XX
PI Rittershaus CW, Thomas LJ;
XX
DR WPI: 1999-302645/25.
XX
PT Vaccine against cholesteryl ester transfer protein
Claim 5; Page 50-52; 61pp; English.

CC its potential antigenicity and high possibility for surface expression
 CC on native CERP. Sequences encoding these 2 epitopes can be used in a DNA
 CC plasmid-based vaccine which comprises sequences encoding at least 1 B
 CC cell epitope of CERP linked in frame with at least one segment encoding
 CC a broad range helper T cell epitope. The vaccines can be used to elevate
 CC the ratio of circulating HDL to circulating LDL, VLDL or total
 CC cholesterol in a human. It can also be used for decreasing the level of
 CC endogenous CERP activity in a human. The vaccine can be used to produce
 CC anti-CERP antibodies in vivo and for treating cardiovascular disease.
 XX
 SQ Sequence 496 AA;

Query Match 42.3%; Score 11; DB 18; Length 496;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDFIQLS 26
 Db 486 hllvdfiqsls 496

RESULT 38
 AAY02467
 ID AAY02467 standard; protein; 496 AA.
 XX
 AC AAY02467;

DT 14-JUL-1999 (first entry)

DE Rabbit cholesterol ester transfer protein (CERP).

XX Vaccine; antibody; endogenous; cholesterol ester transfer protein; CERP;
 KM high-density lipoprotein-associated cholesterol; metabolism;
 KM low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
 KW cholesterol; atherosclerosis; heart disease.
 XX

OS Oryctolagus sp.

XX WO9920302-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WC-US22145.

XX 20-OCT-1997; 97US-0954643.

XX (AVANT) AVANT IMMUNOTHERAPEUTICS INC.

XX Rittershaus CW, Thomas LJ;

XX WPI; 1999-302645/25.

XX N-PSDB; AAX35808.

XX Vaccine against cholesterol ester transfer protein

XX Disclosure; Page 47-49; 61pp; English.

CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesterol ester transfer protein
 CC (CERP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CERP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol; for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents rabbit CERP.

XX Sequence 496 AA;

Query Match 42.3%; Score 11; DB 20; Length 496;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDFIQLS 26
 Db 486 hllvdfiqsls 496

RESULT 39
 AAM31066
 ID AAM31066 standard; protein; 51 AA.
 XX
 AC AAM31066;

DT 17-OCT-2001 (first entry)

DE Peptide #5103 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
 KM genetic disorder.
 KM Homo sapiens.
 OS
 XX WO200157272-A2.
 XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00663.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta -

XX Claim 27; SEQ ID No 31335; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;
 XX see AAI31315-AA157546). The present sequence is a peptide encoded by one
 XX such probe. The probes are useful for producing a microarray for
 XX predicting, measuring and displaying gene expression in samples derived
 XX from human placenta. The probes are useful for antenatal diagnosis of
 XX human genetic disorders.

XX Sequence 51 AA;

Query Match 26.9%; Score 7; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGRFLLQ 8
 Db 18 dgrfllq 24

RESULT 40
 AAU17886
 ID AAU17886 standard; protein; 69 AA.
 XX
 AC AAU17886;

XX	07-NOV-2001	(first entry)	
DE	Novel human respiratory antigen #202.		
KW	Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active.		
OS	Homo sapiens.		
XX	WO200155448-A1.		
XX	02-AUG-2001.		
PD			
PE	17-JAN-2001; 2001WO-US01333.		
XX			
PR	31-JAN-2000; 2000US-0179665.		
PR	04-FEB-2000; 2000US-0180628.		
PR	24-FEB-2000; 2000US-0184664.		
PR	02-MAR-2000; 2000US-0186350.		
PR	16-MAR-2000; 2000US-0189874.		
PR	17-MAR-2000; 2000US-0190076.		
PR	18-APR-2000; 2000US-0198123.		
PR	19-MAY-2000; 2000US-0205515.		
PR	07-JUN-2000; 2000US-0209467.		
PR	28-JUN-2000; 2000US-0214886.		
PR	30-JUN-2000; 2000US-0215135.		
PR	07-JUL-2000; 2000US-0216647.		
PR	07-JUL-2000; 2000US-0216880.		
PR	11-JUL-2000; 2000US-0217487.		
PR	11-JUL-2000; 2000US-0217496.		
PR	14-JUL-2000; 2000US-0218290.		
PR	26-JUL-2000; 2000US-0220963.		
PR	26-JUL-2000; 2000US-0220963.		
PR	14-AUG-2000; 2000US-0224518.		
PR	14-AUG-2000; 2000US-0224519.		
PR	14-AUG-2000; 2000US-0225213.		
PR	14-AUG-2000; 2000US-0225214.		
PR	14-AUG-2000; 2000US-0225266.		
PR	14-AUG-2000; 2000US-0225267.		
PR	14-AUG-2000; 2000US-0225268.		
PR	14-AUG-2000; 2000US-0225470.		
PR	14-AUG-2000; 2000US-0225447.		
PR	14-AUG-2000; 2000US-0225757.		
PR	14-AUG-2000; 2000US-0225758.		
PR	14-AUG-2000; 2000US-0225759.		
PR	18-AUG-2000; 2000US-0226279.		
PR	22-AUG-2000; 2000US-0226681.		
PR	22-AUG-2000; 2000US-0226686.		
PR	22-AUG-2000; 2000US-0227182.		
PR	23-AUG-2000; 2000US-0227009.		
PR	30-AUG-2000; 2000US-0228924.		
PR	01-SEP-2000; 2000US-0229287.		
PR	01-SEP-2000; 2000US-0229343.		
PR	01-SEP-2000; 2000US-0229344.		
PR	01-SEP-2000; 2000US-0229345.		
PR	05-SEP-2000; 2000US-0229509.		
PR	05-SEP-2000; 2000US-0229513.		
PR	06-SEP-2000; 2000US-0230437.		
PR	06-SEP-2000; 2000US-0230438.		
PR	08-SEP-2000; 2000US-0231242.		
PR	08-SEP-2000; 2000US-0231243.		
PR	08-SEP-2000; 2000US-0231244.		
PR	08-SEP-2000; 2000US-0231413.		
PR	08-SEP-2000; 2000US-0231414.		
PR	08-SEP-2000; 2000US-0232080.		
PR	08-SEP-2000; 2000US-0232081.		
PR	12-SEP-2000; 2000US-0231968.		
PR	14-SEP-2000; 2000US-0232397.		
PR	14-SEP-2000; 2000US-0232398.		
PR	14-SEP-2000; 2000US-0232399.		

[illegible]

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476224/51.
DR N-PSDB; AAS28070.
XX
XX Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the respiratory system including respiratory
PT cancers and also for testing and detection e.g. diagnosis -
XX
PS Claim 11; SEQ ID No 504; 546bp; English.
XX
XX The present invention relates to the isolation of novel human
CC respiratory antigens, and cDNA (AAS27869-AAS28159) and genomic
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful for preventing, treating and/or prognosing
CC disorders related to the respiratory system including throat
CC disorders (e.g. vocal cord paralysis, tonsillitis and laryngitis),
CC lung disorders e.g. pneumonia, allergic disorders e.g. asthma,
CC pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of
CC the respiratory tissues e.g. lung cancer. The polynucleotide sequences
CC of the invention are useful in gene therapy and antisense therapy.
CC AA017685-AA017975 represent novel human respiratory antigens.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 69 AA:

Query Match 26.9%; Score 7; DB 22; Length 69;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LITQMDFG 12
|||||||
DB 43 IJQMDfG 49

RESULT 41
ABG07716
ID ABG07716 standard; Protein; 186 AA.
XX
XX
AC ABG07716;
XX
XX 13-FEB-2002 (first entry)
DT
XX
DE Novel human diagnostic protein #7707.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
PN
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
PF
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX

PA (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS71903.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 38075; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful for medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 186 AA:

Query Match 26.9%; Score 7; DB 22; Length 186;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLD 8
|||||||
DB 93 dGflllD 99

RESULT 42
ABG17572
ID ABG17572 standard; Protein; 401 AA.
XX
XX
AC ABG17572;
XX
XX 18-FEB-2002 (first entry)
DT
XX
DE Novel human diagnostic protein #17563.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
PN
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
PF
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.

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XX  Drmanac RT, Liu C, Tang YT;
XX  WPI: 2001-639362/73.
XX  N-PSDB: AAS81759.
XX
XX  New isolated polynucleotide and encoded polypeptides, useful in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits and to assess
XX  biodiversity -
XX
XX  Claim 20: SEQ ID No 47931; 103bp; English.
XX
XX  The invention relates to isolated polynucleotide (I) and
XX  polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX  and gene mapping, and in recombinant production of (II). The
XX  polynucleotides are also used in diagnostics as expressed sequence tags
XX  for identifying expressed genes. (I) is useful in gene therapy techniques
XX  to restore normal activity of (II) or to treat disease states involving
XX  (II). (II) is useful for generating antibodies against it, detecting or
XX  quantitating a polypeptide in tissue, as molecular weight markers and as
XX  a food supplement. (II) and its binding partners are useful in medical
XX  imaging of sites expressing (II). (I) and (II) are useful for treating
XX  disorders involving aberrant protein expression or biological activity.
XX  The polypeptide and polynucleotide sequences have applications in
XX  diagnostics, forensics, gene mapping, identification of mutations in
XX  responsible for genetic disorders or other traits to assess biodiversity
XX  and to produce other types of data and products dependent on DNA and
XX  amino acid sequences. Abg00010-Abg30377 represent novel human
XX  diagnostic amino acid sequences of the invention.
XX  Note: The sequence data for this patent did not appear in the printed
XX  specification, but was obtained in electronic format directly from WIPO
XX  at ftp.wipo.int/pub/published_pct_sequences.
XX
XX  Sequence 401 AA:

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Query Match          26.9%; Score 7; DB 22; Length 401;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY  2 DGFLLQ 8
    |||||
Db  308 dGflllq 314

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RESULT 43
ABG07733
ID  ABG07733 standard; Protein: 417 AA.
XX
XX  ABG07733:
XX
XX  13-FEB-2002 (first entry)
XX
XX  Novel human diagnostic protein #7724.
XX
XX  Human; chromosome mapping; gene mapping; gene therapy; forensics;
XX  food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX  Homo sapiens.
XX
XX  WO200175067-A2.
XX
XX  11-OCT-2001.
XX
XX  30-MAR-2001; 2001MO-US08631.
XX
XX  31-MAR-2000; 2000US-0540217.
XX  23-AUG-2000; 2000US-0649167.
XX
XX  (HYSE-) HYSE0 INC.
XX

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PI  Drmanac RT, Liu C, Tang YT;
XX  WPI: 2001-639362/73.
XX  N-PSDB: AAS71920.
XX
XX  New isolated polynucleotide and encoded polypeptides, useful in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits and to assess
XX  biodiversity -
XX
XX  Claim 20: SEQ ID No 38092; 103bp; English.
XX
XX  The invention relates to isolated polynucleotide (I) and
XX  polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX  and gene mapping, and in recombinant production of (II). The
XX  polynucleotides are also used in diagnostics as expressed sequence tags
XX  for identifying expressed genes. (I) is useful in gene therapy techniques
XX  to restore normal activity of (II) or to treat disease states involving
XX  (II). (II) is useful for generating antibodies against it, detecting or
XX  quantitating a polypeptide in tissue, as molecular weight markers and as
XX  a food supplement. (II) and its binding partners are useful in medical
XX  imaging of sites expressing (II). (I) and (II) are useful for treating
XX  disorders involving aberrant protein expression or biological activity.
XX  The polypeptide and polynucleotide sequences have applications in
XX  diagnostics, forensics, gene mapping, identification of mutations in
XX  responsible for genetic disorders or other traits to assess biodiversity
XX  and to produce other types of data and products dependent on DNA and
XX  amino acid sequences. Abg00010-Abg30377 represent novel human
XX  diagnostic amino acid sequences of the invention.
XX  Note: The sequence data for this patent did not appear in the printed
XX  specification, but was obtained in electronic format directly from WIPO
XX  at ftp.wipo.int/pub/published_pct_sequences.
XX
XX  Sequence 417 AA:

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Query Match          26.9%; Score 7; DB 22; Length 417;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY  2 DGFLLQ 8
    |||||
Db  329 dGflllq 335

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RESULT 44
AAR54202
ID  AAR54202 standard; Protein: 422 AA.
XX
XX  AAR54202:
XX
XX  18-NOV-1994 (first entry)
XX
XX  snaA gene product involved in streptogramin biosynthetic pathway.
XX
XX  Antibiotic; streptogramin; snaA; snab; snac; biosynthesis; enzyme;
XX  biosynthetic pathway; Streptomyces pristinaespiralis.
XX
XX  Streptomyces pristinaespiralis.
XX
XX  FR2696189-A.
XX
XX  01-APR-1994.
XX
XX  25-SEP-1992; 92PR-0011441.
XX
XX  25-SEP-1992; 92PR-0011441.
XX
XX  (RHON ) RHONE POULENC RORER SA.
XX
XX  Blanc V, Blanche F, Crouzet J, Jacques N, Lacroix P,
XX  Thibaut D, Zagorec M,
XX

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XX WPI: 1994-128286/16.
 DR N-PSDB: AAO64202.
 XX
 PT DNA involved in streptogramin antibiotic biosynthesis - for
 PT prodn. or bio-conversion of streptogramin(s) or prodn. of
 PT streptogramin intermediates, derivs. or hybrid antibiotics
 XX
 PS
 CC Claim 21: Page 49-51; 83pp; French.
 CC The snaa gene product is involved in the biosynthesis of
 CC streptogramins, antibiotics active against Gram-positive bacteria.
 CC The identification of the sequences encoding the enzymes involved
 CC in the biosynthetic pathway means that they can be isolated and
 CC manipulated. Mutant microorganisms in which a step in the
 CC streptogramin biosynthetic pathway is blocked can be cultured to
 CC produce streptogramin intermediates, which may later be converted
 CC to streptogramin derivatives. Recombinant cells may also be used
 CC for the bioconversion of streptogramins from one form to another or
 CC for the production of hybrid antibiotics.
 CC
 SQ Sequence 422 AA:

Query Match 26.9%; Score 7; DB 15; Length 422;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 11 RGPEHL 17
 |||||
 Db 143 fgpchl 149

RESULT 45
 ABG16251
 ID ABG16251 standard; Protein; 466 AA.
 XX
 AC ABG16251;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #16242.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 PI
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS80438.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20: SEQ ID No 46610; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at fip.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 466 AA:

Query Match 26.9%; Score 7; DB 22; Length 466;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 DGFLLQ 8
 |||||
 Db 373 dgflilq 379

RESULT 46
 ABG15687
 ID ABG15687 standard; Protein; 478 AA.
 XX
 AC ABG15687;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #15678.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 PI
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS79874.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20: SEQ ID No 46046; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAG00010-ABG3377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIGO
 CC at ftp.wigo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 478 AA:

Query Match 26.9%; Score 7; DB 22; Length 478;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 DGFLLQ 8
 |||||
 Db 151 dGflllq 157

RESULT 47

AAG82878
 ID AAG82878 standard; Protein: 1501 AA.

AC AAG82878;

DT 03-SEP-2001 (first entry)

DE 5. epidermidis open reading frame protein sequence SEQ ID NO:2850.

KW Staphylococcus epidermidis SRI strain; infection; diagnosis;

KW vaccination; endocarditis.

OS Staphylococcus epidermidis.

PN WO200134809-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000MO-US30782.

PR 09-NOV-1999; 99US-0164258.

PA (GLAXO) GLAXO GROUP LTD.

PI Kimmerly WJ;

DR WPI: 2001-316495/33.

DR N-PSDB; AAH53728.

XX

XX

XX

CC

Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 useful for vaccinating against infections, e.g. endocarditis -
 Claim 18; Page 742-743; 2188pp; English.

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 (I) and (II) can have antibacterial activity and therefore can be used
 in vaccination. The nucleic acids (I) may be used to produce the
 S. epidermidis polypeptides (II) via the production of vectors
 containing them which are used to produce hosts cells which express the
 polypeptides. The polypeptides (II) (and/or nucleic acids) may then be

CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.

SQ Sequence 1501 AA:

Query Match 26.9%; Score 7; DB 22; Length 1501;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 17 LTVDFLQ 23
 |||||
 Db 404 ltvdfllq 410

RESULT 48

AAZ27814
 ID AAZ27814 standard; Protein: 14 AA.

AC AAZ27814;

DT 30-JUL-1999 (first entry)

DE Human secreted protein encoded by gene No. 84.

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;

KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW developmental abnormality; foetal deficiency; blood; allergy; renal;

KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

KW inflammation; ischaemic shock; Alzheimer's disease; osteoclast; thymus;

KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

PN WO9924836-A1.

PD 20-MAY-1999.

PF 04-NOV-1998; 98MO-US23435.

PR 17-NOV-1997; 97US-0066100.

PR 07-NOV-1997; 97US-0064900.

PR 07-NOV-1997; 97US-0064908.

PR 07-NOV-1997; 97US-0064911.

PR 07-NOV-1997; 97US-0064912.

PR 07-NOV-1997; 97US-0064983.

PR 07-NOV-1997; 97US-0064984.

PR 07-NOV-1997; 97US-0064985.

PR 07-NOV-1997; 97US-0064987.

PR 07-NOV-1997; 97US-0064988.

PR 17-NOV-1997; 97US-0066090.

PR 17-NOV-1997; 97US-0066094.

PR 17-NOV-1997; 97US-0066095.

PR 17-NOV-1997; 97US-0066099.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Carter KC, Ebner R, Endress GA, Feng P, Janat F;

PI Kyaw H, Lafleur DM, Moore PA, Ni J, Olsen HS, Rosen CA;

PI Ruben SM, Shi Y, Sopet DR, Wei Y;

XX MPI; 1999-337740/28.
 DR N-PSDB; AAX85016.
 XX
 PT New human secreted proteins and coding sequences useful for treating
 disorders of the immune system and hyperproliferative disorders
 PS
 PS Disclosure: Page 119; 507pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAX84924) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 125 novel genes and their fragments (nucleic
 CC acid sequences: AAX84933-85057; amino acid sequences AAY27567-Y27933)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 125
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAX84933 for described uses).
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 23.1%; Score 6; DB 20; Length 14;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 FLOSLIS 26
 |||||
 Db 8 flqsls 13
 RESULT 49
 AAB51836
 ID AAB51836 standard; Protein; 31 AA.
 XX
 AC AAB51836;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 10 SEQ ID NO:69.
 XX
 KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cytoskeletal; cardiac; vasotropic; cerebroprotective;
 KW neurotropic; neuroprotective; antibacterial; virocidic; fungicide;
 KW ophthalmological; vulnerary; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorders; cancer; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; nervous system disorder;
 KW Alzheimer's disease; ocular disorder; wound healing; skin aging.
 XX
 OS Homo sapiens.
 XX
 PN WO200061626-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US09066.
 XX
 PR 09-APR-1999; 99US-0128698.
 PR 20-JAN-2000; 2000US-0176926.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX MPI; 2000-619227/59.
 DR N-PSDB; AAC93488.
 XX

PT New nucleic acid molecules encoding 49 human secreted proteins for
 PT diagnosing, preventing or ameliorating medical conditions and used for
 PT food additives or preservatives -
 XX
 XX Claim 11; Page 466; 516pp; English.
 XX
 CC Polynucleotide sequences AAC93479 - AAC93527 represent cDNA encoding
 CC human secreted proteins AAB51827 - AAB51875. Sequences AAB51876 -
 CC AAB51927 represent alternative polypeptides encoded by the genes, and
 CC amino acid sequences with which they share homology. The genes and
 CC proteins have activities dependent on the tissues and cells in which they
 CC are expressed. Examples of their activities include immunosuppressive;
 CC antirheumatic; antirheumatic; antiproliferative; cytoskeletal; cardiac;
 CC vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;
 CC virocidic; fungicide; ophthalmological; and vulnerary. The secreted
 CC proteins, polynucleotides, antagonists and agonists may be useful in
 CC treating, preventing and/or diagnosing diseases and disorders such as
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. Oligonucleotides AAC93470 - AAC93478 and peptide AAB51826 are
 CC used in the isolation and characterisation of the proteins and
 CC polynucleotides of the invention.
 CC
 XX Sequence 31 AA;
 SQ
 Query Match 23.1%; Score 6; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 LLYVDFL 22
 |||||
 Db 9 llyvdf 14
 RESULT 50
 AAB38991
 ID AAB38991 standard; Protein; 42 AA.
 XX
 AC AAB38991;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human secreted protein #8.
 XX
 KW Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200056880-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 16-MAR-2000; 2000WO-US06781.
 XX
 PR 19-MAR-1999; 99US-0125363.
 PR 08-DEC-1999; 99US-0169617.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI: 2000-602220/57.
DR N-PSDB; AAC59699.

XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating disorders such as Parkinson's and
PT Alzheimer's diseases, cancers and infections -

XX
PS Claim 11; Page 377; 422pp; English.

XX
CC Sequences AA318971-B39020 represent the amino acid sequences of 50
CC human secreted proteins encoded by the genes AAC59679-C59728. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.

XX
SQ Sequence 42 AA;

Query Match 23.1%; Score 6; DB 21; Length 42;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
|||||
DB 11 dgfill 16

Search completed: June 19, 2002, 11:07:39
Job time: 124 sec

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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:06:51 ; Search time 104.14 Seconds

(without alignments)

87.624 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26

Sequence: 1 RKGFLLQMDFGPEHLDVDFLSLS 26

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 3502263 seqs, 351980561 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	1	PCT-US99-139758-106
2	26	100.0	26	1	US-08-433-483-1
3	26	100.0	26	1	US-08-433-483A-1
4	26	100.0	26	11	US-08-785-997-29
5	26	100.0	26	11	US-08-788-882-29
6	26	100.0	26	13	US-08-934-367-29
7	26	100.0	26	13	US-08-945-289-1

8	26	100.0	26	17	US-09-386-591-29	Sequence 29, App1
9	26	100.0	26	17	US-09-387-340-29	Sequence 29, App1
10	26	100.0	26	21	US-09-701-588-106	Sequence 106, App
11	26	100.0	26	23	US-09-943-334-1	Sequence 1, App1
12	26	100.0	26	23	US-09-943-548-1	Sequence 1, App1
13	26	100.0	45	1	PCT-US99-139758-110	Sequence 110, App
14	26	100.0	45	1	PCT-US99-139758-111	Sequence 111, App
15	26	100.0	46	21	US-09-701-588-110	Sequence 110, App
16	26	100.0	46	21	US-09-701-588-111	Sequence 111, App
17	26	100.0	47	19	US-09-518-598-111	Sequence 111, App
18	26	100.0	47	22	US-09-872-128-14	Sequence 14, App1
19	26	100.0	47	10	US-08-640-713-4	Sequence 4, App1
20	26	100.0	47	11	US-08-785-997-28	Sequence 28, App1
21	26	100.0	47	11	US-08-788-882-28	Sequence 28, App1
22	26	100.0	47	12	US-08-802-967A-4	Sequence 4, App1
23	26	100.0	47	13	US-08-934-367-28	Sequence 28, App1
24	26	100.0	47	13	US-08-945-289-4	Sequence 4, App1
25	26	100.0	47	13	US-08-954-643-1	Sequence 1, App1
26	26	100.0	47	17	US-09-386-591-28	Sequence 28, App1
27	26	100.0	47	17	US-09-387-340-28	Sequence 28, App1
28	26	100.0	47	19	US-09-529-762-1	Sequence 1, App1
29	26	100.0	47	23	US-09-943-334-4	Sequence 4, App1
30	26	100.0	47	23	US-09-943-548-4	Sequence 4, App1
31	26	100.0	49	11	US-08-785-997-30	Sequence 30, App1
32	26	100.0	49	11	US-08-788-882-30	Sequence 30, App1
33	26	100.0	49	13	US-08-934-367-30	Sequence 30, App1
34	26	100.0	49	13	US-09-054-272-14	Sequence 14, App1
35	26	100.0	49	14	US-09-054-272-18	Sequence 14, App1
36	26	100.0	49	17	US-09-386-591-30	Sequence 30, App1
37	26	100.0	49	17	US-09-387-340-30	Sequence 30, App1
38	26	100.0	49	22	US-09-802-640-12	Sequence 12, App1
39	26	84.6	22	11	US-08-785-997-10	Sequence 10, App1
40	26	84.6	22	11	US-08-788-882-10	Sequence 10, App1
41	26	84.6	22	11	US-08-788-882-12	Sequence 12, App1
42	26	84.6	22	11	US-08-788-882-14	Sequence 14, App1
43	26	84.6	22	13	US-08-934-367-10	Sequence 10, App1
44	26	84.6	22	13	US-08-934-367-34	Sequence 34, App1
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46	26	84.6	22	17	US-09-386-591-34	Sequence 34, App1
47	26	84.6	22	17	US-09-387-340-10	Sequence 10, App1
48	26	84.6	22	17	US-09-387-340-34	Sequence 34, App1
49	26	84.6	22	17	US-08-954-643-6	Sequence 6, App1
50	26	84.6	49	19	US-09-529-762-6	Sequence 6, App1
51	26	61.5	16	1	PCT-US99-139758-107	Sequence 107, App
52	26	61.5	16	21	US-09-701-588-107	Sequence 107, App
53	26	61.5	16	21	US-08-432-483-2	Sequence 2, App1
54	26	61.5	31	8	US-08-432-483A-2	Sequence 2, App1
55	26	61.5	31	13	US-08-945-289-2	Sequence 7, App1
56	26	61.5	31	13	US-08-954-643-7	Sequence 7, App1
57	26	61.5	31	19	US-09-529-762-7	Sequence 2, App1
58	26	61.5	31	23	US-09-943-334-2	Sequence 2, App1
59	26	61.5	31	23	US-09-943-548-2	Sequence 2, App1
60	26	61.5	35	1	PCT-US99-139758-114	Sequence 114, App
61	26	61.5	35	21	US-09-701-588-114	Sequence 114, App
62	26	61.5	36	1	PCT-US99-139758-112	Sequence 112, App
63	26	61.5	36	1	PCT-US99-139758-113	Sequence 113, App
64	26	61.5	36	1	PCT-US99-139758-115	Sequence 115, App
65	26	61.5	36	21	US-09-701-588-112	Sequence 112, App
66	26	61.5	36	21	US-09-701-588-113	Sequence 113, App
67	26	61.5	36	21	US-09-701-588-115	Sequence 115, App
68	26	61.5	36	21	US-09-701-588-115	Sequence 115, App
69	26	61.5	30	13	US-08-945-289-8	Sequence 8, App1
70	26	61.5	30	13	US-08-945-289-8	Sequence 8, App1
71	26	61.5	50	23	US-09-943-334-8	Sequence 8, App1
72	26	42.3	11	8	US-08-482-454-3	Sequence 3, App1
73	26	42.3	16	1	PCT-US99-139758-108	Sequence 108, App
74	26	42.3	22	11	US-09-701-588-108	Sequence 108, App
75	26	42.3	22	11	US-08-785-997-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
PCT-US99-13975B-106
Sequence 106, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
TITLE OF INVENTION: PEPTIDE IMMUNOGENS
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158PC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-106

Query Match 100.0%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
|||||
Db 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

RESULT 2
US-08-432-483-1
Sequence 1, Application US/08432483
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179 (TCS-95179)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino acids of
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26

US-08-432-483-1

Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
|||||
Db 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

RESULT 3
US-08-432-483A-1
Sequence 1, Application US/08432483A
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: Ten South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-7407
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,483A
FILING DATE: 1-May-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich

REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino acids of
NAME/KEY: human CERP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Dreyer, Dennis, et al.
TITLE: Cloning and sequencing of human
TITLE: cholesterol ester transfer CDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1:FROM 1 TO 26
US-08-432-483A-1

Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLIOMDGFPEHLVDFLOSL 26
DB 1 RDGFLIOMDGFPEHLVDFLOSL 26

RESULT 4
US-08-785-997-29
Sequence 29, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process for Increasing
TITLE OF INVENTION: the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.,
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-08-785-997-29

Query Match 100.0%; Score 26; DB 11; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLIOMDGFPEHLVDFLOSL 26
DB 1 RDGFLIOMDGFPEHLVDFLOSL 26

RESULT 5
US-08-788-882-29
Sequence 29, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamson, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.,
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-08-788-882-29

Query Match 100.0%; Score 26; DB 11; Length 26;

Best Local Similarity 100.0%; Pred. No. 1,7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLILQMDFGFPEHLVDFLOSL 26
|||||
Db 1 RDGFLILQMDFGFPEHLVDFLOSL 26

RESULT 6

US-08-934-367-29
; Sequence 29, Application US/08934367
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,367
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Swenson, T. L.
; AUTHORS: et al.
; JOURNAL: J. Biol. Chem.
; VOLUME: 264
; PAGES: 14318-14326
; DATE: 1989
; US-08-934-367-29

Query Match 100.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,7e-16;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLILQMDFGFPEHLVDFLOSL 26
|||||
Db 1 RDGFLILQMDFGFPEHLVDFLOSL 26

RESULT 7

US-08-945-289-1
; Sequence 1, Application US/08945289
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; APPLICANT: Thomas, Lawrence J.

;; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
;; TITLE OF INVENTION: TRANSFER PROTEIN (CTP) ACTIVITY
;; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Yankwich & Associates

;; STREET: 130 Bishop Allen Drive
;; CITY: Cambridge

;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02139

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 95

;; SOFTWARE: Word 97
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/945,289

;; FILING DATE: October 17, 1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/432,483

;; FILING DATE: May 1, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Leon R. Yankwich

;; REGISTRATION NUMBER: 30,237
;; REFERENCE/DOCKET NUMBER: TCS-411.1P US

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 amino acids
;; TYPE: amino acid

;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; AMINO-ACID:
;; FEATURE:

;; NAME/KEY: Carboxyl terminal 26 amino
;; LOCATION: acids of human CTP

;; PUBLICATION INFORMATION:
;; AUTHORS: Drayna, Dennis, et al.
;; JOURNAL: Nature

;; VOLUME: 327
;; ISSUE:
;; PAGES: 632-634

;; DATE: 18-JUN-1987
;; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26

US-08-945-289-1

Query Match 100.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLILQMDFGFPEHLVDFLOSL 26
|||||
Db 1 RDGFLILQMDFGFPEHLVDFLOSL 26

RESULT 8

US-09-386-591-29
; Sequence 29, Application US/09386591
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago

STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gansson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-386-591-29

Query Match 100.0%; Score 26; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
DB 1 RDGFLLLQMDGFPPEHLVDFLOSL 26

RESULT 9
US-09-387-340-29
Sequence 29, Application US/09387340
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Gansson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-387-340-29

Query Match 100.0%; Score 26; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
DB 1 RDGFLLLQMDGFPPEHLVDFLOSL 26

RESULT 10
US-09-701-588-106
Sequence 106, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LRRH PEPTIDE
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maiba H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-1580S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 106

US-09-701-588-106

Query Match 100.0%; Score 26; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFGPEHLVDFLQSL 26
DB 1 RDGFLLLQMDGFGPEHLVDFLQSL 26

RESULT 11
US-09-943-334-1
; Sequence 1, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943.334
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432.483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945.289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
US-09-943-334-1

Query Match 100.0%; Score 26; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFGPEHLVDFLQSL 26
DB 1 RDGFLLLQMDGFGPEHLVDFLQSL 26

RESULT 12
US-09-943-548-1
; Sequence 1, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943.548
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432.483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945.289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
US-09-943-548-1

Query Match 100.0%; Score 26; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFGPEHLVDFLQSL 26
DB 1 RDGFLLLQMDGFGPEHLVDFLQSL 26

RESULT 13
PCT-US99-13975B-110
; Sequence 110, Application PC/TUS9913975B
; GENERAL INFORMATION:
; APPLICANT: UNITED BIOMEDICAL INC., ET AL.
; TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
; TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/13975B
; FILING DATE: 21-JUNE-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100.412
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4158P01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US99-13975B-110

Query Match 100.0%; Score 26; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFGPEHLVDFLQSL 26
DB 21 RDGFLLLQMDGFGPEHLVDFLQSL 46

RESULT 14
PCT-US99-13975B-111
; Sequence 111, Application PC/TUS9913975B
; GENERAL INFORMATION:
; APPLICANT: UNITED BIOMEDICAL INC., ET AL.
; TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
; TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
; NUMBER OF SEQUENCES: 151

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-158BC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-111

Query Match 100.0%; Score 26; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
Db 21 RDGFLLLQMDGFPPEHLVDFLOSLS 46

RESULT 15
US-09-701-588-110
Sequence 110, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
IMMUNOGENS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin

REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-1580S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 110
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 110
US-09-701-588-110

Query Match 100.0%; Score 26; DB 21; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
Db 21 RDGFLLLQMDGFPPEHLVDFLOSLS 46

RESULT 16
US-09-701-588-111
Sequence 111, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
IMMUNOGENS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-1580S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 111
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 111
US-09-701-588-111

Query Match 100.0%; Score 26; DB 21; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

Db 21 RDGFLLLQMDFGFPEHLVDFLOSL 46

RESULT 17

US-09-518-598-14
Sequence 14, Application US/09518598
GENERAL INFORMATION:
APPLICANT: Beamer, Lesa J.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN;
TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
TITLE OF INVENTION: MOLECULAR MODELING OF RELATED PROTEINS
FILE REFERENCE: 1103/11034US03
CURRENT APPLICATION NUMBER: US/09/518,598
CURRENT FILING DATE: 2000-03-03
EARLIER APPLICATION NUMBER: 08/879,565
EARLIER FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure
US-09-518-598-14

Query Match

Best Local Similarity 100.0%; Score 26; DB 19; Length 470;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDFGFPEHLVDFLOSL 26

Db 445 RDGFLLLQMDFGFPEHLVDFLOSL 470

RESULT 18

US-09-872-128-14
Sequence 14, Application US/09872128
GENERAL INFORMATION:
APPLICANT: Beamer, Lesa J.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN;
TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
TITLE OF INVENTION: MOLECULAR MODELING OF RELATED PROTEINS
FILE REFERENCE: 1103/11034US03
CURRENT APPLICATION NUMBER: US/09/872,128
CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: US/09/518,598
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 08/879,565
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure
US-09-872-128-14

Query Match 100.0%; Score 26; DB 22; Length 470;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDFGFPEHLVDFLOSL 26

Db 445 RDGFLLLQMDFGFPEHLVDFLOSL 470

RESULT 19

US-08-640-713-4
Sequence 4, Application US/08640713
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,713
FILING DATE: May 1, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,1102(TCS-205-999)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence of mature human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Dryana, Dennis, et al.
TITLE: Cloning and sequencing of human
TITLE: cholesterol ester transfer cDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 4:
FROM 1 TO
RELEVANT RESIDUES IN SEQ ID NO: 476
US-08-640-713-4

Query Match

Best Local Similarity 100.0%; Score 26; DB 10; Length 476;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDFGFPEHLVDFLOSL 26

Db 451 RDGFLLLQMDFGFPEHLVDFLOSL 476

RESULT 20

US-08-785-997-28

Sequence 28, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process for Increasing
TITLE OF INVENTION: the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis
AUTHORS: Jarnagin, Alisha Stephens
AUTHORS: McLean, John
AUTHORS: Henzel, William
AUTHORS: Kohr, William
AUTHORS: Fielding, Christopher
AUTHORS: Lawn, Richard
TITLE: Cloning and sequencing of human cholesterol
TITLE: ester transfer protein CDNA
JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: June 18-1987
US-08-785-997-28

Query Match 100.0%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
Db 451 RDGFLLLQMDGFPPEHLVDFLOSL 476

RESULT 21
US-08-788-882-28
Sequence 28, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamson, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis
AUTHORS: Jarnagin, Alisha Stephens
AUTHORS: McLean, John
AUTHORS: Henzel, William
AUTHORS: Kohr, William
AUTHORS: Fielding, Christopher
AUTHORS: Lawn, Richard
TITLE: Cloning and sequencing of human cholesterol
TITLE: ester transfer protein CDNA
JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: June 18-1987
US-08-788-882-28

Query Match 100.0%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
Db 451 RDGFLLLQMDGFPPEHLVDFLOSL 476

RESULT 22
US-08-802-967A-4
Sequence 4, Application US/08802967A
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR
TITLE OF INVENTION: TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,967A
FILING DATE: 21-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 US
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence of mature human
NAME/KEY: CERP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632 - 634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476
US-08-802-967A-4

Query Match 100.0%; Score 26; DB 12; Length 476;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFGPEHLVDFLQSL 26
|||||

DB 451 RDGFLLLQMDGFGPEHLVDFLQSL 476

RESULT 23
US-08-934-367-28
Sequence 28, Application US/08934367
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: For Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF INVENTIONS: Vaccination
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,367

FILING DATE: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gansson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis
AUTHORS: Jarnagin, Alisha Stephens
AUTHORS: McLean, John
AUTHORS: Henzel, William
AUTHORS: Kohr, William
AUTHORS: Fielding, Christopher
AUTHORS: Lawn, Richard
TITLE: Cloning and sequencing of human cholesteryl
JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: June 18-1987
US-08-934-367-28

Query Match 100.0%; Score 26; DB 13; Length 476;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFGPEHLVDFLQSL 26
|||||

DB 451 RDGFLLLQMDGFGPEHLVDFLQSL 476

RESULT 24
US-08-945-289-4
Sequence 4, Application US/08945289
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CERP) ACTIVITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,289
FILING DATE: October 17, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/432,483
FILING DATE: May 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: TCS-411.1P US
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence of mature
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 476
US-08-945-289-4

Query Match 100.0%; Score 26; DB 13; Length 476;
Best Local Similarity 100.0%; Pred. NO. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLOMDGFPPEHLVDFLOSL 26
Db 451 RDGFLLOMDGFPPEHLVDFLOSL 476

RESULT 25
US-08-954-643-1
Sequence 1, Application US/08954643
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: XENOGENEIC CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) FOR MODULATION OF CETP ACTIVITY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,643
FILING DATE: concurrently herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-420.0 US
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: amino acid sequence of mature human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human cholesteryl
TITLE: ester transfer cDNA
JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: 1 to 476
US-08-954-643-1

Query Match 100.0%; Score 26; DB 13; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLOMDGFPPEHLVDFLOSL 26
Db 451 RDGFLLOMDGFPPEHLVDFLOSL 476

RESULT 26
US-09-386-591-28
Sequence 28, Application US/09386591
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ganson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis
AUTHORS: Jarnagin, Alisha Stephens
AUTHORS: McLean, John
AUTHORS: Henzel, William
AUTHORS: Kohr, William
AUTHORS: Fielding, Christopher
AUTHORS: Lawn, Richard
TITLE: Cloning and sequencing of human cholesteryl
TITLE: ester transfer protein cDNA

JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: June 18-1987
US-09-386-591-28

Query Match 100.0%; Score 26; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
|||||
DB 451 RDGFLLLQMDGFPPEHLVDFLOSLS 476

RESULT 27

US-09-387-340-28
Sequence 28, Application US/09187340
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamsom, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamsom, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis
AUTHORS: Jarnagin, Alisha Stephens
AUTHORS: McLean, John
AUTHORS: Henszel, William
AUTHORS: Kohr, William
AUTHORS: Fielding, Christopher
AUTHORS: Lawn, Richard
TITLE: Cloning and sequencing of human cholesteryl
TITLE: ester transfer protein cDNA
JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: June 18-1987
US-09-387-340-28

Query Match 100.0%; Score 26; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
|||||
DB 451 RDGFLLLQMDGFPPEHLVDFLOSLS 476

RESULT 28

US-09-529-762-1
Sequence 1, Application US/09529762
GENERAL INFORMATION:
APPLICANT: AVANT Immunotherapeutics, Inc.
APPLICANT: Rittershaus, Charles
APPLICANT: Thomas, Lawrence
TITLE OF INVENTION: Xenogenic Cholesteryl Ester Transfer Protein (CETP) for
TITLE OF INVENTION: Modulation of CETP Activity
FILE REFERENCE: sequence listing for TCS-420.1 PCT
CURRENT APPLICATION NUMBER: US/09/529,762
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: USSN 08/954,643
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO: 1
LENGTH: 476
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-762-1

Query Match 100.0%; Score 26; DB 19; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
|||||
DB 451 RDGFLLLQMDGFPPEHLVDFLOSLS 476

RESULT 29

US-09-943-334-4
Sequence 4, Application US/09943334
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,334
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentln version 3.1
SEQ ID NO: 4
LENGTH: 476
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-943-334-4

Query Match 100.0%; Score 26; DB 23; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
|||||

Db 451 RDGFLLLQMDGFPPEHLVDFLQSL 476

RESULT 30
US-09-943-548-4
; Sequence 4, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-943-548-4

Query Match 100.0%; Score 26; DB 23; Length 476;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFPPEHLVDFLQSL 26
Db 451 RDGFLLLQMDGFPPEHLVDFLQSL 476

RESULT 31
US-08-785-997-30
; Sequence 30, Application US/08785997
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; TITLE OF INVENTION: An Immunological Process for Increasing
; TITLE OF INVENTION: the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,997
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid

STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Pape, Michael E.
; AUTHORS: Rehberg, Edward F.
; AUTHORS: Marotli, Keith R.
; AUTHORS: Welchior, George W.
; TITLE: Molecular Cloning, Sequence, and Expression
; TITLE: of Cynomolgus Monkey Cholesteryl Ester Transfer
; TITLE: Protein
; JOURNAL: Arteriosclerosis and Thrombosis
; VOLUME: 11
; ISSUE: 6
; PAGES: 1759-1771
; DATE: Nov/Dec 1991
US-08-785-997-30

Query Match 100.0%; Score 26; DB 11; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFPPEHLVDFLQSL 26
Db 468 RDGFLLLQMDGFPPEHLVDFLQSL 493

RESULT 32
US-08-788-882-30
; Sequence 30, Application US/08788882
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,882
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Pape, Michael E.
; AUTHORS: Rehberg, Edward F.
; AUTHORS: Marotli, Keith R.

AUTHORS: Melchior, George W.
TITLE: Molecular Cloning, Sequence, and Expression
of Cynomolgus Monkey Cholesteryl Ester Transfer
Protein
JOURNAL: Arteriosclerosis and Thrombosis
VOLUME: 11
ISSUE: 6
PAGES: 1759-1771
DATE: Nov/Dec-1991
US-08-788-882-30

Query Match 100.0%; Score 26; DB 11; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGFPHLLVDFLOSLS 26
DB 468 RDGFLLLQMDFGFPHLLVDFLOSLS 493

RESULT 33
US-08-934-367-30
Sequence 30, Application US/08934367
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,367
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gansson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Pape, Michael E.
AUTHORS: Rehberg, Edward F.
AUTHORS: Marotli, Keith R.
AUTHORS: Melchior, George W.
TITLE: Molecular Cloning, Sequence, and Expression
of Cynomolgus Monkey Cholesteryl Ester Transfer
Protein
JOURNAL: Arteriosclerosis and Thrombosis
VOLUME: 11
ISSUE: 6
PAGES: 1759-1771

DATE: Nov/Dec-1991
US-08-934-367-30

Query Match 100.0%; Score 26; DB 13; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGFPHLLVDFLOSLS 26
DB 468 RDGFLLLQMDFGFPHLLVDFLOSLS 493

RESULT 34
US-09-054-272-14
Sequence 14, Application US/09054272
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Daley, George Q.
APPLICANT: Carilli, Michele
APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI98-05
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-272-14

Query Match 100.0%; Score 26; DB 14; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGFPHLLVDFLOSLS 26
DB 468 RDGFLLLQMDFGFPHLLVDFLOSLS 493

RESULT 35
US-09-054-272-48

Sequence 48, Application US/09054272
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Daley, George Q.
APPLICANT: Carell, Michele
APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO MILLIE DRIVE
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH198-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-054-272-48

Query Match 100.0%; Score 26; DB 14; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLQMDGFPEHLVDLFQSLIS 26
DB 468 RDGFLLQMDGFPEHLVDLFQSLIS 493

RESULT 35
US-09-386-591-30
Sequence 30, Application US/09386591
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Pape, Michael E.
AUTHORS: Rehberg, Edward F.
AUTHORS: Marotli, Keith R.
AUTHORS: Melchior, George W.
TITLE: Molecular Cloning, Sequence, and Expression
TITLE: of Cynomolgus Monkey Cholesteryl Ester Transfer
TITLE: Protein
JOURNAL: Arteriosclerosis and Thrombosis
VOLUME: 11
ISSUE: 6
PAGES: 1759-1771
DATE: Nov/Dec-1991
US-09-386-591-30

Query Match 100.0%; Score 26; DB 17; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLQMDGFPEHLVDLFQSLIS 26
DB 468 RDGFLLQMDGFPEHLVDLFQSLIS 493

RESULT 37
US-09-387-340-30
Sequence 30, Application US/09387340
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
APPLICANT: Kroll, Elaine
APPLICANT: Gamson, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1500
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Pape, Michael E.
AUTHORS: Rehberg, Edward F.
AUTHORS: Marotti, Keith R.
AUTHORS: Melchior, George W.
TITLE: Molecular Cloning, Sequence, and Expression
TITLE: of Cynomolgus Monkey Cholesteryl Ester Transfer
JOURNAL: Arteriosclerosis and Thrombosis
VOLUME: 11
ISSUE: 6
PAGES: 1759-1771
DATE: Nov/Dec-1991
US-09-387-340-30

Query Match 100.0%; Score 26; DB 17; Length 493;
Best Local Similarity 100.0%; Pred. NO. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLIOMDGFPEHLVDFLOSL 26
DB 468 RDGFLIOMDGFPEHLVDFLOSL 493

RESULT 38
US-09-802-640-12
; Sequence 12, Application US/09802640
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsel Aruna
; APPLICANT: Kiehn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-12

Query Match 100.0%; Score 26; DB 22; Length 493;
Best Local Similarity 100.0%; Pred. NO. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLIOMDGFPEHLVDFLOSL 26
DB 468 RDGFLIOMDGFPEHLVDFLOSL 493

RESULT 39
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```
US-08-785-997-10
; Sequence 10, Application US/08785997
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process for Increasing
; TITLE OF INVENTION: the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,997
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-997-10

Query Match 84.6%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. NO. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LIIOMDGFPEHLVDFLOSL 26
DB 1 LIIOMDGFPEHLVDFLOSL 22

RESULT 40
US-08-785-997-34
; Sequence 34, Application US/08785997
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process for Increasing
; TITLE OF INVENTION: the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,997
```

FILING DATE: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-882-34

Query Match 84.6%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQNDGFPFPHLLVDFLOSLS 26
DB 1 LLLQNDGFPFPHLLVDFLOSLS 22

RESULT 41
US-08-788-882-10
Sequence 10, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-882-10

Query Match 84.6%; Score 22; DB 11; Length 22;

Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LLLQNDGFPFPHLLVDFLOSLS 26
DB 1 LLLQNDGFPFPHLLVDFLOSLS 22

RESULT 42
US-08-788-882-34
Sequence 34, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamsen, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-882-34

Query Match 84.6%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQNDGFPFPHLLVDFLOSLS 26
DB 1 LLLQNDGFPFPHLLVDFLOSLS 22

RESULT 43
US-08-934-367-10
Sequence 10, Application US/08934367
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.

```

: STREET: 120 South Riverside Plaza, 22nd Floor
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/934,367
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamson Ph.D., Edward P.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)655-1501
: TELEFAX: (312)655-1501
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-934-367-10

Query Match      84.6%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 LLLQMDGFPEHLVDLFQSL 26
DB      1 LLLQMDGFPEHLVDLFQSL 22

RESULT 44
US-08-934-367-34
: Sequence 34, Application US/08934367
: GENERAL INFORMATION:
: APPLICANT: Needleman, Philip
: APPLICANT: Glenn, Kevin
: TITLE OF INVENTION: An Immunological Process and Constructs
: TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Welsh & Katz, Ltd.
: STREET: 120 South Riverside Plaza, 22nd Floor
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/934,367
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamson Ph.D., Edward P.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)655-1501
: TELEFAX: (312)655-1501

```

```

: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-934-367-34

Query Match      84.6%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 LLLQMDGFPEHLVDLFQSL 26
DB      1 LLLQMDGFPEHLVDLFQSL 22

RESULT 45
US-09-386-591-10
: Sequence 10, Application US/09386591
: GENERAL INFORMATION:
: APPLICANT: Needleman, Philip
: APPLICANT: Glenn, Kevin
: TITLE OF INVENTION: An Immunological Process and Constructs
: TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Welsh & Katz, Ltd.
: STREET: 120 South Riverside Plaza, 22nd Floor
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/386,591
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamson Ph.D., Edward P.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)655-1501
: TELEFAX: (312)655-1501
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-386-591-10

Query Match      84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 LLLQMDGFPEHLVDLFQSL 26
DB      1 LLLQMDGFPEHLVDLFQSL 22

RESULT 46
US-09-386-591-34

```

```
? Sequence 34, Application US/09386591
? GENERAL INFORMATION:
? APPLICANT: Needleman, Phillip
? APPLICANT: Glenn, Kevin
? TITLE OF INVENTION: An Immunological Process and Constructs
? TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
? NUMBER OF SEQUENCES: 52
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Welsh & Katz, Ltd.
? STREET: 120 South Riverside Plaza, 22nd Floor
? CITY: Chicago
? STATE: IL
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/386,591
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Gansson Ph.D., Edward P.
? REGISTRATION NUMBER: 29,381
? REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312)655-1500
? TELEFAX: (312)655-1501
? INFORMATION FOR SEQ ID NO: 34:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 22 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-09-386-591-34

Query Match      84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPPEHLVDLQSL 26
DB 1 LLLQMDGFPPEHLVDLQSL 22

RESULT 47
US-09-387-340-10
? Sequence 10, Application US/09387340
? GENERAL INFORMATION:
? APPLICANT: Needleman, Phillip
? APPLICANT: Glenn, Kevin
? APPLICANT: Krul, Elaine
? TITLE OF INVENTION: An Immunological Process and Constructs
? TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
? NUMBER OF SEQUENCES: 50
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Welsh & Katz, Ltd.
? STREET: 120 South Riverside Plaza, 22nd Floor
? CITY: Chicago
? STATE: IL
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
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? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/387,340
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Gansson, Edward P.
? REGISTRATION NUMBER: 29,381
? REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312)655-1500
? TELEFAX: (312)655-1501
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 22 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-09-387-340-10

Query Match      84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPPEHLVDLQSL 26
DB 1 LLLQMDGFPPEHLVDLQSL 22

RESULT 48
US-09-387-340-34
? Sequence 34, Application US/09387340
? GENERAL INFORMATION:
? APPLICANT: Needleman, Phillip
? APPLICANT: Glenn, Kevin
? APPLICANT: Krul, Elaine
? TITLE OF INVENTION: An Immunological Process and Constructs
? TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
? NUMBER OF SEQUENCES: 50
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Welsh & Katz, Ltd.
? STREET: 120 South Riverside Plaza, 22nd Floor
? CITY: Chicago
? STATE: IL
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/387,340
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Gansson, Edward P.
? REGISTRATION NUMBER: 29,381
? REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312)655-1500
? TELEFAX: (312)655-1501
? INFORMATION FOR SEQ ID NO: 34:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 22 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-09-387-340-34
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Query Match 84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGPPEHLVDFLOSL 26
|||||
DB 1 LLLQMDFGPPEHLVDFLOSL 22

RESULT 49

US-08-954-643-6
; Sequence 6, Application US/08954643

; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.

; TITLE OF INVENTION: XENOGENIC CHOLESTERYL ESTER

; TITLE OF INVENTION: TRANSFER PROTEIN (CTP) FOR MODULATION OF CTP ACTIVITY

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Yankwich & Associates

; STREET: 130 Bishop Allen Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02139

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/954,643

; FILING DATE: concurrently herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Leon R. Yankwich

; REGISTRATION NUMBER: 30,237

; REFERENCE/DOCKET NUMBER: TCS-420.0 US

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 496 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: amino acid sequence for a humanized

; US-08-954-643-6

Query Match 84.6%; Score 22; DB 13; Length 496;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGPPEHLVDFLOSL 26
|||||
DB 475 LLLQMDFGPPEHLVDFLOSL 496

RESULT 50

US-09-529-762-6
; Sequence 6, Application US/09529762

; GENERAL INFORMATION:

; APPLICANT: AVANT Immunotherapeutics, Inc.

; APPLICANT: Rittershaus, Charles

; APPLICANT: Thomas, Lawrence

; TITLE OF INVENTION: Xenogeneic Cholesteryl Ester Transfer Protein (CTP) for

; TITLE OF INVENTION: Modulation of CTP Activity

; FILE REFERENCE: sequence listing for TCS-420.1 PCT

; CURRENT APPLICATION NUMBER: US/09/529,762
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: USSN 08/954,643
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

; LENGTH: 496

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: humanized

; US-09-529-762-6

Query Match 84.6%; Score 22; DB 19; Length 496;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGPPEHLVDFLOSL 26
|||||
DB 475 LLLQMDFGPPEHLVDFLOSL 496

Search completed: June 19, 2002, 11:10:11
Job time: 200 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 19, 2002, 11:07:06 ; Search time 14.77 Seconds

(without alignments)
152.226 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26
Sequence: 1 RKGFULLQMDFGPPEHLVDFLOSLS 26

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262338 seqs, 86476186 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262338

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

Pending_Patents_AA_New:*
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2: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep:*
3: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep:*
4: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep:*
5: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep:*
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7: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	470	5	US-09-446-415B-6
2	11	42.3	11	5	US-09-523-033A-3
3	7	26.9	405	5	US-09-935-625-15267
4	6	23.1	42	6	US-10-105-299-4676
5	6	23.1	69	6	US-10-106-698-4318
6	6	23.1	97	6	US-10-144-850-423
7	6	23.1	193	7	US-60-360-039-20191
8	6	23.1	239	7	US-60-360-039-16488
9	6	23.1	260	7	US-60-360-039-17364
10	6	23.1	261	7	US-60-360-039-13333
11	6	23.1	269	7	US-60-360-039-17696
12	6	23.1	364	7	US-60-360-039-16535
13	6	23.1	370	5	US-09-895-913A-210
14	6	23.1	397	5	US-09-540-209B-5750
15	6	23.1	430	6	US-10-145-415-8
16	6	23.1	430	6	US-10-145-415-12
17	6	23.1	430	6	US-10-145-415-20
18	6	23.1	430	6	US-10-145-415-30
19	6	23.1	442	6	US-10-106-698-6383
20	6	23.1	481	7	US-60-360-039-4831
21	6	23.1	484	7	US-60-360-039-7590
22	6	23.1	487	7	US-60-360-039-8897
23	6	23.1	892	7	US-60-360-039-22811
24	6	23.1	903	6	US-10-104-047-2951
25	6	23.1	911	7	US-60-360-039-12464
26	6	23.1	1340	7	US-60-360-039-19485

27	5	19.2	7	6	US-10-105-299-3886	Sequence 3886, Ap
28	5	19.2	9	6	US-10-117-937-269	Sequence 269, Ap
29	5	19.2	9	6	US-10-014-340-19	Sequence 19, Appl
30	5	19.2	10	6	US-10-117-937-270	Sequence 270, Appl
31	5	19.2	13	1	PCR-US02-09135-151	Sequence 151, App
32	5	19.2	13	1	PCR-US02-09105-221	Sequence 221, App
33	5	19.2	13	1	PCR-US02-09257-299	Sequence 299, App
34	5	19.2	13	1	PCR-US02-09222-285	Sequence 285, App
35	5	19.2	13	6	US-10-105-299-3814	Sequence 3814, Ap
36	5	19.2	22	6	US-10-105-299-3635	Sequence 3635, Ap
37	5	19.2	24	6	US-10-143-775-636	Sequence 636, App
38	5	19.2	28	6	US-10-105-299-4607	Sequence 4607, App
39	5	19.2	34	6	US-10-105-299-5561	Sequence 5561, Ap
40	5	19.2	35	6	US-10-106-698-5700	Sequence 5700, Ap
41	5	19.2	37	6	US-10-105-299-4199	Sequence 4199, Ap
42	5	19.2	41	6	US-10-143-922-216	Sequence 216, App
43	5	19.2	44	1	PCR-US02-01109-100	Sequence 100, App
44	5	19.2	44	6	US-10-137-337-750	Sequence 750, App
45	5	19.2	46	6	US-10-105-299-5159	Sequence 5159, Ap
46	5	19.2	46	6	US-10-105-299-5161	Sequence 5161, Ap
47	5	19.2	48	1	PCR-US02-09921-928	Sequence 928, App
48	5	19.2	50	6	US-10-105-299-5308	Sequence 5308, App
49	5	19.2	52	6	US-10-143-788-680	Sequence 680, App
50	5	19.2	56	6	US-10-105-299-6077	Sequence 6077, Ap
51	5	19.2	60	6	US-10-106-698-7059	Sequence 7059, Ap
52	5	19.2	60	6	US-10-152-780-462	Sequence 462, App
53	5	19.2	60	6	US-10-152-780-466	Sequence 466, App
54	5	19.2	61	5	US-09-380-693A-55	Sequence 55, Appl
55	5	19.2	62	5	US-09-380-693A-57	Sequence 57, Appl
56	5	19.2	63	5	US-09-380-693A-54	Sequence 54, Appl
57	5	19.2	63	6	US-09-540-209B-9390	Sequence 9390, Ap
58	5	19.2	63	6	US-10-106-698-8030	Sequence 8030, Ap
59	5	19.2	64	6	US-10-144-090-253	Sequence 253, App
60	5	19.2	64	6	US-09-620-333B-5812	Sequence 5812, App
61	5	19.2	65	5	US-09-620-333B-5812	Sequence 5812, App
62	5	19.2	69	5	US-09-380-693A-56	Sequence 56, Appl
63	5	19.2	72	6	US-10-144-702-537	Sequence 537, Appl
64	5	19.2	74	5	US-09-935-625-8321	Sequence 8321, Ap
65	5	19.2	74	6	US-10-105-299-4472	Sequence 4472, Ap
66	5	19.2	78	5	US-10-106-698-8410	Sequence 8410, Ap
67	5	19.2	80	5	US-09-620-333B-4183	Sequence 4183, Ap
68	5	19.2	80	5	US-09-620-333B-8965	Sequence 8965, Ap
69	5	19.2	87	5	US-09-991-150-175	Sequence 175, App
70	5	19.2	87	5	US-09-935-625-8319	Sequence 8319, Ap
71	5	19.2	88	1	PCR-US02-09921-991	Sequence 991, App
72	5	19.2	89	5	US-09-620-333B-548	Sequence 548, App
73	5	19.2	91	5	US-09-620-333B-547	Sequence 547, App
74	5	19.2	91	5	US-09-935-625-9036	Sequence 9036, Ap
75	5	19.2	93	5	US-09-620-333B-5781	Sequence 5781, Ap

ALIGNMENTS

RESULT 1
US-09-446-415B-6
: Sequence 6, Application US/09446415B
: GENERAL INFORMATION:
: APPLICANT: Beamer, Lesa J.
: APPLICANT: Eisenberg, David
: TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
: TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
: TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
: FILE REFERENCE: 11034US02
: CURRENT APPLICATION NUMBER: US/09/446,415B
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: 08/879,565
: PRIOR FILING DATE: 1997-06-20
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6

LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: cholesterol ester transfer protein (CETP) (figure
OTHER INFORMATION: 5)
US-09-446-415B-6

Query Match 100.0%; Score 26; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 3; 7e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGELLQMDGPEPRLHVDLQSL 26
DB 445 RDGELLQMDGPEPRLHVDLQSL 470

RESULT 2
US-09-523-033A-3
Sequence 3, Application US/09523033A
GENERAL INFORMATION:
APPLICANT: Kwok, Deborah Y.
APPLICANT: Brostoff, Steven W.
APPLICANT: Carlo, Dennis J.
TITLE OF INVENTION: METHOD FOR INCREASING HDL CHOLESTEROL LEVEL
FILE REFERENCE: TCS-428.0 US-1
CURRENT APPLICATION NUMBER: US/09/523,033A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 08/482,454
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-523-033A-3

Query Match 42.3%; Score 11; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDLQSL 26
DB 1 HLLVDLQSL 11

RESULT 3
US-09-935-625-15267
Sequence 15267, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
FILE REFERENCE: 2750-148P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 15267
LENGTH: 405
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..405
OTHER INFORMATION: Ceres Seq. ID no. 3440036
US-09-935-625-15267

Query Match 26.9%; Score 7; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 24;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 19 VDFLQSL 25
DB 37 VDFLQSL 43

RESULT 4
US-10-105-299-4676
Sequence 4676, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P5950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4676
LENGTH: 42
TYPE: PRT
ORGANISM: Homo sapiens
US-10-105-299-4676

Query Match 23.1%; Score 6; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLL 7
DB 11 DGFLLL 16

RESULT 5
US-10-106-698-4318
Sequence 4318, Application US/10106698
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCR/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4318
LENGTH: 69
TYPE: PRT
ORGANISM: Homo sapiens
US-10-106-698-4318

Query Match 23.1%; Score 6; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLQSL 26
DB 8 FLQSL 13

RESULT 6
US-10-144-850-423
Sequence 423, Application US/10144850
GENERAL INFORMATION:
APPLICANT: Rosen et al.

```

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM03901N
; CURRENT APPLICATION NUMBER: US/10/144,850
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/758,443
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 423
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-144-850-423
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Query Match          23.1%; Score 6; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 17 LDVDFL 22
      |||||
DB 41 LDVDFL 46
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```

RESULT 7
US-60-360-039-20191
; Sequence 20191: Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20191
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Nostoc punctiforme
US-60-360-039-20191
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Query Match          23.1%; Score 6; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 20 DFLQSL 25
      |||||
DB 78 DFLQSL 83
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RESULT 8
US-60-360-039-16488
; Sequence 16488: Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
```

```

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16488
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-60-360-039-16488
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Query Match          23.1%; Score 6; DB 7; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RDGFLL 6
      |||||
DB 116 RDGFLL 121
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RESULT 9
US-60-360-039-17364
; Sequence 17364: Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17364
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-60-360-039-17364
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Query Match          23.1%; Score 6; DB 7; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RDGFLL 6
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DB 113 RDGFLL 118
```

```

RESULT 10
US-60-360-039-13333
; Sequence 13333: Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13333
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
```

```
; LOCATION: (1)..(261)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-13333
```

```
Query Match          23.1%; Score 6; DB 7; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 21 FLOSLS 26
|||||
Db 109 FLOSLS 114
```

```
RESULT 11
US-60-360-039-17696
; Sequence 17696, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17696
; LENGTH: 269
; TYPE: PRF
; ORGANISM: Bacillus subtilis
US-60-360-039-17696
```

```
Query Match          23.1%; Score 6; DB 7; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 RDGFL 6
|||||
Db 123 RDGFL 128
```

```
RESULT 12
US-60-360-039-16535
; Sequence 16535, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16535
; LENGTH: 364
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-60-360-039-16535
```

```
Query Match          23.1%; Score 6; DB 7; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 21 FLOSLS 26
|||||
```

```
Db 292 FLOSLS 297
```

```
RESULT 13
US-09-895-913A-210
; Sequence 210, Application US/09895913A
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Tomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 370
; TYPE: PRF
; ORGANISM: Helicobacter pylori
US-09-895-913A-210
```

```
Query Match          23.1%; Score 6; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 6 LQMDP 11
|||||
Db 240 LQMDP 245
```

```
RESULT 14
US-09-540-209B-5750
; Sequence 5750, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES
; FILE REFERENCE: 2709, 1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 5750
; LENGTH: 397
; TYPE: PRF
; ORGANISM: B. fragilis
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (44)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are un
US-09-540-209B-5750
```

```
Query Match          23.1%; Score 6; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 17 LVDPL 22
|||||
Db 298 LVDPL 303
```

```
RESULT 15
US-10-145-415-8
; Sequence 8, Application US/10145415
; GENERAL INFORMATION:
```

```

; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces lydicus
US-10-145-415-8
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 GPEPHL 17
        |||||
Db       99 GPEPHL 104
```

```

RESULT 16
US-10-145-415-12
; Sequence 12, Application US/10145415
; GENERAL INFORMATION:
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces chatanoogenensis
US-10-145-415-12
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 GPEPHL 17
        |||||
Db       99 GPEPHL 104
```

```

RESULT 17
US-10-145-415-20
; Sequence 20, Application US/10145415
; GENERAL INFORMATION:
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
```

```

; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces kasugaensis
US-10-145-415-20
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 GPEPHL 17
        |||||
Db       99 GPEPHL 104
```

```

RESULT 18
US-10-145-415-30
; Sequence 30, Application US/10145415
; GENERAL INFORMATION:
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces lydicus
US-10-145-415-30
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 GPEPHL 17
        |||||
Db       99 GPEPHL 104
```

```

RESULT 19
US-10-106-698-6383
; Sequence 6383, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
```

```
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6383
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6383
```

```
Query Match          23.1%; Score 6; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 9 MDGFP 14
    |||||
Db 137 MDGFP 142
```

```
RESULT 20
US-60-360-039-4831
; Sequence 4831, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4831
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-60-360-039-4831
```

```
Query Match          23.1%; Score 6; DB 7; Length 481;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 LLLQMD 10
    |||||
Db 83 LLLQMD 88
```

```
RESULT 21
US-60-360-039-7590
; Sequence 7590, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
```

```
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7590
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-60-360-039-7590
```

```
Query Match          23.1%; Score 6; DB 7; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 LLLQMD 10
    |||||
Db 83 LLLQMD 88
```

```
RESULT 22
US-60-360-039-8897
; Sequence 8897, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8897
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus
US-60-360-039-8897
```

```
Query Match          23.1%; Score 6; DB 7; Length 487;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 LLLQMD 10
    |||||
Db 171 LLLQMD 176
```

```
RESULT 23
US-60-360-039-22811
; Sequence 22811, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22811
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-60-360-039-22811
```

```
Query Match          23.1%; Score 6; DB 7; Length 892;
```

Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSL 26
|||||
DB 405 FLOSL 410

RESULT 24
US-10-104-047-2951

; Sequence 2951, Application US/10104047
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2951
; LENGTH: 903
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2951

Query Match 23.1%; Score 6; DB 6; Length 903;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLOSL 25
|||||
DB 210 DFLOSL 215

RESULT 25
US-60-360-039-12464
; Sequence 12464, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12464
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) (911)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-12464

Query Match 23.1%; Score 6; DB 7; Length 911;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSL 26
|||||
DB 400 FLOSL 405

RESULT 26

US-60-360-039-19485

; Sequence 19485, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19485
; LENGTH: 1340
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-60-360-039-19485

Query Match 23.1%; Score 6; DB 7; Length 1340;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LLYDFL 22
|||||
DB 572 LLYDFL 577

RESULT 27
US-10-105-299-3886
; Sequence 3886, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P8950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; PRIOR APPLICATION removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3886
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-3886

Query Match 19.2%; Score 5; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLL 7
|||||
DB 2 GFLL 6

RESULT 28
US-10-117-937-269
; Sequence 269, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM 027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06

```
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-269
```

```
Query Match          19.2%; Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 GFLL 7
        |||||
Db       5 GFLL 9
```

```
RESULT 29
US-10-014-340-19
; Sequence 19, Application US/10014340
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-19
```

```
Query Match          19.2%; Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      13 FPHL 17
        |||||
Db       2 FPHL 6
```

```
RESULT 30
US-10-117-937-270
; Sequence 270, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Laping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 270
; LENGTH: 10
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-270
```

```
Query Match          19.2%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 GFLL 7
        |||||
Db       6 GFLL 10
```

```
RESULT 31
PCT-US02-09135-151
; Sequence 151, Application PC/TUS0209135
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS956PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09135
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09135-151
```

```
Query Match          19.2%; Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 GFLL 7
        |||||
Db       5 GFLL 9
```

```
RESULT 32
PCT-US02-09105-221
; Sequence 221, Application PC/TUS0209105
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS951PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09105
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 779
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09105-221
```

```
Query Match          19.2%; Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||
DB 5 GFULL 9

RESULT 33
PCT-US02-09257-299

; Sequence 299, Application PC/TUS0209257
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS957PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09257
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 994
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 299
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09257-299

Query Match

Best Local Similarity 19.2%; Score 5; DB 1; Length 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||
DB 5 GFULL 9

RESULT 34

PCT-US02-09922-285
; Sequence 285, Application PC/TUS0209922
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS955PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09922
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 1117
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 285
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09922-285

Query Match 19.2%; Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||
DB 5 GFULL 9

RESULT 35
US-10-105-299-3814

; Sequence 3814, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3814
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-3814

Query Match

Best Local Similarity 19.2%; Score 5; DB 6; Length 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||
DB 5 GFULL 9

RESULT 36

US-10-105-299-5635
; Sequence 5635, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5635
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-5635

Query Match

Best Local Similarity 19.2%; Score 5; DB 6; Length 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSL 25
|||||
DB 11 FLOSL 15

RESULT 37

US-10-143-775-636
; Sequence 636, Application US/10143775
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC02JCIN
; CURRENT APPLICATION NUMBER: US/10/143,775
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1064
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 636
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```
; NAME/KEY: misc_feature
; LOCATION: (14)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-10-143-775-636
```

```
Query Match
Best Local Similarity 19.2%; Score 5; DB 6; Length 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 19 VDFDQ 23
    |||||
Db 8 VDFDQ 12
```

```
RESULT 38
US-10-105-299-4607
; Sequence 4607, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4607
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-4607
```

```
Query Match
Best Local Similarity 19.2%; Score 5; DB 6; Length 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 FLLDQ 8
    |||||
Db 18 FLLDQ 22
```

```
RESULT 39
US-10-105-299-5561
; Sequence 5561, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5561
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-5561
```

```
Query Match
Best Local Similarity 19.2%; Score 5; DB 6; Length 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 3 GFLLD 7
    |||||
Db 17 GFLLD 21
```

```
RESULT 40
US-10-106-698-5700
```

```
; Sequence 5700, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ribben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentln Ver. 3.0
; SEQ ID NO 5700
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-5700
```

```
Query Match
Best Local Similarity 19.2%; Score 5; DB 6; Length 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 18 LVDFL 22
    |||||
Db 3 LVDFL 7
```

```
RESULT 41
US-10-105-299-4199
; Sequence 4199, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4199
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-4199
```

```
Query Match
Best Local Similarity 19.2%; Score 5; DB 6; Length 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 3 GFLLD 7
    |||||
Db 18 GFLLD 22
```

```
RESULT 42
US-10-143-922-216
; Sequence 216, Application US/10143922
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC022C1N
; CURRENT APPLICATION NUMBER: US/10/143,922
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 216
; LENGTH: 41
```

```

: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (13)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-143-922-216
```

```

Query Match          19.2%; Score 5; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 FPEHL 17
      |||||
Db       8 FPEHL 12
```

```

RESULT 43
PCT-US02-01109-100
: Sequence 100, Application PC/TUS0201109
: GENERAL INFORMATION:
: APPLICANT: Human Genome Sciences, Inc.
: TITLE OF INVENTION: 50 Human Secreted Proteins
: FILE REFERENCE: P2016PCT2
: CURRENT APPLICATION NUMBER: PCT/US02/01109
: CURRENT FILING DATE: 2002-01-17
: PRIOR APPLICATION NUMBER: US 60/262,066
: PRIOR FILING DATE: 2001-01-18
: NUMBER OF SEQ ID NOS: 206
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 100
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US02-01109-100
```

```

Query Match          19.2%; Score 5; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GFLL 7
      |||||
Db       12 GFLL 16
```

```

RESULT 44
US-10-137-337-750
: Sequence 750, Application US/10137337
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PM028CIN
: CURRENT APPLICATION NUMBER: US/10/137,337
: CURRENT FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: 09/758,447
: PRIOR FILING DATE: 2001-01-11
: PRIOR APPLICATION NUMBER: 60/179,065
: PRIOR FILING DATE: 2000-01-31
: PRIOR APPLICATION NUMBER: 60/180,628
: PRIOR FILING DATE: 2000-02-04
: NUMBER OF SEQ ID NOS: 812
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 750
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (16)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: FEATURE:
```

```

: NAME/KEY: misc_feature
: LOCATION: (27)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-137-337-750
```

```

Query Match          19.2%; Score 5; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      18 LVDFL 22
      |||||
Db       19 LVDFL 23
```

```

RESULT 45
US-10-105-299-5159
: Sequence 5159, Application US/10105299
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al
: TITLE OF INVENTION: Human Secreted Proteins
: FILE REFERENCE: PS950
: CURRENT APPLICATION NUMBER: US/10/105,299
: CURRENT FILING DATE: 2002-03-26
: NUMBER OF SEQ ID NOS: 15197
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5159
: LENGTH: 46
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-105-299-5159
```

```

Query Match          19.2%; Score 5; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GFLL 7
      |||||
Db       5 GFLL 9
```

```

RESULT 46
US-10-105-299-5161
: Sequence 5161, Application US/10105299
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al
: TITLE OF INVENTION: Human Secreted Proteins
: FILE REFERENCE: PS950
: CURRENT APPLICATION NUMBER: US/10/105,299
: CURRENT FILING DATE: 2002-03-26
: NUMBER OF SEQ ID NOS: 15197
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5161
: LENGTH: 46
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-105-299-5161
```

```

Query Match          19.2%; Score 5; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 EHLV 19
      |||||
Db       34 EHLV 38
```

```

RESULT 47
PCT-US02-09921-928
```

```

; Sequence 928, Application PC/TUS0209921
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAEFO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Darryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHERY, Stefan R.
; APPLICANT: DAUGHERRY, Sean C.
; APPLICANT: DAM, Tam C.
; APPLICANT: LITU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEFELD, Iael
; APPLICANT: GERSTIN JR., Edward H.
; APPLICANT: PERALTA, Careyna H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARMAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael
; TITLE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1232 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09921
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/280,068; 60/291,280; 60/291,849;
; 60/291,849; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17;
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 1146
; SOFTWARE: PERL Program
; SEQ ID NO 928
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyte ID No: LI:260629.7.orf1:2001MAY17
; PCT-US02-09921-928

Query Match          19.2%; Score 5; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 FLQSL 25
      |||||
Db      22 FLQSL 26

RESULT 48
US-10-105-299-5308
; Sequence 5308, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 5308
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-299-5308

Query Match          19.2%; Score 5; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 LVLDF 21
      |||||
Db      1 LVLDF 5

RESULT 49
US-10-143-788-680
; Sequence 680, Application US/10143788
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC017C1N
; CURRENT APPLICATION NUMBER: US/10/143,788
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 930
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 680
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-10-143-788-680

Query Match          19.2%; Score 5; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 MDFGF 13
      |||||
Db      10 MDFGF 14

RESULT 50
US-10-105-299-6077
; Sequence 6077, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6077
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-299-6077

Query Match          19.2%; Score 5; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GFLLL 7
      |||||

```

Wed Jun 19 11:12:08 2002

us-09-943-334-1.oligo.rpn

Page 13

Db 36 GFLTL 40

Search completed: June 19, 2002, 11:10:33
Job time: 207 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:05:55 : Search time 13.15 seconds

(without alignments)
48.294 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 1 RDGFLLLQMPGFPPELLVDFLOSLIS 26

Sequence: 1 RDGFLLLQMPGFPPELLVDFLOSLIS 26

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 2442594 residues

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Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

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6: /cgn2_6/ptodata/2/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	470	3	US-08-879-565-14
2	26	100.0	476	4	US-09-171-969-4
3	11	42.3	50	4	US-09-171-969-7
4	11	42.3	496	4	US-09-171-969-2
5	7	26.9	422	2	US-08-403-8529-17
6	7	26.9	422	3	US-08-510-8468-18
7	7	26.9	422	4	US-09-231-818-17
8	6	23.1	166	4	US-09-339-9138-79
9	6	23.1	166	4	US-09-339-9138-79
10	6	23.1	166	4	US-09-339-9138-79
11	6	23.1	166	4	US-09-339-9138-79
12	6	23.1	189	1	US-08-026-758-11
13	6	23.1	189	1	US-08-026-758-11
14	6	23.1	189	1	US-08-026-758-11
15	6	23.1	189	1	US-08-026-758-11
16	6	23.1	189	1	US-08-026-758-11
17	6	23.1	189	1	US-08-026-758-11
18	6	23.1	189	1	US-08-026-758-11
19	6	23.1	189	1	US-08-026-758-11
20	6	23.1	189	1	US-08-026-758-11
21	6	23.1	189	1	US-08-026-758-11
22	6	23.1	189	1	US-08-026-758-11
23	6	23.1	189	1	US-08-026-758-11
24	6	23.1	189	1	US-08-026-758-11
25	6	23.1	189	1	US-08-026-758-11
26	6	23.1	189	1	US-08-026-758-11
27	6	23.1	189	1	US-08-026-758-11

ALIGNMENTS

RESULT 1
US-08-879-565-14
Sequence 14, Application US/08879565A
Patent No. 6093573
GENERAL INFORMATION:
APPLICANT: Beamier, Lesa J.
APPLICANT: Carroll, Stephen F.
APPLICANT: Elsenberg, David
TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF
FILE REFERENCE: 1103/110340501
CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:

OTHER INFORMATION: cholesterol ester transfer protein (CEP) (Figure
OTHER INFORMATION: 5)
US-08-879-565-14

Query Match 100.0%; Score 26; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 8.8e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLDMDFGPPEHLVDFLOSLS 26
DB 445 RDGFLLDMDFGPPEHLVDFLOSLS 470

RESULT 2
US-09-171-969-4
Sequence 4, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
FEATURE:
NAME/KEY: Amino acid sequence of mature human
NAME/KEY: CEP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Dayana, Dennis, et al.
TITLE: Cloning and sequencing of human
JOURNAL: cholesterol ester transfer CDNA
VOLUME: 327
ISSUE:
PAGES: 632 - 634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476
US-09-171-969-4

Query Match 100.0%; Score 26; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 8.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLDMDFGPPEHLVDFLOSLS 26
DB 451 RDGFLLDMDFGPPEHLVDFLOSLS 476

RESULT 3
US-09-171-969-7
Sequence 7, Application US/09171969
Patent No. 6284533

GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
FEATURE:
NAME/KEY: amino acid sequence of peptide encoded
FEATURE: by bases 10 to 159 of SEQ ID NO:5
NAME/KEY:
LOCATION:
US-09-171-969-7

Query Match 42.3%; Score 11; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLVDLFLSLS 26
DB 40 HLVDLFLSLS 50

RESULT 4
US-09-171-969-2
Sequence 2, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.

TITLE OF INVENTION: PLASMAID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence for mature
NAME/KEY: rabbit CcTP protein.
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Nagashima, Mariko, et al.
TITLE: Cloning and mRNA tissue
TITLE: distribution of rabbit
TITLE: cholesteryl ester transfer
TITLE: protein
JOURNAL: J. Lipid Res.
VOLUME: 29
ISSUE:
PAGES: 1643 - 1649
DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 496
US-09-171-969-2
Query Match 42.3%; Score 11; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSLS 26
|||||

DB 486 HLLVDFLOSLS 496

RESULT 5
US-08-403-852D-17
Sequence 17, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Crouzet, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie

APPLICANT: Lacroix, Patricia
APPLICANT: Thibault, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Faradow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
FAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-852D-17
Query Match 26.9%; Score 7; DB 2; Length 422;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGPEHL 17
|||||

DB 143 FGPEHL 149

RESULT 6
US-08-510-646B-18
Sequence 18, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanchet, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibault, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-510-646B-18

Query Match          26.9%; Score 7; DB 3; Length 422;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCGPEHL 17
      |||||
Db 143 GCGPEHL 149

RESULT 7
US-09-231-818-17
Sequence 17, Application US/09231818
Patent No. 6171846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibault, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.

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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-231-818-17

Query Match          26.9%; Score 7; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCGPEHL 17
      |||||
Db 143 GCGPEHL 149

RESULT 8
US-09-339-913B-79
Sequence 79, Application US/09339913B
Patent No. 630344
GENERAL INFORMATION:
APPLICANT: Patten, Phillip
APPLICANT: Stemmer, William P.C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
FILE REFERENCE: 02-020503US
CURRENT APPLICATION NUMBER: US/09/339,913B
CURRENT FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 08/769,062
PRIOR FILING DATE: 1996-12-18
PRIOR APPLICATION NUMBER: 08/198,431
PRIOR FILING DATE: 1994-02-17
PRIOR APPLICATION NUMBER: 08/425,684
PRIOR FILING DATE: 1995-04-18
PRIOR APPLICATION NUMBER: 08/537,874
PRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 79
LENGTH: 166
TYPE: PRT
ORGANISM: human alpha interferon
US-09-339-913B-79

Query Match          23.1%; Score 6; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 35 DFGPPE 40

RESULT 9
US-09-339-904A-79
; Sequence 79, Application US/09339904A
; Patent No. 6339713
; GENERAL INFORMATION:
; APPLICANT: Patlen, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-02050405
; CURRENT APPLICATION NUMBER: US/09/339,904A
; CURRENT FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 08/769,062
; PRIOR FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 79
; LENGTH: 166
; TYPE: PRT
; ORGANISM: human alpha Interferon
US-09-339-904A-79

Query Match 23.1%; Score 6; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 35 DFGPPE 40

RESULT 10
US-08-769-062B-79
; Sequence 79, Application US/08769062B
; Patent No. 6335160
; GENERAL INFORMATION:
; APPLICANT: Patlen, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-02050005
; CURRENT APPLICATION NUMBER: US/08/769,062B
; CURRENT FILING DATE: 1996-11-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 79
; LENGTH: 166
; TYPE: PRT
; ORGANISM: human alpha Interferon
US-08-769-062B-79

Query Match 23.1%; Score 6; DB 4; Length 166
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 35 DFGPPE 40

RESULT 11
US-09-344-002B-79
; Sequence 79, Application US/09344002B
; Patent No. 6355484
; GENERAL INFORMATION:
; APPLICANT: Patlen, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-02050205
; CURRENT APPLICATION NUMBER: US/09/344,002B
; CURRENT FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 08/769,062
; PRIOR FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 79
; LENGTH: 166
; TYPE: PRT
; ORGANISM: human alpha Interferon
US-09-344-002B-79

Query Match 23.1%; Score 6; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 35 DFGPPE 40

RESULT 12
US-08-026-758-11
; Sequence 11, Application US/08026758
; Patent No. 5780021
; GENERAL INFORMATION:
; APPLICANT: SOBEL, DOUGLAS O.
; TITLE OF INVENTION: A METHOD FOR TREATING AUTOIMMUNE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,758
; FILING DATE: 19930305
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NO. 5780021man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-096-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 24..189
OTHER INFORMATION: /note= "IFN-alpha-4b"
US-08-026-758-11

Query Match 23.1%; Score 6; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 13
US-08-026-758-20
Sequence 20, Application US/08026758
Patent No. 5780021
GENERAL INFORMATION:
APPLICANT: SOBEL, DOUGLAS O.
TITLE OF INVENTION: A METHOD FOR TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES USING ALPHA-INTERFERON AND/OR BETA-INTERFERON
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,758
FILING DATE: 19930305
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5780021man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-096-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 24..189
OTHER INFORMATION: /note= "IFN-alpha-76"
US-08-026-758-20

Query Match 23.1%; Score 6; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 14
US-09-206-935-10
Sequence 10, Application US/09206935
Patent No. 6299877
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Godowski, Paul
APPLICANT: Wood, William I.
APPLICANT: Zhang, Dong-Xiao
TITLE OF INVENTION: NOVEL TYPE I INTERFERONS
FILE REFERENCE: 11669, 50US05
CURRENT APPLICATION NUMBER: US/09/206,935
CURRENT FILING DATE: 1998-12-07
EARLIER APPLICATION NUMBER: 60/084,045
EARLIER FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-09-206-935-10

Query Match 23.1%; Score 6; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 15
US-09-206-936-10
Sequence 10, Application US/09206936A
Patent No. 6300475
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Wood, William I.
TITLE OF INVENTION: NO. 6300475el Interferon
FILE REFERENCE: P1224R1
CURRENT APPLICATION NUMBER: US/09/206,936A
CURRENT FILING DATE: 1998-12-07
EARLIER APPLICATION NUMBER: US 60/067,897
EARLIER FILING DATE: 1998-12-08
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 10
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-09-206-936-10

Query Match 23.1%; Score 6; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 16

5463025-1
 Patent No. 5463025
 APPLICANT: Sumi, Yoshihiko; Ichikawa, Yataro; Aoki, Nobuo
 INVENTOR: Masami
 TITLE OF INVENTION: PROTEIN HAVING HUMAN PLASMIN INHIBITING
 ACTIVITY
 NUMBER OF SEQUENCES: 7
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/185,162
 FILING DATE: 24-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60,691
 FILING DATE: 13-MAY-1993
 APPLICATION NUMBER: 419,913
 FILING DATE: 05-SEP-1989
 SEQ ID NO: 1:
 LENGTH: 464
 5463025-1

Query Match 23.1%; Score 6; DB 6; Length 464;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 DFFSL 25
 DB 428 DFFSL 433

RESULT 17
 US-08-928-692-59
 Sequence 59, Application US/08928692
 Patent No. 5958727
 GENERAL INFORMATION:
 APPLICANT: Brody, Howard
 APPLICANT: Yaver, Deborah S.
 APPLICANT: Hansen, Kim
 TITLE OF INVENTION: Methods for Modifying the Production of
 TITLE OF INVENTION: a Polypeptide
 NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 59587270 No. 59587270disk of No. 5958727 America, Inc.
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928,692
 FILING DATE: 12-SEP-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4844,200-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 911 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 5958727e
 US-08-928-692-59

Query Match 23.1%; Score 6; DB 2; Length 911;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFFLL 8
 DB 635 GFFLL 640

RESULT 18
 US-09-413-814-42
 Sequence 42, Application US/09413814
 Patent No. 6225064
 GENERAL INFORMATION:
 APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 APPLICANT: Bristol-Myers Squibb, CO.
 APPLICANT: Beyer, Stefan
 APPLICANT: Bloeker, Helmut
 APPLICANT: Brandt, Petra
 APPLICANT: Cino, Paul M
 APPLICANT: Dougherty, Brian A
 APPLICANT: Goldberg, Steven L
 APPLICANT: Hotte, Gerhard
 APPLICANT: Mueller, Joachim
 TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
 TITLE OF INVENTION: heteropolypeptide compounds
 FILE REFERENCE: PCT/US 99/23535
 CURRENT APPLICATION NUMBER: US/09/413,814
 CURRENT FILING DATE: 1999-10-07
 EARLIER APPLICATION NUMBER: DE 198 46 493.2
 EARLIER FILING DATE: 1998-10-09
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 42
 LENGTH: 2539
 TYPE: PRT
 ORGANISM: Sorangium cellulosum
 US-09-413-814-42

Query Match 23.1%; Score 6; DB 4; Length 2539;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DFFLL 7
 DB 1319 DFFLL 1324

RESULT 19
 US-09-335-409-5
 Sequence 5, Application US/09335409
 Patent No. 6121029
 GENERAL INFORMATION:
 APPLICANT: Schupp, Thomas
 APPLICANT: Ligon, James
 APPLICANT: Molnar, Istvan
 APPLICANT: Zirkle, Ross
 APPLICANT: Cyr, Devon
 TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTILONES
 FILE REFERENCE: 4-30582A
 CURRENT APPLICATION NUMBER: US/09/335,409
 CURRENT FILING DATE: 1999-06-17
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 7257
 TYPE: PRT
 ORGANISM: Sorangium cellulosum
 US-09-335-409-5

Query Match 23.1%; Score 6; DB 3; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 20
US-09-568-102-5
; Sequence 5, Application US/09568102
; Patent No. 6346404
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHIIONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568.102
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-102-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 21
US-09-567-969-5
; Sequence 5, Application US/09567969
; Patent No. 6353457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHIIONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,969
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-969-5

Query Match 23.1%; Score 6; DB 4; Length 7257;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 22
US-09-568-480-5
; Sequence 5, Application US/09568480
; Patent No. 6355458
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHIIONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-480-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 23
US-09-568-486-5
; Sequence 5, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHIIONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-486-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 EHLVD 20
|11111
Db 2999 EHLVD 3004

RESULT 24
US-09-568-472-5
; Sequence 5, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligou, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Deyon
; APPLICANT: Soetlich, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHLIONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 7257
; TYPE: PR1
; ORGANISM: Sorangium cellulosum
US-09-568-472-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 EHLVD 20
|11111
Db 2999 EHLVD 3004

RESULT 25
US-09-057-897-20
; Sequence 20, Application US/09057897
; Patent No. 6300476
; GENERAL INFORMATION:
; APPLICANT: Lu, Anthony Y.H.
; APPLICANT: Meng, Regine W.
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human
; TITLE OF INVENTION: Cyclochrome P450 3A4
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-3905
; TELEFAX: (732)594-4720

; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-057-897-20

Query Match 19.2%; Score 5; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFIQ 23
|11111
Db 3 VDFIQ 7

RESULT 26
US-08-159-339A-1184
; Sequence 1184, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esben
; TITLE OF INVENTION: HLA Binding peptides and their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 28-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-00503005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1184:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1184

Query Match 19.2%; Score 5; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GFULL 7
| | | | |
Db 3 GFULL 7

RESULT 27

US-08-159-339A-95
; Sequence 95, Application US/08159339A
; Patent No. 6037135

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: HLA Binding peptides and their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-0050300S

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX:

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-95

Query Match 19.2%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GFULL 7
| | | | |
Db 4 GFULL 8

RESULT 28

US-08-164-839-66
; Sequence 66, Application US/08164839

; Patent No. 5514573
; GENERAL INFORMATION:

APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO

APPLICANT: MOTOKI, MASAO

APPLICANT: NAGASE, KAZUO

APPLICANT: MATSUI, HIROSHI

TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/164,839

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/004,729

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, No. 5514573man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-599-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)412-3000

TELEFAX: (703)413-2220

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-164-839-66

Query Match 19.2%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 LVDF 21
| | | | |
Db 1 LVDF 5

RESULT 29

US-08-583-799-66
; Sequence 66, Application US/08583799
; Patent No. 5607849

GENERAL INFORMATION:

APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO

APPLICANT: MOTOKI, MASAO

APPLICANT: NAGASE, KAZUO

APPLICANT: MATSUI, HIROSHI

TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Odion, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-583-799-66

Query Match 19.2% Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LVDF 21
Db 1 LVDF 5

RESULT 30
US-08-159-339A-593
Sequence 593, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 593:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-593

Query Match 19.2% Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLL 7
Db 5 GFLLL 9

RESULT 31
US-09-057-897-18
Sequence 18, Application US/09057897
Patent No. 6300476
GENERAL INFORMATION:
APPLICANT: Lu, Anthony Y.H.
APPLICANT: Wang, Regina W.
TITLE OF INVENTION: Anti-Peptide Antibody Against Human
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732)594-3905
TELEFAX: (732)594-4720
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-057-897-18

Query Match 19.2%; Score 5; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 23
|||||
DB 7 VDFLQ 11

RESULT 32
US-09-060-039-9
; Sequence 9, Application US/09060039
; Patent No. 6130036
; GENERAL INFORMATION:
; APPLICANT: Kim, Lawrence A.
; APPLICANT: Kim, Baek
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; TITLE OF INVENTION: FOR ANTI-AIDS DRUGS
; FILE REFERENCE: 920010.410C3
; CURRENT APPLICATION NUMBER: US/09/060,039
; CURRENT FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Randomly generated mutation of segment of HIV RT
; OTHER INFORMATION: gene which encodes a portion of the putative
; OTHER INFORMATION: nucleotide binding site
US-09-060-039-9

Query Match 19.2%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLYDF 21
|||||
DB 7 LLYDF 11

RESULT 33
5169933-6
; Patent No. 5169933
; APPLICANT: ANDERSON, DAVID C.; MORGAN, CHARLES JR.; FRITZBERG,
; ALAN R.; NICHOLS, EVERETT J.
; TITLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS
; FOR ENHANCED CYTOTOXICITY AND IMAGING
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/390,241
; FILING DATE: 07-AUG-1999
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 232,337
; FILING DATE: 15-AUG-1988
; SEQ ID NO: 6
; LENGTH: 14
5169933-6

Query Match 19.2%; Score 5; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLLL 7
|||||
DB 7 GFLLL 11

RESULT 34

US-07-918-181A-17
; Sequence 17, Application US/07918181A
; Patent No. 5338833
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Mutelins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: POW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-07-918-181A-17

Query Match 19.2%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLOS 24
|||||
DB 3 DFLOS 7

RESULT 35
US-07-918-181A-21
; Sequence 21, Application US/07918181A
; Patent No. 5338833
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Mutelins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-07-918-181A-21

Query Match 19.2%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DPLQS 24
|||||
DB 3 DPLQS 7

RESULT 36
US-08-231-575-17
Sequence 17, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varlick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-08-231-575-17

Query Match 19.2%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DPLQS 24
|||||
DB 3 DPLQS 7

RESULT 37
US-08-231-575-21
Sequence 21, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varlick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-08-231-575-21

Query Match 19.2%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DPLQS 24
|||||
DB 3 DPLQS 7

RESULT 38
US-08-159-339A-1183

Sequence 1183, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-00503005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 1183:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-1183

Query Match 19.2%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLL 7
DB 10 GFLLL 14

RESULT 39
PCT-US93-06928-17
Sequence 17, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
PCT-US93-06928-17

Query Match 19.2%; Score 5; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLOS 24
DB 3 DFLOS 7

RESULT 40
PCT-US93-06928-21
Sequence 21, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
PCT-US93-06928-21

Query Match 19.2%; Score 5; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQS 24
DB 3 DFLQS 7

RESULT 41
US-09-162-934-18
Sequence 18, Application US/09162934
Patent No. 6258597
GENERAL INFORMATION:
APPLICANT: Bachovchin, William
APPLICANT: 71 Marwick Road
APPLICANT: Melrose, MA 02176
APPLICANT: U.S.A.
APPLICANT: Wallner, Barbara
APPLICANT: 64 Arrowhead Road
APPLICANT: Weston, MA 02193
APPLICANT: U.S.A.
TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
VITRO
FILE REFERENCE: 10248/7005
CURRENT APPLICATION NUMBER: US/09/162,934
CURRENT FILING DATE: 1998-09-29
EARLIER APPLICATION NUMBER: US 60/060,306
EARLIER FILING DATE: 1997-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 20
TYPE: PRT
ORGANISM: homo sapiens
US-09-162-934-18

Query Match 19.2%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQMPF 11
DB 11 LQMPF 15

RESULT 42
US-09-057-897-1
Sequence 1, Application US/09057897
Patent No. 6300476
GENERAL INFORMATION:
APPLICANT: Lu, Anthony Y.H.
APPLICANT: Wang, Regina W.
TITLE OF INVENTION: Anti-Peptide Antibody Against Human
CYTOCHROME P450 3A4
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732)594-4720
TELEFAX: (732)594-3905
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-057-897-1

Query Match 19.2%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 23
DB 17 VDFLQ 21

RESULT 43
US-09-057-897-32
Sequence 32, Application US/09057897
Patent No. 6300476
GENERAL INFORMATION:
APPLICANT: Lu, Anthony Y.H.
APPLICANT: Wang, Regina W.
TITLE OF INVENTION: Anti-Peptide Antibody Against Human
CYTOCHROME P450 3A4
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732)594-3905

TELEFAX: (732)594-4720
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-057-897-32

Query Match 19.2%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 23
DB 17 VDFLQ 21

RESULT 44
US-09-248-588-24
Sequence 24, Application US/09248588
Patent No. 6231864
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
TITLE OF INVENTION: their Derivatives
FILE REFERENCE: SYN-101 4564/69529
CURRENT APPLICATION NUMBER: US/09/248,588
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/074537
EARLIER FILING DATE: 1998-02-12
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 22
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-248-588-24

Query Match 19.2%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 23
DB 18 VDFLQ 22

RESULT 45
US-09-162-934-17
Sequence 17, Application US/09162934
Patent No. 6258597
GENERAL INFORMATION:
APPLICANT: Bachovchin, William
APPLICANT: 71 Warwick Road
APPLICANT: Melrose, MA 02176
APPLICANT: U.S.A.
APPLICANT: Wallner, Barbara
APPLICANT: 64 Arrowhead Road
APPLICANT: Weston, MA 02193
APPLICANT: U.S.A.
TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
TITLE OF INVENTION: VITRO
FILE REFERENCE: 10248/7005
CURRENT APPLICATION NUMBER: US/09/162,934
CURRENT FILING DATE: 1998-09-29
EARLIER APPLICATION NUMBER: US 60/060,306
EARLIER FILING DATE: 1997-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 17
LENGTH: 22
TYPE: PRT
ORGANISM: homo sapiens
US-09-162-934-17

Query Match 19.2%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQWDF 11
DB 13 LQWDF 17

RESULT 46
US-09-057-897-2
Sequence 2, Application US/09057897
Patent No. 6300476
GENERAL INFORMATION:
APPLICANT: Lu, Anthony Y.H.
APPLICANT: Wang, Regina W.
TITLE OF INVENTION: Anti-Peptide Antibody Against Human
TITLE OF INVENTION: Cytochrome P450 3A4
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732)594-3905
TELEFAX: (732)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-057-897-2

Query Match 19.2%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 23
DB 18 VDFLQ 22

RESULT 47
US-08-220-378-3
Sequence 3, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-3

Query Match 19.2%; Score 5; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDF 21
DB 6 LVDF 10

RESULT 48
US-08-696-012-3
Sequence 3, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-012-3

Query Match 19.2%; Score 5; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDF 21
DB 6 LVDF 10

RESULT 49
US-08-126-587C-2
Sequence 2, Application US/08126587C
Patent No. 5534438
GENERAL INFORMATION:
APPLICANT: Hayden, Michael
APPLICANT: Goldberg, Paul
APPLICANT: Andrew, Susan
APPLICANT: Rommens, Johanna M.
APPLICANT: Lin, Biobang
TITLE OF INVENTION: Process for Isolating Genes and the Gene
TITLE OF INVENTION: Causative of Huntington's Disease and Differential 3'
TITLE OF INVENTION: Polyadenylation in the Gene
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 1211 E. Morehead Street
CITY: Charlotte
STATE: NC 5534438th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,587C
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Layton Jr., Samuel G.
REGISTRATION NUMBER: 22,807
REFERENCE/DOCKET NUMBER: 3477-84
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-377-1561

TELEFAX: 704-334-2014
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-08-126-587C-2

Query Match 19.2%; Score 5; DB 1; Length 35;
 Best local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 LOSLS 26
 Db 16 LOSLS 20

RESULT 50
 US-08-868-435-10
 ; Sequence 10, Application US/08868435
 ; Patent No. 6291221
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Loon, Adolphus
 ; APPLICANT: Mitchell, David
 ; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingsland Street
 ; CITY: Nutley
 ; STATE: New Jersey
 ; COUNTRY: United States of America
 ; ZIP: 07110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/868,435
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/744,231
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kass, Alan P
 ; REGISTRATION NUMBER: 32142
 ; REFERENCE/DOCKET NUMBER: Case Docket 9339
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (201) 235-4205
 ; TELEFAX: (201) 235-2363
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 36 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-868-435-10

Db 30 LOSLS 34

Search completed: June 19, 2002, 11:07:59
 Job time: 124 sec

Query Match 19.2%; Score 5; DB 4; Length 36;
 Best local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 LOSLS 26
 Db 16 LOSLS 20

, and support the concept that inhibition of CETP activity in vivo can be anti-atherogenic. Currently, this vaccine is in clin. trials.

ST **atherosclerosis vaccine cholesteryl ester transfer protein peptide HDL cholesterol**

IT **Proteins**

RL: BSU (Biological study, unclassified); BIOL (Biological study) (cholesterol ester-exchanging, peptide, conjugate with tetanus toxin peptide; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **Lipoproteins**

RL: BSU (Biological study, unclassified); BIOL (Biological study) (high-d., cholesterol; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **Toxins**

RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (tetanus, peptide, conjugate with CETP peptide; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **Atherosclerosis**

Immunotherapy

Vaccines

(vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **57-88-5, Cholesterol**

RL: BSU (Biological study, unclassified); BIOL (Biological study) (HDL; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **430455-98-4**

RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L42 ANSWER 2 OF 15 HCAPLUS COPYRIGHT 2002 ACS
AN 2001:651566 HCAPLUS
DN 135:225853

TI Plasmid-based **vaccine** for treating **atherosclerosis**
 IN **Thomas, Lawrence J.**
 PA AVANT Immunotherapeutics, Inc., USA
 SO U.S., 35 pp., Cont.-in-part of U.S. Ser. No. 802,967.
 CODEN: USXXAM
 DT Patent
 LA English
 IC ICM C12N018-88
 ICS A61K048-00
 NCL 435320100
 CC 15-2 (Immunochemistry)
 Section cross-reference(s): 3, 63

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6284533	B1	20010904	US 1998-171969	19981002
	WO 9741227	A1	19971106	WO 1997-US7294	19970501
	W:		AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
	RW:		GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG		
PRAI	US 1996-52983P	P	19960501		
	US 1997-802967	A2	19970221		
	WO 1997-US7294	W	19970501		
	US 1996-640713	A	19960501		

AB A plasmid-based **vaccine** is provided herein based on the combination of DNA segments coding for one or more B cell **epitopes** of **cholesteryl ester transfer protein** (CETP) and one or more broad range helper T cell **epitopes**. Administration of the plasmids as a **vaccine** to a vertebrate subject provides an immune response to the subject's endogenous CETP and modulation of CETP activity, leading to prevention or reversal of various manifestations of heart disease. The **vaccines** provide an advantageous strategy for the prevention or treatment of **atherosclerosis**.

ST plasmid **vaccine** **cholesteryl ester transfer protein**; **atherosclerosis** autoantibody **cholesteryl ester transfer protein**

IT Histocompatibility antigens

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (MHC (major histocompatibility complex), class II; plasmid-based **vaccine** encoding B cell **epitope** of **cholesteryl ester transfer protein** and helper T cell **epitope** of **tetanus toxoid** or **diphtheria toxoid** for treating **atherosclerosis**)

IT Antibodies

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); THU (Therapeutic use); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
 (autoantibodies; plasmid-based **vaccine** encoding B cell **epitope** of **cholesteryl ester transfer protein** and helper T cell **epitope** of **tetanus toxoid** or **diphtheria toxoid** for treating **atherosclerosis**)

IT **Proteins**, specific or class

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(cholesterol ester-exchanging;
 plasmid-based vaccine encoding B cell epitope of
 cholesteryl ester transfer protein
 and helper T cell epitope of tetanus toxoid
 or diphtheria toxoid for treating
 atherosclerosis)

IT Toxoids

RL: BSU (Biological study, unclassified); PRP (Properties); THU
 (Therapeutic use); BIOL (Biological study); USES (Uses)

(diphtheria; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT B cell (lymphocyte)

(epitope; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT T cell (lymphocyte)

(helper cell; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Influenza

(hemagglutinin; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Fissurella

(hemocyanin; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Lipoproteins

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU
 (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(high-d., increase; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Gene, microbial

RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
 (Biological study); USES (Uses)

(immediate early, enhancer; plasmid-based vaccine encoding B
 cell epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Enhancer (genetic element)

Promoter (genetic element)

RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
 (Biological study); USES (Uses)

(immediate early; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

- IT Hemagglutinins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(influenza; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Drug delivery systems
(injections, i.m.; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Drug delivery systems
(intradermal; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Hemocyanins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(keyhole limpet; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Lipoproteins
RL: BSU (Biological study, unclassified); REM (Removal or disposal); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(low-d., decrease; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Animal cell
(mammalian; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Infection
(measles, vaccine; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Lipids, processes
RL: REM (Removal or disposal); PROC (Process)
(neutral; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Salivary gland
(parotid, mumps, vaccine; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)

- IT **Atherosclerosis**
DNA sequences
Epitopes
Heart, disease
Molecular cloning
Mycobacterium BCG
Plasmids
Protein sequences
T cell (lymphocyte)
Vaccines
Vertebrate (Vertebrata)
(plasmid-based vaccine encoding B cell epitope of
cholesteryl ester transfer protein
and helper T cell epitope of tetanus toxoid
or diphtheria toxoid for treating
atherosclerosis)
- IT DNA
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified);
PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP
(Preparation); USES (Uses)
(plasmid-based vaccine encoding B cell epitope of
cholesteryl ester transfer protein
and helper T cell epitope of tetanus toxoid
or diphtheria toxoid for treating
atherosclerosis)
- IT Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(plasmid-based vaccine encoding B cell epitope of
cholesteryl ester transfer protein
and helper T cell epitope of tetanus toxoid
or diphtheria toxoid for treating
atherosclerosis)
- IT TCR (T cell receptors)
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
(Biological study); PROC (Process)
(plasmid-based vaccine encoding B cell epitope of
cholesteryl ester transfer protein
and helper T cell epitope of tetanus toxoid
or diphtheria toxoid for treating
atherosclerosis)
- IT Invariant chain (class II antigen)
RL: BSU (Biological study, unclassified); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); USES (Uses)
(plasmid-based vaccine encoding B cell epitope of
cholesteryl ester transfer protein
and helper T cell epitope of tetanus toxoid
or diphtheria toxoid for treating
atherosclerosis)
- IT Human herpesvirus 5
(promoter; plasmid-based vaccine encoding B cell
epitope of cholesteryl ester
transfer protein and helper T cell epitope
of tetanus toxoid or diphtheria
toxoid for treating atherosclerosis)
- IT Tuberculin
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(purified protein deriv.; plasmid-based vaccine
encoding B cell epitope of cholesteryl
ester transfer protein and helper T cell
epitope of tetanus toxoid or
diphtheria toxoid for treating

- atherosclerosis)**
- IT **Toxoids**
 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (tetanus; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **Pertussis**
Poliomyelitis
Rubella
Tuberculosis
 (vaccine; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **111274-16-9 122525-86-4**, Sialoglycoprotein CETP
 (rabbit clone .lambda.RCETP.2/.lambda.RCETP.1 protein moiety reduced) 199062-33-4
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **199063-97-3 359035-23-7 359035-24-8**
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (nucleotide sequence; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **172273-70-0P 172273-71-1P 172273-72-2P 172273-73-3P 172273-74-4P 172273-75-5P 253309-86-3P 359016-11-8P**
 RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **119260-99-0 184882-09-5 359016-20-9 359016-22-1**
 RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **359035-61-3, 6: PN: US6284533 SEQID: 6 unclaimed DNA 359035-62-4, 8: PN: US6284533 SEQID: 8 unclaimed DNA**
 RL: PRP (Properties)
 (unclaimed nucleotide sequence; plasmid-based vaccine for treating atherosclerosis)
- IT **88265-18-3, Toxin (Corynebacterium diphtheriae strain C7 reduced)**
 RL: PRP (Properties)
 (unclaimed protein sequence; plasmid-based vaccine for

treating atherosclerosis)
IT 126779-14-4
RL: PRP (Properties)
(unclaimed sequence; plasmid-based vaccine for treating
atherosclerosis)
RE.CNT 110 THERE ARE 110 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L42 ANSWER 3 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 2000:709161 HCAPLUS

DN 134:40763

TI Vaccine-induced antibodies inhibit CETP activity in vivo and reduce aortic lesions in a rabbit model of

atherosclerosis

- AU **Rittershaus, Charles W.; Miller, David P.; Thomas, Lawrence J.; Picard, Michele D.; Honan, Christopher M.; Emmett, Constance D.; Pettey, Carolyn L.; Adari, Hedy; Hammond, Russell A.; Beattie, David T.; Callow, Allan D.; Marsh, Henry C.; Ryan, Una S.**
- CS AVANT Immunotherapeutics, Inc, Needham, MA, 02494, USA
- SO Arteriosclerosis, Thrombosis, and Vascular Biology (2000), 20(9), 2106-2112
- CODEN: ATVBFA; ISSN: 1079-5642
- PB Lippincott Williams & Wilkins
- DT Journal
- LA English
- CC 15-2 (Immunochemistry)
- Section cross-reference(s): 14
- AB Using a **vaccine** approach, the authors immunized New Zealand White rabbits with a peptide contg. a region of **cholesteryl ester transfer protein (CETP)** known to be required for neutral lipid **transfer** function. These rabbits had significantly reduced plasma **CETP** activity and an altered lipoprotein profile. In a **cholesterol**-fed rabbit model of **atherosclerosis**, the fraction of plasma **cholesterol** in HDL was 42% higher and the fraction of plasma **cholesterol** in LDL was 24% lower in the **CETP-vaccinated** group than in the control-**vaccinated** group. Moreover, the percentage of the aorta surface exhibiting **atherosclerotic** lesion was 39.6% smaller in the **CETP-vaccinated** rabbits than in controls. The data reported here demonstrate that **CETP** activity can be reduced in vivo by **vaccination** with a peptide derived from **CETP** and support the concept that inhibition of **CETP** activity in vivo can be anti-atherogenic. In addn., these studies suggest that **vaccination** against a self-antigen is a viable therapeutic strategy for disease management.
- ST **vaccine antibody cholesteryl ester transfer protein atherosclerosis**
- IT **Antiarteriosclerotics**
(**antiatherosclerotics**; **vaccination** with **cholesteryl ester transfer protein** alters lipoprotein profiles and ameliorates lesions in **atherosclerosis** model in relation to)
- IT **Proteins, specific or class**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**cholesterol ester-exchanging**; **vaccination** with **cholesteryl ester transfer protein** alters lipoprotein profiles and ameliorates lesions in **atherosclerosis** model)
- IT **Lipoproteins**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(high-d.; **vaccination** with **cholesteryl ester transfer protein** alters **cholesterol** content of)
- IT **Lipoproteins**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(low-d.; **vaccination** with **cholesteryl ester transfer protein** alters **cholesterol** content of)
- IT **Vaccines**
(synthetic; **vaccination** with **cholesteryl ester transfer protein** alters lipoprotein profiles and ameliorates lesions in **atherosclerosis** model)

- IT Antibodies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(to cholesteryl ester transfer
protein in relation to immunotherapy of atherosclerosis
)
- IT Atherosclerosis
(vaccination with cholesteryl ester
transfer protein alters lipoprotein profiles and
ameliorates lesions in atherosclerosis model)
- IT 57-88-5, Cholesterol, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(vaccination with cholesteryl ester
transfer protein alters plasma lipoprotein content
of)

RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD
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TI Current, new and future treatments in dyslipidemia and
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AB A review with 294 refs. The new therapeutic options available to clinicians treating dyslipidemia in the last decade have enabled effective treatment for many patients. The development of the HMG-CoA reductase inhibitors (statins) have been a major advance in that they possess multiple pharmacol. effects (pleiotropic effects) resulting in potent redns. of low d. lipoproteins (LDL) and prevention of the **atherosclerotic** process. More recently, the newer fibric acid derivs. have also reduced LDL to levels comparable to those achieved with statins, have reduced triglycerides, and gemfibrozil has been shown to increase high d. lipoprotein (HDL) levels. Nicotinic acid has been made tolerable with sustained-release formulations, and is still considered an excellent choice in elevating HDL **cholesterol** and is potentially effective in reducing lipoprotein(a) [Lp(a)] levels, an emerging risk factor for coronary heart disease (CHD). Furthermore, recent studies have reported pos. lipid-lowering effects from estrogen and/or progestogen in postmenopausal women but there are still conflicting reports on the use of these agents in dyslipidemia and in females at risk for CHD. In addn. to lowering lipid levels, these antihyperlipidemic agents may have directly or indirectly targeted thrombogenic, fibrinolytic and **atherosclerotic** processes which may have been unaccounted for in their overall success in clin. trials. Although LDL **cholesterol** is still the major target for therapy, it is likely that over the next several years other lipid/lipoprotein and nonlipid parameters will become more generally accepted targets for specific therapeutic interventions. Some important emerging lipid/lipoprotein parameters that have been assocd. with CHD include elevated triglyceride, oxidized LDL **cholesterol** and Lp(a) levels, and low HDL levels. The nonlipid parameters include elevated homocysteine and fibrinogen, and decreased endothelial-derived nitric oxide prodn. Among the new investigational agents are inhibitors of squalene synthetase, acylCoA: **cholesterol** acyltransferase, **cholesteryl ester transfer protein**, monocyte-macrophages and LDL **cholesterol** oxidn. Future applications may include thyromimetic therapy, **cholesterol** **vaccination**, somatic gene therapy, and recombinant **proteins**, in particular, apolipoproteins A-I and E. Non-LDL-related targets such as peroxisome proliferator-activating receptors, matrix metalloproteinases and scavenger receptor class B type I may also have clin. significance in the treatment of **atherosclerosis** in the near future. Before lipid-lowering therapy, dietary and lifestyle modification is and should be the first therapeutic intervention in the management of dyslipidemia. Although current recommendations from the US and Europe are slightly different,

adherence to these recommendations is essential to lower the risk of **atherosclerotic** vascular disease, more specifically CHD. New guidelines that are expected in the near future will encompass global opinions from the expert scientific community addressing the issue of target LDL goal (aggressive vs. moderate lowering) and the application of therapy for newer emerging CHD risk factors.

ST review antilipidemic agent dyslipidemia **atherosclerosis**

IT **Atherosclerosis**

Hypolipemic agents

(current, new and future treatments in dyslipidemia and **atherosclerosis**)

IT Lipids, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dyslipidemia; current, new and future treatments in dyslipidemia and **atherosclerosis**)

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L42 ANSWER 5 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:819268 HCAPLUS

DN 132:77607

TI Artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens

IN Wang, Chang Yi

PA United Biomedical Inc., USA

SO PCT Int. Appl., 129 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K045-00

ICS C07K019-00

CC 15-2 (Immunochimistry)

Section cross-reference(s): 2

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9966957	A2	19991229	WO 1999-US13975	19990621
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 9945808 A1 20000110 AU 1999-45808 19990621 BR 9912177 A 20010410 BR 1999-12177 19990621 EP 1089760 A1 20010411 EP 1999-928826 19990621 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI US 1998-100412 A2 19980620

WO 1999-US13975 W 19990621

AB Disclosed are immunogenic peptide compns. comprising a T helper **epitope** linked to a target antigenic site or a synthetic B cell **epitope**, and optionally with an immunostimulatory sequence for inducing T helper cell-mediated immune response and producing high level of antibodies directed against the "target antigen". The disclosed immunogenic peptide compns. are useful for contraception or control of hormone-dependent tumor (with LH-releasing hormone as target), growth promotion in farm animal (with somatostatin as target), treatment of allergy (with IgE as target), prevention of HIV infection (with CD4 receptor as target), prevention of foot-and-mouth disease (with FMDV capsid protein as target), treatment of malaria (with circumsporozoite antigen of Plasmodium falciparum as target), and treatment of **arteriosclerosis** (with cholesteryl ester transport protein as target).

ST T helper cell **epitope** antigen immunostimulant; vaccine

T B cell **epitope**

- IT Antigens
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (CS (circumsporozoite); artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Immunoglobulins
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (E; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Proteins, specific or class
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (VP1; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Measles virus
 (antigen; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Allergy
Arteriosclerosis
Epitopes
 Foot-and-mouth disease virus
 Human immunodeficiency virus
 Human immunodeficiency virus 1
 Human immunodeficiency virus 2
 Immunotherapy
 Infection
 Livestock
 Malaria
 Neoplasm
 Pathogen
 Plasmodium falciparum
 Protein sequences
 Rat
 Simian immunodeficiency virus
Vaccines
 Veterinary medicine
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Antibodies
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT CD4 (antigen)
 Haptens
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Antigens
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (autoantigens; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT **Proteins**, specific or class
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (cholesterol ester-exchanging; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT **Vaccines**
 (contraceptive; artificial T helper cell **epitopes** as immune

stimulators for synthetic peptide immunogens)

IT Cardiovascular system
(disease; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Immunity
(disorder; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT B cell (lymphocyte)
(**epitope**; artificial T helper cell **epitopes** as
immune stimulators for synthetic peptide immunogens)

IT T cell (lymphocyte)
(helper cell, **epitope**; artificial T helper cell
epitopes as immune stimulators for synthetic peptide
immunogens)

IT Fissurella
(hemocyanin; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Antigens
RL: BSU (Biological study, unclassified); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); USES (Uses)
(hepatitis B surface; artificial T helper cell **epitopes** as
immune stimulators for synthetic peptide immunogens)

IT CD4-positive T cell
(immune response mediated by; artificial T helper cell **epitopes**
as immune stimulators for synthetic peptide immunogens)

IT Castration
(immuno-; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Proteins, specific or class
RL: BSU (Biological study, unclassified); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); USES (Uses)
(invasins; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Hemocyanins
RL: BSU (Biological study, unclassified); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); USES (Uses)
(**keyhole limpet**; artificial T helper cell
epitopes as immune stimulators for synthetic peptide
immunogens)

IT Antibodies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU
(Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(neutralizing; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Antigens
RL: BSU (Biological study, unclassified); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); USES (Uses)
(peptide; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Growth, animal
(promotion; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Immunostimulants
(sequence; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Amino acids, biological studies
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(stimulatory; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Swine
(taint; artificial T helper cell **epitopes** as immune
stimulators for synthetic peptide immunogens)

IT Antigenes
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (tumor-assocd.; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Contraceptives
 (vaccines; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT 9034-40-6, LH-releasing hormone 40958-31-4, Somatostatin (sheep reduced)
 51110-01-1, Somatostatin 60556-70-9 92463-35-9 109489-04-5
 123202-49-3 130540-86-2 143201-20-1 150241-81-9 159347-89-4
 160824-82-8 184882-09-5 221550-30-7 232933-99-2 232934-00-8
 232934-04-2 232934-05-3 253196-73-5 253196-75-7 253196-76-8
 253196-77-9 253196-78-0 253196-79-1 253196-81-5 253196-82-6
 253196-84-8 253196-85-9 253196-86-0 253196-87-1 253196-88-2
 253196-89-3 253196-90-6 253196-91-7 253196-92-8 253196-94-0
 253196-95-1 253196-96-2 253196-97-3 253196-98-4 253196-99-5
 253197-01-2 253197-03-4 253197-05-6 253197-07-8 253197-09-0
 253197-11-4 253197-13-6 253197-15-8 253197-18-1 253197-20-5
 253197-22-7 253197-24-9 253197-26-1 253197-27-2 253197-28-3
 253197-29-4 253197-30-7 253197-31-8 253197-32-9 253273-61-9
 253273-62-0 253274-37-2 253309-62-5 253309-63-6 253309-64-7
 253309-65-8 253309-66-9 253309-67-0 253309-68-1 253309-69-2
 253309-70-5 253309-71-6 253309-72-7 253309-73-8 253309-74-9
 253309-75-0 253309-76-1 253309-77-2 253309-78-3 253309-79-4
 253309-80-7 253309-81-8 253309-82-9 253309-83-0 253309-84-1
 253309-85-2 253309-86-3 253309-87-4 253309-88-5 253309-89-6
 253332-84-2 253332-85-3 253332-86-4 253332-87-5 253332-88-6
 253332-89-7 253332-91-1 253332-93-3 253332-94-4 253332-95-5
 253332-99-9 253333-01-6 253333-14-1 253333-25-4 253333-32-3
 253333-33-4 253333-34-5 253333-37-8 253333-38-9 253333-39-0
 253333-40-3 253333-41-4 253335-01-2 253335-03-4 253335-04-5
 253335-24-9 253335-66-9 253335-70-5 253335-82-9 253335-96-5
 253336-07-1 253336-50-4 253336-54-8 253336-57-1 253336-62-8
 253336-67-3 253336-69-5 253336-70-8 253336-71-9 253336-73-1
 253336-75-3 253336-76-4 253336-81-1 253336-96-8 253336-97-9
 253336-99-1 253337-01-8 253337-02-9 253337-03-0 253337-04-1
 253337-05-2 253337-07-4 253337-15-4 253337-67-6 253602-91-4
 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

L42 ANSWER 6 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:454264 HCAPLUS

DN 131:83997

TI Assay for predicting the angiographic response to LDL cholesterol-lowering therapy in patients, and cholesterol ester transfer protein gene for the use thereof

IN Kuivenhoven, Jan Albert; Kastelein, Johannes Jacobus Pieter

PA Academisch Ziekenhuis bij de Universiteit van Amsterdam, Neth.

SO PCT Int. Appl., 25 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C12Q001-68

ICS C07K014-47

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 1, 13

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9935286	A2	19990715	WO 1999-EP150	19990106

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

EP 939136 A1 19990901 EP 1998-200022 19980107

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

CA 2317940 AA 19990715 CA 1999-2317940 19990106

AU 9922791 A1 19990726 AU 1999-22791 19990106

EP 1049805 A2 20001108 EP 1999-902536 19990106

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

JP 2002504315 T2 20020212 JP 2000-527668 19990106

PRAI EP 1998-200022 A 19980107

WO 1999-EP150 W 19990106

AB The present invention relates to an assay for testing a genetic predisposition in patients with coronary artery disease (CAD) to respond to LDL **cholesterol**-lowering therapy. The method comprises screening for the presence (B1) or absence (B2) of a TaqI restriction site in intron 1 of both alleles of the **cholesterol ester transfer protein (CETP)** gene. A novel interaction was revealed between pravastatin treatment for CAD, this **CETP** gene polymorphism, and predicting the progression of coronary **atherosclerosis**. The response to pravastatin with regard to coronary **atherosclerosis** was greatest for homozygotes for B1B1 while B2B2 homozygotes did not appear to benefit from this treatment. Thus, according to the invention, the TaqIB polymorphism of **CETP** is found to be a genetic marker for identifying subjects who will or will not exhibit regression of coronary **atherosclerosis** in response to LDL **cholesterol**-lowering therapy, such as pravastatin.

ST therapy coronary **atherosclerosis cholesterol ester transfer protein** gene

IT Gene, animal

RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(**CETP**; assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in patients, and **cholesterol ester transfer protein** gene for the use thereof)

IT Primers (nucleic acid)

RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (PCR; assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)

IT Genetic polymorphism

(TaqIB restriction site in intron 1 of **CETP** gene; assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)

IT DNA sequences

PCR (polymerase chain reaction)

Test kits

(assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein**

gene for the use thereof)

IT Anticholesteremic agents
Susceptibility (genetic)
(assay for predicting the angiog. response to LDL cholesterol
-lowering therapy in patients, and **cholesterol ester
transfer protein** gene for the use thereof)

IT **Proteins**, specific or class
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**cholesterol ester-exchanging**, gene;
assay for predicting the angiog. response to LDL cholesterol
-lowering therapy in patients, and **cholesterol ester
transfer protein** gene for the use thereof)

IT Artery, disease
(coronary; assay for predicting the angiog. response to LDL
cholesterol-lowering therapy in coronary artery disease
patients, and **cholesterol ester transfer
protein** gene for the use thereof)

IT Genetic markers
(use of **CETP** gene as; assay for predicting the angiog.
response to LDL cholesterol-lowering therapy in coronary
artery disease patients, and **cholesterol ester
transfer protein** gene for the use thereof)

IT 81093-37-0, Pravastatin
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(assay for predicting the angiog. response to LDL cholesterol
-lowering therapy in coronary artery disease patients, and
cholesterol ester transfer protein
gene for the use thereof)

IT 140027-68-5, DNA (human **CETP** gene fragment)
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study,
unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL
(Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; assay for predicting the angiog. response to LDL
cholesterol-lowering therapy in coronary artery disease
patients, and **cholesterol ester transfer
protein** gene for the use thereof)

IT 229482-34-2 229482-35-3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(primer; assay for predicting the angiog. response to LDL
cholesterol-lowering therapy in coronary artery disease
patients, and **cholesterol ester transfer
protein** gene for the use thereof)

L42 ANSWER 7 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:282118 HCAPLUS

DN 130:310673

TI Xenogeneic **cholesteryl ester transfer
protein (CETP)** for modulation of **CETP** activity
in treatment of atherosclerosis

IN Rittershaus, Charles W.; Thomas, Lawrence J.

PA Avant Immunotherapeutics, Inc., USA

SO PCT Int. Appl., 62 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K039-00

ICS A61K039-39; A61K048-00; C07K014-47

CC 15-2 (Immunochemistry)

Section cross-reference(s): 3, 63

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	---	-----	-----	-----
PI	WO 9920302	A1	19990429	WO 1998-US22145	19981020

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2307012 AA 19990429 CA 1998-2307012 19981020

AU 9911048 A1 19990510 AU 1999-11048 19981020

EP 1024825 A1 20000809 EP 1998-953762 19981020

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

JP 2001520204 T2 20011030 JP 2000-516697 19981020

PRAI US 1997-954643 A2 19971020

WO 1998-US22145 W 19981020

AB Methods for modulating **cholesteryl ester transfer protein (CETP)** activity and the plasma levels of lipoproteins involved in heart disease involve administration of a non-endogenous **CETP** or a plasmid-based **vaccine** for expression of such non-endogenous **CETP** to elicit prodn. in a mammal of antibodies that recognize (bind to) the mammal's native (endogenous) **CETP**.

ST **cholesteryl ester transfer protein antiatherosclerotic sequence**

IT Promoter (genetic element)

RL: PEP (Physical, engineering or chemical process); PROC (Process) (Cytomegalovirus immediate early promoter/enhancer; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Immunostimulants (adjuvants, Freund's; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Immunostimulants (adjuvants, Ribi; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Immunostimulants (adjuvants; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT **Antiarteriosclerotics** (antiatherosclerotics; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Antibodies

RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process) (**cholesteryl ester transfer protein-binding**; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Transport proteins

RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) (**cholesteryl ester**; xenogeneic **cholesteryl ester transfer protein (CETP)** for

- modulation of CETP activity in treatment of
atherosclerosis)
- IT Cytomegalovirus
(immediate early promoter/enhancer of; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of CETP activity in treatment of **atherosclerosis)**
- IT Gene, microbial
RL: PEP (Physical, engineering or chemical process); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(immediate early, promoter of; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of CETP activity in treatment of **atherosclerosis)**
- IT Lipoproteins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(low-d., **cholesterol** conjugates, metab. of; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of CETP activity in treatment of **atherosclerosis)**
- IT Anticholesteremic agents
Genetic polymorphism
Immunostimulants
Monkey
Mouse
Plasmid vectors
Protein sequences
Rabbit
Vaccines
cDNA sequences
(xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of CETP activity in treatment of **atherosclerosis)**
- IT 223577-55-7P
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of CETP activity in treatment of **atherosclerosis)**
- IT 57-88-5D, **Cholesterol**, LDL conjugates
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of CETP activity in treatment of **atherosclerosis)**
- IT 81669-55-8P, **Cholesteryl ester transferase**
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of CETP activity in treatment of **atherosclerosis)**
- RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
- (1) Hesler, C; J BIOL CHEM 1987, V262(5), P2275 HCAPLUS
 - (2) Hesler, C; J BIOL CHEM 1988, V263(11), P5020 HCAPLUS
 - (3) Immune Response Corp Inc; WO 9639168 A 1996 HCAPLUS
 - (4) Smith, A; MEDICAL SCIENCE RESEARCH 1993, V21(24), P911 HCAPLUS
 - (5) T Cell Sciences Inc; WO 9634888 A 1996 HCAPLUS

- (6) T Cell Sciences Inc; WO 9741227 A 1997 HCAPLUS
 (7) Thomas, L; FASEB JOURNAL 1998, V12(4), Pa310

L42 ANSWER 8 OF 15 HCAPLUS COPYRIGHT 2002 ACS
 AN 1999:223038 HCAPLUS
 DN 130:250711

TI Vector **vaccines** against **cholesterol ester transfer protein** for the treatment of **atherosclerosis**

IN Needleman, Philip; Glenn, Kevin

PA Monsanto Company, USA

SO PCT Int. Appl., 99 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-12

ICS A61K048-00

CC 14-5 (Mammalian Pathological Biochemistry)

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9915655	A1	19990401	WO 1998-US19366	19980917
	W:				
	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW:				
	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2302778	AA	19990401	CA 1998-2302778	19980917
	AU 9892317	A1	19990412	AU 1998-92317	19980917
	EP 1015584	A1	20000705	EP 1998-944877	19980917
	R:				
	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI				
	JP 2002516656	T2	20020611	JP 2000-512947	19980917
PRAI	US 1997-934367	A	19970919		
	WO 1998-US19366	W	19980917		
AB	Expression vectors for manuf. of antigenic fragments of cholesteryl ester transfer protein (CETP) that can be used to inactivate the protein are described. The protein plays a key role in the transfer of cholesterol from HDL to LDL and VLDL and inhibition of CETP synthesis can be used to prevent LDL and VLDL formation in the prophylaxis of atherosclerosis . Immunogens, inocula, DNA segments, and recombinant DNA mol. vectors useful for carrying out the invention are also disclosed. The use of antigenic fragments of rabbit CETP to raise autoantibodies in rabbits is demonstrated. Antibodies to three such peptides cross-reacted with human CETP . Rabbits vaccinated with these antigens showed a .apprx.10% increase in serum HDL. Antigens were manufd. as fusion proteins with hepatitis B core antigens in Escherichia coli, in a baculovirus system, and in mammalian cell culture.				
ST	cholesteryl ester transfer protein antigen vaccine atherosclerosis ; autoantibody cholesteryl ester transfer protein atherosclerosis HDL				
IT	Antibodies RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses) (autoantibodies, to cholesteryl ester transfer protein ; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)				
IT	Proteins , specific or class				

RL: ADV (Adverse effect, including toxicity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(cholesterol ester-exchanging; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Toxoids

RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(diphtheria, fusion proteins with cholesteryl ester transfer protein, as antigens; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Antigens

RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(hepatitis B core, fusion proteins with cholesteryl ester transfer protein, as antigens; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Lipoproteins

RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(high-d., prevention of cholesterol ester transfer from; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Lipoproteins

RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(low-d., prevention of cholesterol ester transfer to; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Plasmid vectors

(pCMV-SPORT-HBcAg/CETP/HBcAg, vector vaccine against cholesteryl ester transfer protein; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Plasmid vectors

(pcDNA1/AMP-HBcAg/CETP/HBcAg-1, vector vaccine against cholesteryl ester transfer protein; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Plasmid vectors

(pcDNA1/AMP-HBcAg/CETP/HBcAg-2, vector vaccine against cholesteryl ester transfer protein; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Vaccines

(synthetic; vector vaccines against cholesterol ester transfer protein for treatment of atherosclerosis)

IT Toxoids

RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(tetanus, fusion **proteins with cholesteryl ester transfer protein**, as antigens; vector **vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT **Atherosclerosis**

(vector **vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT Lipoproteins

RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(very-low-d., prevention of **cholesterol ester transfer to; vector vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT 123202-49-3 221550-30-7

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(antigenic peptide of **cholesteryl ester transfer protein; vector vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT 221550-31-8 221550-32-9 221550-33-0 221550-34-1 221550-35-2 221550-37-4

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(antigenic peptide of rabbit **cholesteryl ester transfer protein; vector vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

- (1) Evans, E; Journal of Lipid Research 1994, P1634
- (2) Gaynor, E; Atherosclerosis 1994, V110, P101
- (3) Melchior, E; Journal of Biological Chemistry 1995, V270, P21068
- (4) Melchior, E; Trends in Cardiovascular Medicine 1995, V5, P83
- (5) O'Brien, C; Molecular Medicine Today 1997, V3(6), P231 MEDLINE
- (6) Schodel, E; Journal of Virology 1992, V66, P106
- (7) Sugano, E; Journal of Biological Chemistry 1996, V271, P19080
- (8) T Cell Sciences Inc; WO 9634888 A 1996 HCAPLUS
- (9) Thomas, L; WO 9741227 A 1997 HCAPLUS
- (10) Thomas, L; Journal of Allergy and Clinical Immunology 1997, V99(1)

L42 ANSWER 9 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:127088 HCAPLUS

DN 130:192774

TI Cholesterylester transfer protein (CETP)-mRNA as target molecule in therapy of **atherosclerosis**, transcription constructs and drug screening

IN Budzinski, Ralph; Krist, Bernd; Mark, Michael; Mueller, Peter

PA Boehringer Ingelheim Pharma K.-G., Germany

SO Ger. Offen., 24 pp.

CODEN: GWXXBX

DT Patent

LA German

IC ICM C12N015-11

ICS C12N015-54; C07H021-00; C12Q001-68; A61K048-00

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 1

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI  DE 19731609      A1  19990218      DE 1997-19731609 19970723
DE 19731609      C2  19991230
AB  The invention concerns the cholesteryl ester
transfer protein-mRNA (CETP-mRNA) as target
mol. for gene therapy; transcription constructs of the human CETP
gene contg. 5'-non-translating regions with regulatory sequences; the
usage of the transcription constructs for mol. recognition in high
throughput screening of drugs for atherosclerosis therapy via
the suppression of CETP gene expression; and therapeutic
antisense oligonucleotides that inhibit the translation of CETP.
CETP expression can be inhibited by antisense nucleotides
including 3'-dideoxynucleosides, phosphorothioate, methoxy and
methylphosphonate derivs; or non nucleotide mols. Drug screening is
performed in a cell free system contg. reticulocyte lysate, aminoacids,
radiolabeled leucin, synthesized CETP-mRNA and the antisense
nucleotide; after incubation the presence of radiolabeled CETP
is measured using monoclonal antibodies to CETP. Similar
screening is performed when hepatoma cells are incubated with the
therapeutic oligonucleotide; the CETP expression is measured
using RIA. Binding of the prospective drug substance to the nucleic acid
can also be tested in a BiaCore system using surface plasmon resonance
detection .
ST  cholesteryl ester transfer protein
CETP mRNA gene therapy atherosclerosis
IT  Proteins, specific or class
RL: BUU (Biological use, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
    (cholesterol ester-exchanging;
    cholesteryl ester-transfer protein
    -mRNA (CETP-mRNA) as target mol. in therapy of
    atherosclerosis, transcription constructs and drug screening)
IT  Atherosclerosis
    Drug screening
    Gene therapy
    Molecular recognition
    Transcriptional regulation
    (cholesteryl ester-transfer
    protein-mRNA (CETP-mRNA) as target mol. in therapy of
    atherosclerosis, transcription constructs and drug screening)
IT  Antisense oligonucleotides
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); USES (Uses)
    (cholesteryl ester-transfer
    protein-mRNA (CETP-mRNA) as target mol. in therapy of
    atherosclerosis, transcription constructs and drug screening)
IT  mRNA
RL: BUU (Biological use, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
    (cholesteryl ester-transfer
    protein-mRNA (CETP-mRNA) as target mol. in therapy of
    atherosclerosis, transcription constructs and drug screening)
IT  Translation, genetic
    (in reticulocyte lysates, for screening of antisense mRNAs;
    cholesteryl ester-transfer protein
    -mRNA (CETP-mRNA) as target mol. in therapy of
    atherosclerosis, transcription constructs and drug screening)
IT  Animal tissue culture
    (mammalian; cholesteryl ester-transfer
    protein-mRNA (CETP-mRNA) as target mol. in therapy of
    atherosclerosis, transcription constructs and drug screening)
IT  Antibodies
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)

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- (monoclonal, for quantifying CETP prodn.; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**, transcription constructs and drug screening)
- IT Immunoassay
(radioimmunoassay, for quantifying CETP prodn.; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**, transcription constructs and drug screening)
- IT Surface plasmon
(resonance for detecting mol. recognition; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**, transcription constructs and drug screening)
- IT 220791-39-9
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -11 to 4 position; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-30-0
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -18 to 2 position; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-32-2
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -23 to 15 position; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-37-7
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -24 to -13 position; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-45-7
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -26 to -12 position; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-28-6
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -26 to 3 position; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-44-6
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 1584 to 1594 position; **cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of

- atherosclerosis)**
- IT 220791-41-3
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 168 to 183 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis)**
- IT 220791-36-6
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 568 to 584 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis)**
- IT 220735-58-0
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 64 to 71 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis)**
- IT 220791-43-5
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 743 to 760 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis)**
- IT 220791-46-8
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 753 to 768 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis)**
- IT 220791-40-2
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 9 to 24 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis)**
- IT 220791-48-0 220791-49-1 220791-50-4 220791-51-5
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence, 5'-non-translating region of human **CETP ; cholesteryl ester-transfer protein-mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis, transcription constructs and drug screening)**
- IT 220791-47-9
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence, coding for human **CETP; cholesteryl ester-transfer protein -mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis, transcription constructs and drug screening)**

L42 ANSWER 10 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1997:740308 HCAPLUS

DN 128:10315

TI Plasmid-based vaccine for treating atherosclerosis

IN Thomas, Lawrence J.

PA T Cell Sciences, Inc., USA; Thomas, Lawrence J.
 SO PCT Int. Appl., 66 pp.
 CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-12

ICS A61K031-70

CC 1-7 (Pharmacology)

Section cross-reference(s): 3, 14, 63

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9741227	A1	19971106	WO 1997-US7294	19970501
	W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
	CA 2250428	AA	19971106	CA 1997-2250428	19970501
	AU 9729946	A1	19971119	AU 1997-29946	19970501
	AU 721729	B2	20000713		
	EP 914427	A1	19990512	EP 1997-924549	19970501
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
	JP 2001508760	T2	20010703	JP 1997-539202	19970501
	US 6284533	B1	20010904	US 1998-171969	19981002
PRAI	US 1996-640713	A	19960501		
	US 1997-802967	A2	19970221		
	US 1996-52983P	P	19960501		
	WO 1997-US7294	W	19970501		
AB	A plasmid-based vaccine is provided that is based on the combination of DNA segments coding for one or more B cell epitopes of CETP and one or more broad range helper T cell epitopes . Administration of the plasmids as a vaccine to a vertebrate subject provides an immune response to the subject's endogenous CETP and modulation of CETP activity, leading to prevention or reversal of various manifestations of heart disease. The vaccines provide an advantageous strategy for the prevention or treatment of atherosclerosis .				
ST	atherosclerosis plasmid vaccine treatment sequence CETP ; cholesteryl ester transfer protein vaccine atherosclerosis ; epitope CETP fusion protein vaccine atherosclerosis				
IT	B cell (lymphocyte) (CETP B-cell epitope ; plasmid vaccine for atherosclerosis treatment)				
IT	Protein motifs (CETP neutral lipid binding domain or neutral lipid transfer domain; plasmid vaccine for atherosclerosis treatment)				
IT	Fissurella (Keyhole limpet hemocyanin; plasmid vaccine for atherosclerosis treatment)				
IT	Hemocyanins RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses) (Keyhole limpet hemocyanin; helper T cell epitope derived from; plasmid vaccine for atherosclerosis treatment)				
IT	Antiarteriosclerotics				

- (**antiatherosclerotics, vaccine as; plasmid vaccine for atherosclerosis treatment**)
- IT Antibodies
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
 (autoantibodies, **CETP** induces formation of autoantibodies which inhibit **CETP** activity; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Lipids, biological studies
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (blood, **CETP** domains for binding and transfer of; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Proteins, specific or class
 RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
 (**cholesterol ester-exchanging, CETP** induces formation of autoantibodies which inhibit **CETP** activity; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Toxins
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (**diphtheria**, helper T cell **epitope** derived from; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Cardiovascular system
 (disease, method for treatment of; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Tuberculin
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (helper T cell **epitope** derived from; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Antigens
 RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (helper T cell **epitope**; plasmid **vaccine** for **atherosclerosis treatment**)
- IT T cell (lymphocyte)
 (helper cell, **vaccine** comprising **CETP** B cell **epitope** and broad range helper T cell **epitopes**; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Lipoproteins
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (high-d., method to reducing circulating ratio of HDL and LDL and VLDL to cholesterol; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Lipoproteins
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (low-d., method to reducing circulating ratio of HDL and LDL and VLDL to cholesterol; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Animal cell
 (mammalian, promoter for transcription in mammalian cells; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Heart, disease
 (method for treatment of; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Salivary gland
 (parotid, diseases, **mumps, vaccines**; helper T cell **epitope** derived from; plasmid **vaccine** for

- atherosclerosis treatment)
- IT Salivary gland
(parotid, mumps, vaccines; helper T cell
epitope derived from; plasmid vaccine for
atherosclerosis treatment)
- IT Atherosclerosis
Plasmid vectors
Protein sequences
Vertebrate (Vertebrata)
cDNA sequences
(plasmid vaccine for atherosclerosis treatment)
- IT Transcription, genetic
(promoter for transcription in mammalian cells; plasmid vaccine
for atherosclerosis treatment)
- IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(promoter for transcription in mammalian cells; plasmid vaccine
for atherosclerosis treatment)
- IT Vaccines
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(synthetic, rubella and mumps and measles; helper T cell
epitope derived from; plasmid vaccine for
atherosclerosis treatment)
- IT Toxoids
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES
(Uses)
(tetanus, helper T cell epitope derived from;
plasmid vaccine for atherosclerosis treatment)
- IT Epitopes
(vaccine comprising CETP B cell epitope
and broad range helper T cell epitopes; plasmid
vaccine for atherosclerosis treatment)
- IT Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL
(Biological study); PREP (Preparation); USES (Uses)
(vaccine comprising CETP B cell epitope
and broad range helper T cell epitopes; plasmid
vaccine for atherosclerosis treatment)
- IT Pertussis
(vaccine; helper T cell epitope derived from;
plasmid vaccine for atherosclerosis treatment)
- IT Rubella
(vaccines; helper T cell epitope derived from;
plasmid vaccine for atherosclerosis treatment)
- IT Lipoproteins
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU
(Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(very-low-d., method to reducing circulating ratio of HDL and LDL and
VLDL to cholesterol; plasmid vaccine for
atherosclerosis treatment)
- IT 111274-16-9P, Cholesteryl ester
transfer protein (human clone .lambda.CETP
.10/.lambda.CETP.307) 199062-23-2P
199062-31-2P
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; plasmid vaccine for
atherosclerosis treatment)
- IT 199062-11-8 199062-33-4
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES
(Uses)

(amino acid sequence; plasmid **vaccine** for **atherosclerosis** treatment)

IT 57-88-5, Cholesterol, biological studies
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (method to reducing circulating ratio of HDL and LDL and VLDL to cholesterol; plasmid **vaccine** for **atherosclerosis** treatment)

IT 111274-10-3P, DNA (human clone .lambda.CETP.10/.lambda.CETP.307 cholesterol ester-exchanging protein cDNA) 199063-45-1P 199063-46-2P 199063-97-3P 199063-98-4P 199063-99-5P
 RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (nucleotide sequence; plasmid **vaccine** for **atherosclerosis** treatment)

L42 ANSWER 11 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1997:97190 HCAPLUS

DN 126:99323

TI Immunostimulation method for increasing HDL **cholesterol** level using **cholesterol ester transfer protein (CETP)** or fragments thereof

IN Kwoh, Deborah Y.; Brostoff, Steven W.; Carlo, Dennis J.

PA The Immune Response Corporation, USA

SO PCT Int. Appl., 25 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K038-17

CC 1-10 (Pharmacology)

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9639168	A1	19961212	WO 1996-US9143	19960605	<--
	W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG				
	RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
	CA 2223177	AA	19961212	CA 1996-2223177	19960605	<--
	AU 9660912	A1	19961224	AU 1996-60912	19960605	<--
	AU 715410	B2	20000203			
	EP 831881	A1	19980401	EP 1996-918201	19960605	<--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 11507910	T2	19990713	JP 1996-501533	19960605	<--
PRAI	US 1995-482454		19950606	<--		
	WO 1996-US9143		19960605			

AB A method is provided for increasing HDL cholesterol in a mammal by stimulating an immune response that inhibits the function of **CETP**. Such an immune response can be induced by immunizing with **CETP** or fragments of **CETP** (together termed **CETP** peptides) which contain an **epitope** capable of stimulating such a response. The peptides can be conjugated to a carrier, e.g. **KLH** or ovalbumin, in order to increase immunogenicity. Adjuvants can also be administered.

ST **CETP** peptide immunostimulation HDL cholesterol

IT Antigens

Peptides, biological studies

RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(**CETP** immunogenic **epitopes**; immunostimulation

- method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Antiarteriosclerotics
(antiatherosclerotics; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT **Proteins**, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**cholesterol ester-exchanging, CETP immunogenic epitope**; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Hemocyanins
Ovalbumin
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(conjugates, with **CETP** peptides; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT **Toxoids**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**diphtheria**, conjugates with **CETP** peptides; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT B cell (lymphocyte)
(**epitope**; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Lipoproteins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(high-d.; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Immunostimulants
(immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT **Toxoids**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**tetanus**, conjugates with **CETP** peptides; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Antibodies
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(to **CETP**; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT 155381-67-2D, conjugates
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein**)

(CETP) or fragments)
 IT 57-88-5, **Cholesterol**, biological studies
 RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
 (immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein** (CETP) or fragments)
 IT 125377-61-9 125377-61-9D, conjugates 155381-67-2 186002-92-6 186002-92-6D, conjugates
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein** (CETP) or fragments)

L42 ANSWER 12 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1997:12606 HCAPLUS

DN 126:46315

TI Modulation of **cholesteryl ester transfer protein** (CETP) activity

IN Rittershaus, Charles W.; Thomas, Lawrence J.

PA T Cell Sciences, Inc., USA; Rittershaus, Charles W.; Thomas, Lawrence J.

SO PCT Int. Appl., 81 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C07K014-775

ICS C07K014-47; A61K038-17; A61K039-00

CC 15-2 (Immunochemistry)

Section cross-reference(s): 14

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9634888	A1	19961107	WO 1996-US6147	19960501	<--
	W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK				
	RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2219795	AA	19961107	CA 1996-2219795	19960501	<--
	AU 9656360	A1	19961121	AU 1996-56360	19960501	<--
	AU 707752	B2	19990722			
	EP 827509	A1	19980311	EP 1996-913320	19960501	<--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 11504635	T2	19990427	JP 1996-533487	19960501	<--
	US 2002042364	A1	20020411	US 2001-943548	20010830	<--
PRAI	US 1995-432483	A	19950501	<--		
	WO 1996-US6147	W	19960501			
	US 1997-945289	A3	19971017			
AB	This invention relates to peptides comprising a helper T cell epitope portion and a B cell epitope portion for eliciting an immune response against endogenous cholesteryl ester transfer protein (CETP) activity, to prevent or treat cardiovascular disease, such as atherosclerosis . The T helper T cell epitope may be derived from an antigenic peptide selected from the group consisting tetanus toxoid, diphtheria toxoid, pertussis vaccine, Bacille Calmette-Guerin, polio vaccine, measles vaccine, mumps vaccine, rubella vaccine, purified					

- protein deriv. of tuberculin, keyhole
limpet hemocyanin, hsp70 and combination thereof.
- ST cholesteryl ester transfer protein
antigen vaccine; atherosclerosis helper T cell
epitope vaccine
- IT Heat-shock proteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(HSP 70; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Proteins, specific or class
RL: ADV (Adverse effect, including toxicity); BSU (Biological study,
unclassified); BIOL (Biological study)
(cholesterol ester-exchanging; peptide
vaccine comprising helper T cell epitope and B cell
epitope that inhibits cholesteryl ester
transfer protein activity for treating
atherosclerosis)
- IT Toxoids
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(diphtheria; peptide vaccine comprising helper T
cell epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Cardiovascular system
(disease; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT B cell (lymphocyte)
(epitope; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT T cell (lymphocyte)
(helper cell, epitope; peptide vaccine comprising
helper T cell epitope and B cell epitope that
inhibits cholesteryl ester transfer
protein activity for treating atherosclerosis)
- IT Lipoproteins
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
BSU (Biological study, unclassified); BIOL (Biological study); OCCU
(Occurrence)
(high-d.; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Hemocyanins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(keyhole limpet; peptide vaccine
comprising helper T cell epitope and B cell epitope
that inhibits cholesteryl ester transfer
protein activity for treating atherosclerosis)
- IT Lipoproteins
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
BSU (Biological study, unclassified); BIOL (Biological study); OCCU
(Occurrence)
(low-d.; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Infection

- (measles, vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Lipids, biological studies
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (neutral, binding; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Salivary gland
 (parotid, diseases, mumps, vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Salivary gland
 (parotid, mumps, vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Atherosclerosis
 Hypercholesterolemia
 Mycobacterium BCG
 Protein sequences
 (peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Antibodies
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Vaccines
 (peptide; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Toxoids
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (pertussis; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Tuberculin
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (protein deriv.; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Toxoids
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (tetanus; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Poliomyelitis
 Rubella
 (vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits

cholesteryl ester transfer protein
 activity for treating **atherosclerosis**)

IT Peptides, biological studies
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (vaccine; peptide vaccine comprising helper T cell
epitope and B cell **epitope** that inhibits
cholesteryl ester transfer protein
 activity for treating **atherosclerosis**)

IT Lipoproteins
 RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
 BSU (Biological study, unclassified); BIOL (Biological study); OCCU
 (Occurrence)
 (very-low-d.; peptide vaccine comprising helper T cell
epitope and B cell **epitope** that inhibits
cholesteryl ester transfer protein
 activity for treating **atherosclerosis**)

IT 57-88-5, **Cholesterol**, biological studies
 RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
 BSU (Biological study, unclassified); BIOL (Biological study); OCCU
 (Occurrence)
 (peptide vaccine comprising helper T cell **epitope**
 and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
 treating **atherosclerosis**)

IT 111274-16-9, **Protein** (human clone .lambda.CETP
 .10/.lambda.CETP.307 **cholesterol ester-**
exchanging reduced)
 RL: BPR (Biological process); BSU (Biological study, unclassified); PRP
 (Properties); THU (Therapeutic use); BIOL (Biological study); PROC
 (Process); USES (Uses)
 (peptide vaccine comprising helper T cell **epitope**
 and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
 treating **atherosclerosis**)

IT 80295-45-0, Complement C3d
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (peptide vaccine comprising helper T cell **epitope**
 and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
 treating **atherosclerosis**)

IT 119260-99-0 123202-49-3 126779-14-4 184882-08-4 184882-09-5
 184882-10-8 184882-11-9
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (peptide vaccine comprising helper T cell **epitope**
 and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
 treating **atherosclerosis**)

L42 ANSWER 13 OF 15 HCAPLUS COPYRIGHT 2002 ACS
 AN 1995:541414 HCAPLUS
 DN 122:299055
 TI **Cholesteryl ester transfer protein**
 inhibitor polypeptide, antibodies against the synthetic polypeptide and
 prophylactic and therapeutic anti-**atherosclerosis** treatments
 IN Kushwaha, Rampratap S.; McGill, Henry C., Jr.; Kanda, Patrick
 PA Southwest Foundation for Biomedical Research, USA
 SO PCT Int. Appl., 47 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC ICM C07K014-435
 ICS C07K016-18; A61K038-17
 CC 63-3 (Pharmaceuticals)

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9504755	A1	19950216	WO 1994-US8624	19940802 <--
	W: AU, CA, JP, KR				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2145767	AA	19950216	CA 1994-2145767	19940802 <--
	AU 9475526	A1	19950228	AU 1994-75526	19940802 <--
	AU 683295	B2	19971106		
	EP 664813	A1	19950802	EP 1994-925711	19940802 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	JP 08502525	T2	19960319	JP 1994-506464	19940802 <--
	US 5519001	A	19960521	US 1995-394066	19950224 <--
PRAI	US 1993-102160		19930804 <--		
	US 1991-811049		19911219 <--		
	WO 1994-US8624		19940802 <--		
AB	A polypeptide and analogs thereof inhibit cholesteryl ester transfer protein (CETP) . An anti- atherosclerosis compn. comprises an anti- atherosclerosis effective amt. of the polypeptide and a pharmaceutically acceptable carrier. An anti- atherosclerosis kit comprises in sep. sterile containers at least one unit of the compn. contg. the polypeptide, one syringe, and one needle. An antibody has specificity for the polypeptide of the invention, the baboon CETP 4-kDa polypeptide inhibitor, the 1-36 amino acid N-terminal fragment of apoC-I, modified apo A-I (mol. wt. 31 kDa), or modified apoE (mol. wt. 41 kDa). A method of preventing atherosclerosis in a mammal being predisposed to that condition comprises administering to the mammal a prophylactically effective amt. of the polypeptide of the invention, and a method of treating a mammal afflicted with atherosclerosis comprises the administration of a therapeutically effective amt. of the polypeptide. The peptides consist of the N-terminal 36 residues of baboon apoC-I, a synthetic peptide adding an N-terminal Ala-Pro dipeptide, the human 38-residue analog, and active fragments and substituted analogs.				
ST	atherosclerosis inhibitor peptide; cholesteryl ester transfer protein inhibitor peptide				
IT	Peptides, biological studies				
	RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)				
	(cholesterol ester-exchanging protein-inhibiting; cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti- atherosclerosis treatments)				
IT	Baboon				
	(cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti- atherosclerosis treatments)				
IT	Antibodies				
	RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)				
	(cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti- atherosclerosis treatments)				
IT	Protein sequences				
	(of cholesteryl ester transfer protein inhibitor polypeptide from baboon and human)				
IT	Antiarteriosclerotics				
	(antiatherosclerotics, cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic				

anti-atherosclerosis treatments)

IT Lipoproteins
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(apo-, A-I, **cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT Lipoproteins
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(apo-, C-I, **cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT Lipoproteins
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(apo-, E, **cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT **Proteins, specific or class**
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(**cholesterol ester-exchanging, cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT 150027-05-7 161051-55-4 163062-88-2
RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

L42 ANSWER 14 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1993:552092 HCAPLUS

DN 119:152092

TI **Cholesteryl ester transfer protein (CETP)** inhibitor polypeptide, antibodies against the synthetic polypeptide, and prophylactic and therapeutic anti-**atherosclerosis** treatments

IN Kushwaha, Rampratap; Born, Kathleen; McGill, Henry C., Jr.; Kanda, Patrick; Dunham, Raymond G.

PA Southwest Foundation for Biomedical Research, USA

SO PCT Int. Appl., 46 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K037-00

ICS A61K037-02; A61K037-64; A61K037-04

CC 1-8 (Pharmacology)

Section cross-reference(s): 15

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9311782	A1	19930624	WO 1992-US10846	19921215 <--
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	EP 618803	A1	19941012	EP 1993-901360	19921215 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	US 5512548	A	19960430	US 1994-193515	19940208 <--
	US 5519001	A	19960521	US 1995-394066	19950224 <--
PRAI	US 1991-811049		19911219	<--	
	WO 1992-US10846		19921215	<--	
	US 1993-102160		19930804	<--	

- AB A polypeptide and analogs thereof inhibit CETP. Also disclosed are methods using the polypeptide of the invention for prevention and treatment of **atherosclerosis**, an anti-**atherosclerosis** compn., and an anti-**atherosclerosis** kit. An antibody is disclosed which has specificity for the polypeptide of the invention, the baboon **CETP** 4 kDa polypeptide inhibitor, the 1-36 apo C-I amino-terminal fragment, modified apo A-I (31 kDa mol. wt.), or modified apo E (41 kDa mol. wt.). Sequences of polypeptide inhibitors are included. Detection of the **CETP** inhibitor peptide in the plasma of baboons with a high HDL1 phenotype is described, as is **CETP** inhibition by various peptide fragments.
- ST **cholesteryl ester transfer protein**
inhibitor peptide; antibody **cholesteryl ester**
transfer protein inhibitor
- IT Antibodies
RL: BIOL (Biological study)
(to **cholesteryl ester transfer**
protein inhibitor peptides)
- IT Sialoglycoproteins
RL: BIOL (Biological study)
(**CETP** (**cholesterol ester-transfer**
protein), peptide inhibitor of)
- IT **Antiarteriosclerotics**
(**antiatherosclerotics**, **cholesteryl ester**
transfer protein inhibitor peptides)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, A-I, modified, antibody specific for **cholesteryl**
ester transfer protein inhibitor peptide
reactive with)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, C-I, antibody specific for **cholesteryl ester**
transfer protein inhibitor peptide reactive with)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, E, modified, antibody specific for **cholesteryl**
ester transfer protein inhibitor peptide
reactive with)
- IT Lipoproteins
RL: BIOL (Biological study)
(high-d., 1, **cholesteryl ester transfer**
protein inhibitory peptide in baboon with high)
- IT 149930-28-9 149930-29-0 149930-30-3 150027-05-7
RL: BIOL (Biological study)
(**cholesteryl ester transfer**
protein inhibitor peptide amino acid sequence)
- IT 150027-05-7D, analogs
RL: BIOL (Biological study)
(**cholesteryl ester transfer**
protein inhibitor peptides)
- L42 ANSWER 15 OF 15 HCAPLUS COPYRIGHT 2002 ACS
- AN 1993:36917 HCAPLUS
- DN 118:36917
- TI Molecular cloning, sequence, and expression of cynomolgus monkey
cholesteryl ester transfer protein.
Inverse correlation between hepatic **cholesteryl ester**
transfer protein mRNA levels and plasma high density
lipoprotein levels
- AU Pape, Michael E.; Rehberg, Edward F.; Marotti, Keith R.; Melchior, George
W.
- CS Upjohn Co., Kalamazoo, MI, 49001, USA

- SO Arterioscler. Thromb. (1991), 11(6), 1759-71
CODEN: ARTTE5; ISSN: 1049-8834
- DT Journal
- LA English
- CC 14-5 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 3, 6
- AB A cDNA clone contg. the coding region for cynomolgus monkey **cholesteryl ester transfer protein** (**CETP**) was isolated by the polymerase chain reaction with primers based on the human **CETP** cDNA sequence and cDNA synthesized from liver poly (A+) RNA. Anal. of that cDNA indicated that the nucleotide and amino acid sequences of cynomolgus monkey **CETP** were greater than 95% homologous with the human sequences. A fragment of the cDNA was used to develop an internal-std./RNAse protection assay that allowed precise quantification of **CETP** mRNA levels. Anal. of total RNA from various tissues with this assay revealed that the liver and thoracic aorta expressed high levels of **CETP** mRNA; the mesenteric fat, adrenal gland, spleen, and abdominal aorta had low but detectable levels of the mRNA; and the brain, kidney, intestine, and skeletal muscle had undetectable levels of that mRNA. When the monkeys were made hypercholesterolemic by a high-fat, high-**cholesterol** (HFHC) diet, hepatic levels of **CETP** mRNA increased from 1.6 pg/.mu.g total RNA to 4.1 pg/.mu.g; mesenteric fat **CETP** mRNA increased from 0.4 pg/.mu.g total RNA to 5.3 pg/.mu.g; and plasma CET activity increased approx. fourfold. The **CETP** mRNA levels in the thoracic and abdominal aortas were not significantly increased in monkeys fed the HFHC diet, even though those animals had gross **atherosclerosis**. The apoprotein E mRNA levels, however, were markedly increased in the aortas of monkeys with **atherosclerosis**, with the largest increase occurring in the abdominal aorta. Taken together, these data suggest that lipid deposition in the artery was not accompanied by increased expression of the **CETP** gene in that tissue. Statistical anal. showed that a strong, neg. correlation existed between hepatic **CETP** mRNA levels and both high d. lipoprotein **cholesterol** and apoprotein A-I. These data suggest that HFHC diet-induced changes in high d. lipoprotein metab. may be linked to altered expression of a functional **CETP** gene.
- ST **cholesterol ester transfer protein**
atherosclerosis monkey; **cholesterol ester transfer protein** sequence monkey
- IT Adipose tissue, composition
(**cholesteryl ester transfer protein** mRNA of mesenteric, in **atherosclerosis** in cynomolgus monkey)
- IT Liver, composition
Organ
(**cholesteryl ester transfer protein** mRNA of, in **atherosclerosis** in cynomolgus monkey)
- IT Blood plasma
(**cholesteryl ester transfer protein** of, in **atherosclerosis** in cynomolgus monkey)
- IT Macaca irus
(**cholesteryl ester transfer protein** of, mol. cloning and sequence and expression of, in **atherosclerosis**)
- IT Gene, animal
RL: BIOL (Biological study)
(for **cholesteryl ester transfer protein**, nucleotide sequence of and predicted amino acid sequence from and expression of, in **atherosclerosis** in cynomolgus monkey)
- IT Ribonucleic acids, messenger

- RL: BIOL (Biological study)
(for **cholesteryl ester transfer protein**, of liver in **atherosclerosis** in cynomolgus monkey, high-d. lipoproteins of blood plasma in relation to)
- IT Molecular cloning
(of **cholesteryl ester transfer protein** cDNA of cynomolgus monkey)
- IT Protein sequences
(of **cholesteryl ester transfer protein**, of cynomolgus monkey liver)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, A-I, mRNA for, of liver, in **atherosclerosis** in cynomolgus monkey, **cholesteryl ester transfer protein** in relation to)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, E, mRNA for, of aorta and liver, in **atherosclerosis** in cynomolgus monkey, **cholesteryl ester transfer protein** in relation to)
- IT Arteriosclerosis
(**atherosclerosis**, **cholesteryl ester transfer protein** mRNA of aorta and liver and other organs in, in cynomolgus monkey)
- IT Deoxyribonucleic acid sequences
(complementary, for **cholesteryl ester transfer protein**, of cynomolgus monkey liver)
- IT Lipoproteins
RL: BIOL (Biological study)
(high-d., **cholesterol** of, of blood plasma in **atherosclerosis** in cynomolgus monkey, **cholesteryl ester transfer protein** in relation to)
- IT Proteins, specific or class
RL: BIOL (Biological study)
(lipid-exchanging I, gene for, nucleotide sequence of and predicted amino acid sequence from and expression of, in **atherosclerosis** in cynomolgus monkey)
- IT 145170-17-8, Glycoprotein (Macaca irus **cholesterol ester-exchanging protein** moiety reduced)
RL: PRP (Properties)
(amino acid sequence of, complete)
- IT 145170-15-6
RL: PRP (Properties)
(nucleotide sequence of)
- IT 145170-16-7, Deoxyribonucleic acid (Macaca irus **cholesterol ester-exchanging glycoprotein messenger RNA-complementary**)
RL: PRP (Properties)
(nucleotide sequence of, complete)
- IT 57-88-5D, Cholest-5-en-3-ol (3.beta.)-, esters
RL: BIOL (Biological study)
(transfer protein for, gene for, nucleotide sequence of and predicted amino acid sequence from and expression of, in **atherosclerosis** in cynomolgus monkey)

=> fil biosis

FILE 'BIOSIS' ENTERED AT 11:58:18 ON 19 JUN 2002

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FILE COVERS 1969 TO DATE.

CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 12 June 2002 (20020612/ED)

=> d all tot

L60 ANSWER 1 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:517733 BIOSIS
DN PREV200100517733
TI Plasmid-based **vaccine** for treating **atherosclerosis**.
AU **Thomas, Lawrence J. (1)**
CS (1) Easton, MA USA
ASSIGNEE: AVANT Immunotherapeutics, Inc.
PI US 6284533 September 04, 2001
SO Official Gazette of the United States Patent and Trademark Office Patents,
(Sep. 4, 2001) Vol. 1250, No. 1, pp. No Pagination. e-file.
ISSN: 0098-1133.
DT Patent
LA English
AB A plasmid-based **vaccine** is provided herein based on the
combination of DNA segments coding for one or more B cell epitopes of
cholesteryl ester transfer protein (CETP) and one or more broad range helper T cell epitopes.
Administration of the plasmids as a **vaccine** to a vertebrate
subject provides an immune response to the subject's endogenous
CETP and modulation of CETP activity, leading to
prevention or reversal of various manifestations of heart disease. The
vaccines provide an advantageous strategy for the prevention or
treatment of **atherosclerosis**.
NCL 435320000
IT Major Concepts
Cardiovascular Medicine (Human Medicine, Medical Sciences);
Pharmacology
IT Diseases
atherosclerosis: vascular disease
IT Chemicals & Biochemicals
plasmid-based **vaccine**: **vaccine**
IT Alternate Indexing
Atherosclerosis (MeSH)

L60 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:298985 BIOSIS
DN PREV200100298985
TI An extended toxicologic evaluation of an immunoneutralizing
vaccine to produce anti-CETP antibodies for the
prevention/treatment of **atherosclerosis**.
AU **Thomas, Lawrence J. (1)**; Picard, Michele D. (1); Miller, David
P. (1); Emmett, Constance D. (1); Scesney, Susanne M. (1); Pisano, Milissa
L. (1); Adari, Hedy (1); Hammond, Russell A. (1); Marsh, Henry C. (1);
Rittershaus, Charles W. (1); Pettey, Carolyn L. (1)
CS (1) AVANT Immunotherapeutics, 119 Fourth Ave., Needham, MA, 02494 USA
SO FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. A566. print.
Meeting Info.: Annual Meeting of the Federation of American Societies for
Experimental Biology on Experimental Biology 2001 Orlando, Florida, USA
March 31-April 04, 2001
ISSN: 0892-6638.
DT Conference
LA English
SL English
AB A toxicology study was conducted with an immunoneutralizing
vaccine designed to elicit antibodies that would bind to and block
the function of **cholesteryl ester transfer protein (CETP)**, in order to prevent
atherosclerosis. The **vaccine** consisted of a dimer of a

31 a.a. synthetic chimeric peptide containing an N-terminal cysteine, a T cell epitope (residues 830-843 of tetanus toxin), and a B cell epitope (residues 461-476 of human CESTP), formulated with an alum adjuvant. In this study NZW rabbits were immunized with either 0 mg (4 males and 4 females), 0.1 mg (2 males and 2 females), 0.25 mg (4 males and 4 females) or 1.0 mg (4 males and 4 females) of the vaccine on days 1, 29 and 57. On day 197 (at a relative antibody minimum) half of the animals from groups 1, 3 and 4 were sacrificed. The remaining animals were boosted and euthanized on day 211, at an expected antibody maximum. Blood samples were taken periodically throughout the study and were assessed for hematology, clinical chemistry, and antibody titers. All rabbits in the non-control groups developed anti-rabbit CESTP antibody titers, thus validating the immunogenicity of the vaccine. In all other measurements the vaccinated groups were indistinguishable from the control group. All animals were monitored for clinical abnormalities throughout the study, and at necropsy, gross pathology was assessed, selected organs were weighed, and samples of 44 tissues were taken for histopathology. By all the above parameters, no significant test article-related pathology was observed. This study demonstrated the administration of this CESTP immunoneutralizing vaccine produced specific self-reactive antibody titers but no detectable test article-related pathology.

- CC Cytology and Cytochemistry - Animal *02506
 - General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
 - Pathology, General and Miscellaneous - Therapy *12512
 - Cardiovascular System - Blood Vessel Pathology *14508
 - Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
 - Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
 - Pharmacology - General *22002
 - Pharmacology - Immunological Processes and Allergy *22018
 - Toxicology - General; Methods and Experimental *22501
 - Toxicology - Pharmacological Toxicology *22504
 - Immunology and Immunochemistry - General; Methods *34502
- BC Leporidae 86040
- IT Major Concepts
 - Pharmacology; Toxicology
- IT Parts, Structures, & Systems of Organisms
 - B cell: blood and lymphatics, immune system; T cell: blood and lymphatics, immune system; blood: blood and lymphatics
- IT Diseases
 - atherosclerosis: prevention, treatment, vascular disease
- IT Chemicals & Biochemicals
 - anti-cholesteryl ester transfer protein antibodies [anti-CESTP antibodies]; cholesteryl ester transfer protein [CESTP]; cholesteryl ester transfer protein immunoneutralizing vaccine [CESTP immunoneutralizing vaccine]: immunogenicity, immunostimulant - drug; immunoneutralizing vaccine: immunostimulant - drug, toxicity
- IT Alternate Indexing
 - Atherosclerosis (MeSH)
- IT Methods & Equipment
 - toxicology study
- IT Miscellaneous Descriptors
 - Meeting Abstract
- ORGN Super Taxa
 - Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia
- ORGN Organism Name
 - NZW rabbit (Leporidae): female, male
- ORGN Organism Superterms

Animals; Chordates; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman
Vertebrates; Vertebrates

L60 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2000:476466 BIOSIS
DN PREV200000476466
TI **Vaccine-induced antibodies inhibit CETP activity in vivo and reduce aortic lesions in a rabbit model of atherosclerosis.**
AU **Rittershaus, Charles W. (1); Miller, David P.; Thomas, Lawrence J.; Picard, Michele D.; Honan, Christopher M.; Emmett, Constance D.; Pettey, Carolyn L.; Adari, Hedy; Hammond, Russell A.; Beattie, David T.; Callow, Allan D.; Marsh, Henry C.; Ryan, Una S.**
CS (1) AVANT Immunotherapeutics, Inc, 119 Fourth Ave, Needham, MA, 02494 USA
SO Arteriosclerosis Thrombosis and Vascular Biology, (September, 2000) Vol. 20, No. 9, pp. 2106-2112. print.
ISSN: 1079-5642.
DT Article
LA English
SL English
AB Using a vaccine approach, we immunized New Zealand White rabbits with a peptide containing a region of **cholesteryl ester transfer protein (CETP)** known to be required for neutral lipid transfer function. These rabbits had significantly reduced plasma CETP activity and an altered lipoprotein profile. In a **cholesterol-fed** rabbit model of **atherosclerosis**, the fraction of plasma **cholesterol** in HDL was 42% higher and the fraction of plasma **cholesterol** in LDL was 24% lower in the **CETP-vaccinated** group than in the control-vaccinated group. Moreover, the percentage of the aorta surface exhibiting **atherosclerotic** lesion was 39.6% smaller in the **CETP-vaccinated** rabbits than in controls. The data reported here demonstrate that **CETP** activity can be reduced in vivo by **vaccination** with a peptide derived from **CETP** and support the concept that inhibition of **CETP** activity in vivo can be antiatherogenic. In addition, these studies suggest that **vaccination** against a self-antigen is a viable therapeutic strategy for disease management.
CC Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - General *10060
Biochemical Studies - Lipids *10066
Cardiovascular System - Physiology and Biochemistry *14504
Cardiovascular System - Blood Vessel Pathology *14508
BC Leporidae 86040
IT Major Concepts
Biochemistry and Molecular Biophysics; Cardiovascular System (Transport and Circulation)
IT Diseases
atherosclerosis: vascular disease
IT Chemicals & Biochemicals
cholesteryl ester transfer protein: inhibition, plasma activity; cholesteryl ester transfer protein vaccine; high-density lipoprotein: plasma fraction; low-density lipoprotein: plasma fraction
IT Alternate Indexing
Atherosclerosis (MeSH)
ORGN Super Taxa
Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
rabbit (Leporidae): animal model
ORGN Organism Superterms
Animals; Chordates; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman

Vertebrates; Vertebrates

L60 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 AN 1999:282999 BIOSIS
 DN PREV199900282999
 TI A vaccine to produce anti-cholesteryl ester transfer protein (CETP) antibodies for the prevention/treatment of atherosclerosis.
 AU Thomas, L. J. (1); Picard, M. D. (1); Miller, D. P. (1); Honan, C. M. (1); Adari, H. (1); Emmett, C. D. (1); Marsh, H. C. (1); Ryan, U. S. (1); Pettey, C. L. (1); Rittershaus, C. W. (1)
 CS (1) Avant Immunotherapeutics, Inc., Needham, MA, 02494 USA
 SO FASEB Journal, (March 15, 1999) Vol. 13, No. 5 PART 2, pp. A693.
 Meeting Info.: Annual Meeting of the Professional Research Scientists on Experimental Biology 99 Washington, D.C., USA April 17-21, 1999 Federation of American Societies for Experimental Biology
 . ISSN: 0892-6638.
 DT Conference
 LA English
 CC Pharmacology - General *22002
 Biochemical Studies - General *10060
 Nutrition - General Studies, Nutritional Status and Methods *13202
 Immunology and Immunochemistry - General; Methods *34502
 Cardiovascular System - General; Methods *14501
 General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
 BC Leporidae 86040
 IT Major Concepts
 Cardiovascular System (Transport and Circulation); Pharmacology
 IT Diseases
 atherosclerosis: vascular disease; fatty streak lesion:
 vascular disease
 IT Chemicals & Biochemicals
 anti-cholesteryl ester transfer protein; anti-cholesteryl ester transfer protein antibody producing vaccine
 ; cholesterol supplemented diet
 IT Alternate Indexing
 Atherosclerosis (MeSH)
 IT Methods & Equipment
 atherosclerosis prevention: prevention method;
 atherosclerosis treatment: therapeutic method
 IT Miscellaneous Descriptors
 Meeting Abstract
 ORGN Super Taxa
 Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia
 ORGN Organism Name
 New Zealand White rabbit (Leporidae)
 ORGN Organism Superterms
 Animals; Chordates; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
 RN 20910-06-9D (CHOLESTERYL)
 57-88-5 (CHOLESTEROL)

L60 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 AN 1998:200178 BIOSIS
 DN PREV199800200178
 TI Use of xenogeneic cholesteryl ester transfer protein (CETP) in a plasmid-based vaccine to produce anti-CETP autoantibodies for the prevention/treatment of atherosclerosis.
 AU Thomas, L. J.; Adari, H.; Picard, M. D.; Honan, C. M.; Miller, D. P.; Rittershaus, C. W.; Pettey, C. L.

- CS T Cell Sciences Inc., Needham, MA USA
 SO FASEB Journal, (March 17, 1998) Vol. 12, No. 4, pp. A310.
 Meeting Info.: Annual Meeting of the Professional Research Scientists on
 Experimental Biology 98, Part 1 San Francisco, California, USA April
 18-22, 1998 Federation of American Societies for Experimental Biology
 . ISSN: 0892-6638.
- DT Conference
 LA English
 CC Cardiovascular System - Blood Vessel Pathology *14508
 Biochemical Studies - General *10060
 General Biology - Symposia, Transactions and Proceedings of Conferences,
 Congresses, Review Annuals *00520
 Biochemical Studies - Proteins, Peptides and Amino Acids *10064
- IT Major Concepts
 Cardiovascular System (Transport and Circulation)
- IT Diseases
 atherosclerosis: prevention, treatment, vascular disease
- IT Chemicals & Biochemicals
 plasmid-based vaccine; xenogenic cholesteryl
 ester transfer protein: autoantibodies
- IT Miscellaneous Descriptors
 Meeting Abstract
- RN 20910-06-9D (CHOLESTERYL)
- L60 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 AN 1997:144273 BIOSIS
 DN PREV199799443476
 TI A plasmid-based vaccine to elicit autoantibodies to
 cholesteryl ester transfer protein (CETP) for the prevention/treatment of atherosclerosis.
- AU Thomas, L. J.; Picard, M. D.; Stewart, S. E.; Waite, B. C. D.;
 Lin, A. Y.; Rittershaus, C. W.; Pettey, C. L.
- CS T Cell Sci. Inc., Needham, MA USA
 SO Journal of Allergy and Clinical Immunology, (1997) Vol. 99, No. 1 PART 2,
 pp. S187.
 Meeting Info.: Joint Meeting of the American Academy of Allergy, Asthma
 and Immunology, the American Association of Immunologists and the Clinical
 Immunology Society San Francisco, California, USA February 21-26, 1997
 ISSN: 0091-6749.
- DT Conference; Abstract
 LA English
 CC General Biology - Symposia, Transactions and Proceedings of Conferences,
 Congresses, Review Annuals 00520
 Biochemical Studies - Proteins, Peptides and Amino Acids 10064
 Biochemical Studies - Sterols and Steroids 10067
 Biochemical Studies - Carbohydrates 10068
 Metabolism - Carbohydrates *13004
 Metabolism - Sterols and Steroids *13008
 Metabolism - Proteins, Peptides and Amino Acids *13012
 Cardiovascular System - Blood Vessel Pathology *14508
 Pharmacology - Drug Metabolism; Metabolic Stimulators *22003
 Pharmacology - Cardiovascular System *22010
 Pharmacology - Immunological Processes and Allergy *22018
 Routes of Immunization, Infection and Therapy 22100
 Genetics of Bacteria and Viruses 31500
 Immunology and Immunochemistry - Immunopathology, Tissue Immunology
 *34508
- BC Leporidae *86040
- IT Major Concepts
 Cardiovascular System (Transport and Circulation); Immune System
 (Chemical Coordination and Homeostasis); Metabolism; Pharmacology
- IT Chemicals & Biochemicals
 CHOLESTERYL; CHOLESTEROL

IT Miscellaneous Descriptors
 ANIMAL MODEL; **ATHEROSCLEROSIS**; CARDIOVASCULAR SYSTEM;
CHOLESTEROL ESTER TRANSFER PROTEIN
 AUTOANTIBODY INDUCTION; **CHOLESTERYL ESTER**
TRANSFER PROTEIN; CYTOMEGALOVIRUS PROMOTER/ENHANCER
 GENE; IMMUNE SYSTEM; IMMUNOTHERAPEUTIC METHOD; PLASMID-BASED
VACCINE TREATMENT; **VACCINE PREVENTION**;
VACCINE TREATMENT; VASCULAR DISEASE

ORGN Super Taxa
 Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
 rabbit (Leporidae)

ORGN Organism Superterms
 animals; chordates; lagomorphs; mammals; nonhuman mammals; nonhuman
 vertebrates; vertebrates

RN 20910-06-9D (CHOLESTERYL)
 57-88-5D (CHOLESTEROL)

=> fil wpix

FILE 'WPIX' ENTERED AT 12:08:58 ON 19 JUN 2002

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L73 ANSWER 1 OF 4 WPIX (C) 2002 THOMSON DERWENT
 AN 1999-302645 [25] WPIX
 DNC C1999-088748
 TI **Vaccine against cholesteryl ester**
transfer protein.
 DC B04 D16
 IN RITTERSHAUS, C W; THOMAS, L J
 PA (AVAN-N) AVANT IMMUNOTHERAPEUTICS INC
 CYC 83
 PI WO 9920302 A1 19990429 (199925)* EN 61p A61K039-00
 RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
 OA PT SD SE SZ UG ZW
 W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE
 GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG
 MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG
 US UZ VN YU ZW
 AU 9911048 A 19990510 (199938)
 EP 1024825 A1 20000809 (200039) EN A61K039-00

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
 JP 2001520204 W 20011030 (200202) 67p A61K039-00
 ADT WO 9920302 A1 WO 1998-US22145 19981020; AU 9911048 A AU 1999-11048
 19981020; EP 1024825 A1 EP 1998-953762 19981020, WO 1998-US22145 19981020;
 JP 2001520204 W WO 1998-US22145 19981020, JP 2000-516697 19981020
 FDT AU 9911048 A Based on WO 9920302; EP 1024825 A1 Based on WO 9920302; JP
 2001520204 W Based on WO 9920302
 PRAI US 1997-954643 19971020
 IC ICM A61K039-00
 ICS A61K039-39; A61K048-00; A61P009-00; A61P009-10; C07K014-47;
 C12N015-09
 AB WO 9920302 A UPAB: 20011203

NOVELTY - **Vaccine** that promotes production of antibodies that bind endogenous **cholesteryl ester transfer protein (CETP)** in a mammal comprises a non-endogenous, optionally mammalianized, **CETP**, optionally combined with an adjuvant, for non-specific stimulation of the mammal's immune response.
 DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a plasmid-based **vaccine** comprising a promoter, functional in mammalian cells, linked to a sequence encoding a non-endogenous **CETP**.

ACTIVITY - Anti-atherosclerotic.

MECHANISM OF ACTION - Antibodies raised against the **vaccine** recognize endogenous **CETP**, reducing its activity, and thus the transfer of **cholesterol** from high-density lipoprotein (HDL) to (very) low-density lipoprotein (LDL).

USE - The **vaccines** (and equivalent plasmid-based **vaccines**) are used:

(1) to increase the ratio of circulating high-density lipoprotein (HDL)-associated **cholesterol** to low-density lipoprotein (LDL)-associated **cholesterol**;

(2) to decrease the level of endogenous **CETP** activity in humans or other animals;

(3) to alter metabolism of LDL-associated **cholesterol**, for inhibiting development of **atherosclerotic** lesions;

(4) to lower circulating levels of LDL and total **cholesterol**;

(5) to treat or prevent **atherosclerosis** (or more generally heart disease)

FS CPI

FA AB; DCN

MC CPI: B04-C01G; B04-E08; B04-N02A; B05-A01A; B05-C05; B14-F06; B14-F07; B14-S11; D05-H07; D05-H12E

TECH UPTX: 19990630

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred **vaccine**: The non-endogenous **CETP** is from rabbit, mouse or monkey, or is a humanized form of these, or it is an allelic variant or polymorph of a human **CETP**. Particularly preferred is a humanized rabbit **CETP** of 447 amino acids (sequence given in the specification. This lacks the region from 393Ala to 411Ala, so resembles the human protein more closely than the wild-type rabbit protein. Alternatively, where the host is a rabbit, the non-endogenous **CETP** is the human protein. Suitable adjuvants are alum, complete or incomplete Freund's adjuvant or the RIBI adjuvant system. Optionally the non-endogenous **CETP** is dimerized or linked to a related protein (e.g. phospholipid transfer protein) or other conventional carrier protein to increase its immunogenicity. It may also contain a source of T helper cells epitopes. Plasmid-based **vaccines** express the same **CETP** as above, and include a cytomegalovirus immediate-early promoter-enhancer. Preparation: **CETP** may be expressed by standard recombinant DNA methods. A typical expression vector is pCMV-CETP-TT (ATCC 98038) in which the cytomegalovirus promoter controls expression of a **vaccinating** peptide described in PCT/US96/06147. It is modified

conventionally to express full-length **CETP** proteins.

TECHNOLOGY FOCUS - PHARMACEUTICALS - Preferred vaccine: The non-endogenous **CETP** is from rabbit, mouse or monkey, or is a humanized form of these, or it is an allelic variant or polymorph of a human **CETP**. Particularly preferred is a humanized rabbit **CETP** of 447 amino acids (reproduced). This lacks the region from 393Ala to 411Ala, so resembles the human protein more closely than the wild-type rabbit protein. Alternatively, where the host is a rabbit, the non-endogenous **CETP** is the human protein. Suitable adjuvants are alum, complete or incomplete Freund's adjuvant or the RIBI adjuvant system. Optionally the non-endogenous **CETP** is dimerized or linked to a related protein (e.g. phospholipid transfer protein) or other conventional carrier protein to increase its immunogenicity. It may also contain a source of T helper cells epitopes. Plasmid-based **vaccines** express the same **CETP** as above, and include a cytomegalovirus immediate-early promoter-enhancer.

TECHNOLOGY FOCUS - ORGANIC CHEMISTRY - Preparation: **CETP** are produced by usual methods of automated peptide synthesis, and coupled to carriers or other peptides through usual bifunctional crosslinkers.

L73 ANSWER 2 OF 4 WPIX (C) 2002 THOMSON DERWENT

AN 1999-276984 [23] WPIX

DNC C1999-081276

TI New recombinant DNA **vaccines** lessening **cholesterol ester transfer** contain DNA encoding **cholesterylester transfer protein**.

DC B04 D16

IN GLENN, K; NEEDLEMAN, P

PA (MONS) MONSANTO CO

CYC 83

PI WO 9915655 A1 19990401 (199923)* EN 98p C12N015-12

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE
GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG
MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG
US UZ VN YU ZW

AU 9892317 A 19990412 (199934) C12N015-12

EP 1015584 A1 20000705 (200035) EN C12N015-12

R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU NL PT SE

ADT WO 9915655 A1 WO 1998-US19366 19980917; AU 9892317 A AU 1998-92317
19980917; EP 1015584 A1 EP 1998-944877 19980917, WO 1998-US19366 19980917

FDT AU 9892317 A Based on WO 9915655; EP 1015584 A1 Based on WO 9915655

PRAI US 1997-934367 19970919

IC ICM C12N015-12

ICS A61K048-00

AB WO 9915655 A UPAB: 19991103

NOVELTY - New recombinant DNA **vaccines** contain DNA encoding **cholesteryl ester transfer protein**, for producing antibodies to lessen the **transfer** of **cholesteryl esters** from HDL.

DETAILED DESCRIPTION - A novel process for producing antibodies to **cholesteryl ester transfer protein** (**CETP**) in a mammal comprises:

(a) **immunizing** the mammal with an inoculum containing a vehicle in which is dissolved or dispersed a recombinant DNA molecule comprising a DNA sequence that contains:

(i) a sequence encoding a **CETP** immunogen linked to;

(ii) a promoter sequence that controls the expression of the **CETP** immunogen DNA sequence in the mammal, the **CETP** immunogen being an immunogenic polypeptide having a **CETP** amino acid residue sequence, the **immunization** providing an amount of

the recombinant DNA molecule to induce antibodies to **CETP**;

(b) maintaining the immunized mammal for the production of antibodies that bind to **CETP**.

INDEPENDENT CLAIMS are also included for:

(1) a process for increasing the concentration of high density lipoprotein (HDL) **cholesterol** in the blood of a mammal whose blood contains **CETP** comprising:

(a) step (a) as above;

(b) maintaining the immunized mammal for the **CETP** immunogen to be expressed and for the production of antibodies that bind to **CETP** and lessen the transfer of **cholesteryl esters** from HDL;

(2) an inoculum that comprises a recombinant DNA molecule comprising a DNA sequence that contains:

(1) a sequence encoding a **CETP** immunogen linked to;

(2) a promoter sequence that controls the expression of the **CETP** immunogen DNA sequence in a mammal, the recombinant DNA molecule being dissolved or dispersed in a vehicle.

USE - The method can provide an autogeneic immunological process for lessening the transfer of **cholesteryl esters** from HDL particles and for increasing the HDL **cholesterol** concentration of a mammal whose blood also contains **CETP**. The method may be useful in treating human pro-atherogenic dyslipoproteinemias characterized by low HDL/LDL **cholesterol** ratios.

ADVANTAGE - The method can have an effect that lasts for months as compared to the short-term effects of the small molecule drugs now available.

Dwg.0/0

FS

CPI

FA

AB; DCN

MC

CPI: B04-B04D5; B04-E02F; B04-G01; B04-N02A0E; B14-F02; B14-S11;
D05-H07; D05-H12C; D05-H12E; D05-H17C

TECH

UPTX: 20001114

TECHNOLOGY FOCUS - BIOTECHNOLOGY - The encoded **CETP** immunogen may comprise an immunogenic polypeptide fused to an exogenous antigen carrier polypeptide, e.g. hepatitis B core protein, tetanus toxoid, or diphtheria toxoid. The DNA may be dissolved or dispersed in a vehicle, e.g. PBS or isotonic saline.

In the process for producing antibodies the blood of the mammal contains **CETP**.

In (1) step (a) may be repeated several times, preferably at intervals of about 3 months to six months until the HDL cholesterol levels is increased by about 10%. In (1) the recombinant DNA encodes human or rabbit **CETP** as the immunogenic polypeptide. The immunogenic polypeptide may be fused (especially by either termini) to an exogenous antigenic carrier polypeptide, where the antigen is especially hepatitis B core protein, tetanus toxoid or diphtheria toxoid. The antigenic carriers may optionally be fused to the C terminus and N terminus of the immunogenic polypeptide. When the antigenic carriers are fused to both termini the immunogenic portion is 10-30 amino acids in length, and is fused to an amino terminal and carboxy-terminal flanking sequence where:

(a) the amino terminal flanking sequence consists of 70-90 amino acid residues of the hepatitis B core protein sequences from amino acids 1-90, the C terminal sequence is 65-85 amino acid residues in length having the hepatitis B core protein sequence from amino acids 80-183 (sic); or

(b) the amino terminal flanking sequence consists of 10-20 amino acid residues of the hepatitis B core protein sequences from amino acids 1-35 (sic), the C terminal sequence is 120-160 amino acid residues in length having the hepatitis B core protein sequence from amino acids 10-183 (sic).

When the antigenic carriers are fused to both termini the immunogenic portion is about equal in number to the number of amino acid residues absent from the hepatitis B core protein between the C termini of the

flanking sequence of the amino terminal flanking sequence and the amino termini of the flanking sequence of the C terminal flanking sequence. The encoded immunogenic polypeptide has one of the two 26 or amino acid sequences given in the specification.

L73 ANSWER 3 OF 4 WPIX (C) 2002 THOMSON DERWENT
 AN 1997-549731 [50] WPIX
 DNC C1997-175370
 TI DNA plasmid-based **vaccine** encodes **CETP** B cell and helper T cell epitope(s) - used for elevating high density lipoprotein levels, and for treating cardiovascular disease.
 DC B04 D16
 IN **THOMAS, L J**
 PA (TCEL-N) T CELL SCI INC; (AVAN-N) **AVANT IMMUNOTHERAPEUTICS INC**
 CYC 73
 PI WO 9741227 A1 19971106 (199750)* EN 67p C12N015-12
 RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT
 SD SE SZ UG
 W: AL AM AT AU AZ BB BG BR BY CA CH CN CZ DE DK EE ES FI GB GE GH HU
 IL IS JP KE KG KP KR KZ LK LR LS LT LU LV MD MG MK MN MW MX NO NZ
 PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN
 AU 9729946 A 19971119 (199812) C12N015-12
 EP 914427 A1 19990512 (199923) EN C12N015-12
 R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
 AU 721729 B 20000713 (200039) C12N015-12
 JP 2001508760 W 20010703 (200142) 75p A61K039-00
 US 6284533 B1 20010904 (200154) C12N015-12
 ADT WO 9741227 A1 WO 1997-US7294 19970501; AU 9729946 A AU 1997-29946
 19970501; EP 914427 A1 EP 1997-924549 19970501; WO 1997-US7294 19970501;
 AU 721729 B AU 1997-29946 19970501; JP 2001508760 W JP 1997-539202
 19970501; WO 1997-US7294 19970501; US 6284533 B1 Provisional US
 1996-52983P 19960501, CIP of US 1997-802967 19970221, WO 1997-US7294
 19970501, US 1998-171969 19981002
 FDT AU 9729946 A Based on WO 9741227; EP 914427 A1 Based on WO 9741227; AU
 721729 B Previous Publ. AU 9729946, Based on WO 9741227; JP 2001508760 W
 Based on WO 9741227; US 6284533 B1 Based on WO 9634888
 PRAI US 1997-802967 19970221; US 1996-640713 19960501; US 1996-52983P
 19960501; US 1998-171969 19981002
 REP 2.Jnl.Ref; WO 9634888
 IC ICM A61K039-00; C12N015-12
 ICS A61K031-70; A61K048-00; A61P009-10; C12N005-10; C12N015-09
 AB WO 9741227 A UPAB: 19971217
 A novel DNA plasmid-based **vaccine** comprises a nucleotide sequence encoding an immunogenic polypeptide, which includes at least one segment encoding a B cell epitope of **cholesteryl ester transferase protein (CETP)** linked in frame with at least one segment encoding a broad range helper T cell epitope, where the nucleotide segment is operably linked to a promoter sequence suitable for directing the transcription of the nucleotide sequence in a mammalian cell.
 USE - The **vaccines** can be used to elevate the ratio of circulating high density lipoproteins (HDL) to circulating low density lipoproteins (LDL), very low density lipoproteins (VLDL) or total **cholesterol** in a human. It can also be used for decreasing the level of endogenous **CETP** activity in a human. The **vaccine** can also be used to produce anti-**CETP** antibodies in a human and for treating cardiovascular disease in a human (all claimed).
 Dwg.0/10
 FS CPI
 FA AB
 MC CPI: B04-E08; B04-F11; **B14-S11**; D05-H07; D05-H12E; D05-H17C

L73 ANSWER 4 OF 4 WPIX (C) 2002 THOMSON DERWENT
 AN 1996-506103 [50] WPIX
 DNC C1996-158783
 TI **Cholesteryl ester transfer protein**
 B cell epitope linked to T cell epitope - used to generate
vaccine to regulate CETP activity for decreasing the
 risk of developing a cardiovascular disease e.g. **atherosclerosis**
 .

DC B04 C06 D16
 IN **RITTERSHAUS, C W; THOMAS, L J**
 PA (AVAN-N) **AVANT IMMUNOTHERAPEUTICS INC;** (TCEL-N) T CELL SCI INC;
 (RITT-I) **RITTERSHAUS C W;** (THOM-I) **THOMAS L J**
 CYC 70
 PI WO 9634888 A1 19961107 (199650)* EN 72p C07K014-775
 RW: AT BE CH DE DK ES FI FR GB GR IE IT KE LS LU MC MW NL OA PT SD SE
 SZ UG
 W: AL AM AT AU AZ BB BG BR BY CA CH CN CZ DE DK EE ES FI GB GE HU IS
 JP KE KG KP KR KZ LK LR LT LU LV MD MG MK MN MW MX NO NZ PL PT RO
 RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN
 AU 9656360 A 19961121 (199711) C07K014-775
 EP 827509 A1 19980311 (199814) EN C07K014-775
 R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
 JP 11504635 W 19990427 (199927) 87p C07K014-47
 AU 707752 B 19990722 (199940) C07K014-775
 CA 2219795 C 20000808 (200051) EN C12N009-96
 US 2002042364 A1 20020411 (200227) A61K039-00

ADT WO 9634888 A1 WO 1996-US6147 19960501; AU 9656360 A AU 1996-56360
 19960501; EP 827509 A1 EP 1996-913320 19960501; WO 1996-US6147 19960501;
 JP 11504635 W JP 1996-533487 19960501; WO 1996-US6147 19960501; AU 707752
 B AU 1996-56360 19960501; CA 2219795 C CA 1996-2219795 19960501; WO
 1996-US6147 19960501; US 2002042364 A1 CIP of US 1995-432483 19950501, Div
 ex WO 1996-US6147 19960501, Div ex US 1997-945289 19971017, US 2001-943548
 20010830

FDT AU 9656360 A Based on WO 9634888; EP 827509 A1 Based on WO 9634888; JP
 11504635 W Based on WO 9634888; AU 707752 B Previous Publ. AU 9656360,
 Based on WO 9634888; CA 2219795 C Based on WO 9634888

PRAI US 1995-432483 19950501; US 1997-945289 19971017; US 2001-943548
 20010830

REP 3.Jnl.Ref; WO 9425060
 IC ICM A61K039-00; C07K014-47; C07K014-775; C12N009-96
 ICS A61K038-17; A61K038-45; A61K039-04; A61K039-05; A61K039-07;
 A61K039-08; A61K039-10; A61K039-13; A61K039-165; A61K039-20;
 A61K039-385; C07K014-33; C07K016-18; C12N009-10; C12N015-09

ICA C12P021-08
 AB WO 9634888 A UPAB: 19961211
 An isolated peptide comprising a broad range helper T cell epitope and a B
 cell epitope of the **cholesteryl ester transfer**
protein (CETP) is new. Also claimed is a method of
 making an anti-**CETP vaccine** to modulate endogenous
CETP activity or to treat **atherosclerosis**
 therapeutically or prophylactically by: (a) selecting a **CETP B**
 cell epitope which does not include a Class I major histocompatibility
 complex T cell antigen; (b) selecting a helper T cell epitope derived from
 a non-**CETP** antigenic peptide; and (c) linking the B and T cell
 epitopes to form an immunogenic moiety.
 USE - The peptide maybe used in a claimed **vaccine** to
 decrease the level of endogenous **CETP** activity in a human or
 animal so as to alter the catabolism of high density lipoprotein (HDL)-
cholesterol, resulting in an elevated ratio of HDL-
cholesterol versus low density (LDL)- or very LDL (VLDL)-
cholesterol (claimed). This leads to a decreased risk of
 developing a cardiovascular disease, esp. **atherosclerosis**.
 Dwg.0/13

FS CPI
 FA AB; DCN
 MC CPI: B04-B04C1; B04-C01G; B04-L05A; B04-N02B; B14-D02A2; **B14-F07**
 ; **B14-S11**; B04-B04C1; C04-B04C1; B04-C01G; C04-C01G;
 B04-L05A; C04-L05A; B04-N02B; C04-N02B; B14-D02A2; C14-D02A2;
 B14-F07; C14-F07; B14-S11;
 C14-S11; C04-B04C1; C04-C01G; C04-L05A; C04-N02B; C14-D02A2;
 C14-F07; C14-S11; D05-H07; D05-H17C

=> fil medline

FILE 'MEDLINE' ENTERED AT 12:14:46 ON 19 JUN 2002

FILE LAST UPDATED: 18 JUN 2002 (20020618/UP). FILE COVERS 1958 TO DATE.

On June 9, 2002, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2002 vocabulary. Enter HELP THESAURUS for details.

THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY AND ACCURATE SUBSTANCE IDENTIFICATION.

=> d all tot

L88 ANSWER 1 OF 5 MEDLINE
 AN 2002099139 MEDLINE
 DN 21687251 PubMed ID: 11828696
 TI Down with the bad, up with the good. A biotech firm develops a **vaccine** to raise good cholesterol levels.
 AU Maeder Thomas
 SO SCIENTIFIC AMERICAN, (2002 Feb) 286 (2) 32-3.
 Journal code: 0404400. ISSN: 0036-8733.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200202
 ED Entered STN: 20020207
 Last Updated on STN: 20020222
 Entered Medline: 20020221
 CT Check Tags: Animal; Human
 ***Arteriosclerosis: PC, prevention & control**
 *Biotechnology
 *Carrier Proteins: IM, immunology
 Clinical Trials, Phase II
 *Lipoproteins, HDL Cholesterol: BL, blood
 Tetanus Toxin: IM, immunology
 ***Vaccines**
 CN 0 (Carrier Proteins); 0 (Lipoproteins, HDL Cholesterol); 0 (Tetanus Toxin); 0 (**Vaccines**); 0 (**cholesterol ester transfer proteins**)

L88 ANSWER 2 OF 5 MEDLINE
 AN 2001058876 MEDLINE
 DN 20383755 PubMed ID: 10929930
 TI Current, new and future treatments in dyslipidaemia and **atherosclerosis**.
 AU Chong P H; Bachenheimer B S
 CS College of Pharmacy, University of Illinois, and Cook County Hospital, Chicago 60612-3785, USA.. cpang@tigger.cc.uic.edu
 SO DRUGS, (2000 Jul) 60 (1) 55-93. Ref: 294
 Journal code: 7600076. ISSN: 0012-6667.

CY New Zealand
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 200012
 ED Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001222
 AB The new therapeutic options available to clinicians treating dyslipidaemia in the last decade have enabled effective treatment for many patients. The development of the HMG-CoA reductase inhibitors (statins) have been a major advance in that they possess multiple pharmacological effects (pleiotropic effects) resulting in potent reductions of low density lipoproteins (LDL) and prevention of the **atherosclerotic** process. More recently, the newer fibric acid derivatives have also reduced LDL to levels comparable to those achieved with statins, have reduced triglycerides, and gemfibrozil has been shown to increase high density lipoprotein (HDL) levels. Nicotinic acid has been made tolerable with sustained-release formulations, and is still considered an excellent choice in elevating HDL **cholesterol** and is potentially effective in reducing lipoprotein(a) [Lp(a)] levels, an emerging risk factor for coronary heart disease (CHD). Furthermore, recent studies have reported positive lipid-lowering effects from estrogen and/or progestogen in postmenopausal women but there are still conflicting reports on the use of these agents in dyslipidaemia and in females at risk for CHD. In addition to lowering lipid levels, these antihyperlipidaemic agents may have directly or indirectly targeted thrombogenic, fibrinolytic and **atherosclerotic** processes which may have been unaccounted for in their overall success in clinical trials. Although LDL **cholesterol** is still the major target for therapy, it is likely that over the next several years other lipid/lipoprotein and nonlipid parameters will become more generally accepted targets for specific therapeutic interventions. Some important emerging lipid/lipoprotein parameters that have been associated with CHD include elevated triglyceride, oxidised LDL **cholesterol** and Lp(a) levels, and low HDL levels. The nonlipid parameters include elevated homocysteine and fibrinogen, and decreased endothelial-derived nitric oxide production. Among the new investigational agents are inhibitors of squalene synthetase, acylCoA: **cholesterol** acyltransferase, **cholesteryl ester transfer protein**, monocyte-macrophages and LDL **cholesterol** oxidation. Future applications may include thromimetic therapy, **cholesterol** vaccination, somatic gene therapy, and recombinant **proteins**, in particular, apolipoproteins A-I and E. Non-LDL-related targets such as peroxisome proliferator-activating receptors, matrix metalloproteinases and scavenger receptor class B type I may also have clinical significance in the treatment of **atherosclerosis** in the near future. Before lipid-lowering therapy, dietary and lifestyle modification is and should be the first therapeutic intervention in the management of dyslipidaemia. Although current recommendations from the US and Europe are slightly different, adherence to these recommendations is essential to lower the risk of **atherosclerotic** vascular disease, more specifically CHD. New guidelines that are expected in the near future will encompass global opinions from the expert scientific community addressing the issue of target LDL goal (aggressive versus moderate lowering) and the application of therapy for newer emerging CHD risk factors.
 CT Check Tags: Human
 *Anticholesteremic Agents: TU, therapeutic use
 *Arteriosclerosis: DT, drug therapy
 Arteriosclerosis: PP, physiopathology
 Arteriosclerosis: PC, prevention & control

*Cholesterol: ME, metabolism
 Diet
 Forecasting
 *Hyperlipidemia: DT, drug therapy
 Hyperlipidemia: PP, physiopathology
 Hyperlipidemia: PC, prevention & control
 Life Style
 *Lipoproteins: DE, drug effects
 *Lipoproteins: ME, metabolism

RN 57-88-5 (Cholesterol)
 CN 0 (Anticholesteremic Agents); 0 (Lipoproteins)

L88 ANSWER 3 OF 5 MEDLINE
 AN 2000482102 MEDLINE
 DN 20436374 PubMed ID: 10978256
 TI **Vaccine-induced antibodies inhibit CETP activity in vivo and reduce aortic lesions in a rabbit model of atherosclerosis.**
 CM Comment in: Arterioscler Thromb Vasc Biol. 2000 Sep;20(9):2029-31
 AU Rittershaus C W; Miller D P; Thomas L J; Picard M D; Honan C M; Emmett C D; Pettey C L; Adari H; Hammond R A; Beattie D T; Callow A D; Marsh H C; Ryan U S
 CS AVANT Immunotherapeutics, Inc, Needham, MA 02494, USA..
 crittershaus@avantimmune.com
 NC HL-59122 (NHLBI)
 SO ARTERIOSCLEROSIS, THROMBOSIS, AND VASCULAR BIOLOGY, (2000 Sep) 20 (9) 2106-12.
 Journal code: 9505803. ISSN: 1524-4636.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200010
 ED Entered STN: 20001019
 Last Updated on STN: 20010521
 Entered Medline: 20001012
 AB Using a vaccine approach, we immunized New Zealand White rabbits with a peptide containing a region of **cholesteryl ester transfer protein (CETP)** known to be required for neutral lipid transfer function. These rabbits had significantly reduced plasma CETP activity and an altered lipoprotein profile. In a **cholesterol-fed** rabbit model of **atherosclerosis**, the fraction of plasma **cholesterol** in HDL was 42% higher and the fraction of plasma **cholesterol** in LDL was 24% lower in the **CETP-vaccinated** group than in the control-**vaccinated** group. Moreover, the percentage of the aorta surface exhibiting **atherosclerotic** lesion was 39.6% smaller in the **CETP-vaccinated** rabbits than in controls. The data reported here demonstrate that CETP activity can be reduced in vivo by vaccination with a peptide derived from CETP and support the concept that inhibition of CETP activity in vivo can be antiatherogenic. In addition, these studies suggest that vaccination against a self-antigen is a viable therapeutic strategy for disease management.
 CT Check Tags: Animal; Human; Support, U.S. Gov't, P.H.S.
 Antibodies: BL, blood
 *Aorta: PA, pathology
 Arteriosclerosis: IM, immunology
 *Arteriosclerosis: ME, metabolism
 Arteriosclerosis: PA, pathology
 Arteriosclerosis: TH, therapy
 Blotting, Western
 CHO Cells

Carrier Proteins: GE, genetics
 *Carrier Proteins: IM, immunology
 Carrier Proteins: ME, metabolism
 Cholesterol, Dietary: PD, pharmacology
 Disease Models, Animal
 Hamsters
 Kidney Function Tests
 Lipoproteins: AN, analysis
 Rabbits
 Recombinant Proteins: IM, immunology
 Recombinant Proteins: ME, metabolism

Vaccines, Synthetic: AD, administration & dosage

***Vaccines, Synthetic: IM, immunology**

CN 0 (Antibodies); 0 (Carrier Proteins); 0 (Cholesterol, Dietary); 0
 (Lipoproteins); 0 (Recombinant Proteins); 0 (Vaccines,
 Synthetic); 0 (cholesterol ester transfer
 proteins)

L88 ANSWER 4 OF 5 MEDLINE

AN 1999307576 MEDLINE

DN 99307576 PubMed ID: 10377515

TI A vaccine approach to healthy lipoprotein levels.

AU Fricker J

SO MOLECULAR MEDICINE TODAY, (1999 Jul) 5 (7) 281.

Journal code: 9508560. ISSN: 1357-4310.

CY ENGLAND: United Kingdom

DT News Announcement

LA English

FS Priority Journals

EM 199909

ED Entered STN: 19991005

Last Updated on STN: 19991005

Entered Medline: 19990921

CT Check Tags: Animal; Human; Male

Aged

Aged, 80 and over

Antibodies: CH, chemistry

***Arteriosclerosis: PC, prevention & control**

Carrier Proteins: GE, genetics

*Carrier Proteins: IM, immunology

Clinical Trials

Japan

*Lipoproteins, HDL: BL, blood

Peptides: CS, chemical synthesis

Peptides: IM, immunology

Rabbits

Vaccines: AD, administration & dosage

Vaccines: CS, chemical synthesis

***Vaccines: IM, immunology**

CN 0 (Antibodies); 0 (Carrier Proteins); 0 (Lipoproteins, HDL); 0 (Peptides);
 0 (Vaccines); 0 (cholesterol ester
 transfer proteins)

L88 ANSWER 5 OF 5 MEDLINE

AN 97355212 MEDLINE

DN 97355212 PubMed ID: 9211407

TI Vaccine for atherosclerosis.

AU O'Brien C

SO MOLECULAR MEDICINE TODAY, (1997 Jun) 3 (6) 231.

Journal code: 9508560. ISSN: 1357-4310.

CY ENGLAND: United Kingdom

DT News Announcement

LA English

FS Priority Journals
 EM 199708
 ED Entered STN: 19970908
 Last Updated on STN: 19970908
 Entered Medline: 19970822
 CT Check Tags: Animal; Human
 Apolipoproteins: BI, biosynthesis
 Apolipoproteins: IM, immunology
 *Arteriosclerosis: TH, therapy
 Carrier Proteins: BI, biosynthesis
 Carrier Proteins: GE, genetics
 *Carrier Proteins: IM, immunology
 Mice
 Mice, Transgenic
 Rabbits
 *Vaccines, DNA
 CN 0 (Apolipoproteins); 0 (Carrier Proteins); 0 (Vaccines, DNA); 0
 (cholesterol ester transfer proteins
)

=> d his

(FILE 'HOME' ENTERED AT 11:33:14 ON 19 JUN 2002)
 SET COST OFF

FILE 'REGISTRY' ENTERED AT 11:33:30 ON 19 JUN 2002
 E CHOLESTERYL ESTER TRANSFER PROTEIN/CN

L1 1 S E4
 E CETP/CN
 E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L2 13 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L3 13 S CETP
 L4 13 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
 L5 1 S L1 AND L2-L4
 L6 24 S L2-L4 NOT L5

FILE 'HCAPLUS' ENTERED AT 11:37:36 ON 19 JUN 2002

L7 876 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
 E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L8 883 S CETP
 L9 1325 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L10 16 S L5 OR L6
 L11 16 S L7-L9 AND L10
 L12 57 S ?ARTHEROSCLERO?
 L13 34932 S ?ATHEROSCLERO?
 L14 19 S ?ARTHERIOSCLERO?
 L15 13496 S ?ARTERIOSCLERO?
 L16 9 S L11 AND L12-L15
 L17 4 S L11 AND VACCIN?
 L18 4 S L17 AND L16
 E ATHEROSCLEROSIS/CT
 E E3+ALL
 L19 20165 S E7-E9, E6
 L20 32452 S E6, E8, E9/BI
 E E5+ALL
 L21 22555 S E5+NT
 L22 8925 S E5/BI
 L23 9 S L11 AND L19-L22
 L24 4 S L16, L23 AND VACCIN?
 L25 5 S L16, L23 NOT L24
 L26 9 S L23-L25
 L27 331 S L7-L9 AND L12-L15, L19-L22

L28 9 S L27 AND VACCIN?
L29 24 S L7-L9,L10 AND EPITOP?
L30 5 S L29 AND (TETANUS OR DIPHTHER? OR TOXOID OR TOXIN OR BCG OR BA
L31 15 S L26,L28,L30
L32 19 S L29 NOT L31
E RITTERSHAUS C/AU
L33 20 S E3-E6
E THOMAS L/AU
L34 219 S E3,E14,E15
E THOMAS LARRY/AU
L35 4 S E3
L36 23 S E26,E29
L37 6 S L33-L36 AND L7-L10
L38 6 S L31 AND L37
L39 9 S L31 NOT L38
L40 15 S L38,L39
L41 5 S L40 AND (PY<=1995 OR PRY<=1995 OR AY<=1995)
L42 15 S L40,L41

FILE 'HCAPLUS' ENTERED AT 11:52:33 ON 19 JUN 2002

FILE 'BIOSIS' ENTERED AT 11:52:55 ON 19 JUN 2002

L43 1 S L5 OR L6
L44 1529 S L7-L9
L45 1529 S L43,L44
L46 324 S L45 AND L12-L15,L20,L22
L47 8 S L45 AND VACCIN?
L48 7 S L45 AND (IMMUNIZ? OR IMMUNIS?)
L49 6 S L46 AND L47,L48
L50 17 S 22100/CC AND L45
L51 15 S 34508/CC AND L45
L52 3 S 22018/CC AND L45
L53 37 S L49-L52
L54 10 S L53 AND L46
SEL DN AN 1 5 9 10
L55 6 S L54 NOT E1-E8
E RITTERSHAUS C/AU
L56 37 S E3-E6
E THOMAS L/AU
L57 491 S E3,E16-E19
E THOMAS LAWRENCE/AU
L58 9 S E3,E5
L59 6 S L45 AND L56-L58
L60 6 S L55,L59

FILE 'BIOSIS' ENTERED AT 11:58:18 ON 19 JUN 2002

FILE 'WPIX' ENTERED AT 11:58:47 ON 19 JUN 2002

L61 94 S L7-L9
L62 64 S L61 AND L12-L15,L20,L22
L63 53 S L61 AND (B14-F07 OR C14-F07 OR B12-H03 OR C12-H03)/MC
L64 64 S L61 AND (?ATHEROSCLERO? OR ?ATHERIOSCLERO? OR ?ARTERIOSCLERO?
L65 65 S L62-L64
L66 4 S L61 AND (VACCIN? OR IMMUNIZ? OR IMMUNIS? OR (B14-S11 OR C14-S
L67 2 S L66 AND L65
L68 2 S L66 NOT L67
E RITTERSHAUS C/AU
L69 9 S E3,E4
E THOMAS L/AU
L70 95 S E3,E11
L71 3 S L61 AND L69,L70
L72 3 S AVANT?/PA AND L61
L73 4 S L66-L68,L71,L72

FILE 'WPIX' ENTERED AT 12:08:58 ON 19 JUN 2002

FILE 'MEDLINE' ENTERED AT 12:09:11 ON 19 JUN 2002

L74 1433 S L7-L10
L75 264 S L74 AND L12-L15,L19-L22
L76 253 S L74 AND (?ATHEROSCLERO? OR ?ATHERIOSCLERO? OR ?ARTERIOSCLERO?
E ATHEROSCLERO/CT
E E8+ALL
E E2+ALL
L77 89148 S E4+NT
L78 154 S L74 AND L77
L79 264 S L75,L76,L78
L80 5 S L79 AND (VACCIN? OR IMMUNIZ? OR IMMUNIS?)
E VACCINE/CT
E E4+ALL
E E2+ALL
L81 0 S L79 AND E44+NT
E E44+ALL
E VACCINES/CT
E E3+ALL
L82 4 S L79 AND E7+NT
L83 5 S L80,L82
L84 265 S L74 AND C14./CT
L85 47 S L74 AND A7./CT
L86 4 S L84,L85 AND (VACCIN? OR IMMUNIZ? OR IMMUNIS?)/CT
L87 4 S L84 AND VACCINES+NT/CT
L88 5 S L83,L86,L87

FILE 'MEDLINE' ENTERED AT 12:14:46 ON 19 JUN 2002

